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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"			
(57) Abstract			
<p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>			

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

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Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

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Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

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In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

20 The invention is also directed to methods of identifying an ORFX polypeptide or nucleic acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

30 In a another aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is
5 preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

10 In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in
15 a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

20 In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

25 Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and
30 examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF n according to the invention (wherein n is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 n -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 n . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of 7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

Amyloid

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoetin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

Apoptosis-related proteins

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

	Abbrev:	Title:
10	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_rna_bind	DNA/RNA binding protein/factor
	dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
10	glucoamylase	glucoamylase
	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase PIR	phosphorylase PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase potassium_channel prostaglandin protease proteaseinhib reductase	polymerase potassium channel protein prostaglandin protease protease inhibitor reductase
10	ribosomalprot RTR	ribosomal associated protein EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM SPTR	similar EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
20	struct sulfotransferase SWP	structural associated protein sulfotransferase SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN synthase	SWISS-PROT Update (release 11-NOV-98) synthase
25	tgf tgfreceptor thioesterase thiolase tm7	transforming growth factor transforming growth factor receptor thioesterase thiolase seven transmembrane domain G-protein coupled receptor
30	tnf traffic tnfreceptor TRN	necrosis factor receptor tumor necrosis factor tumor trafficking associated protein EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor transferase transport tubulin ubiquitin unclassified	transcription factor transferase transport protein tubulin ubiquitin
40	water channel	Protein not categorized into one of the aforementioned protein families water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analog and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, e.g., Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (e.g., as employed for cross-species hybridizations). See, e.g., Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2*n*-1 for the corresponding *n*, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (e.g., the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2n (wherein n = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (e.g., SEQ ID NO:2n-1 (wherein n = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxycarboxymethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methyl ester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaître *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch 1970 J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or (F_{ab})₂, that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated
5 herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotype to a ORFX protein may be produced by
15 techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F₁ fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J. Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2n-1 (wherein $n = 1$ to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For
transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, 10 peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained 15 using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are 20 applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993) 25 *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409), 30 plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (e.g., drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (e.g., the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: __ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

20 An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

25 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

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would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA
5 containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological
10 sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid
15 probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, e.g., proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (e.g., mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (e.g., serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample is obtained and ORFX protein or nucleic acid is detected (e.g., wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS* 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein.

Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (e.g., benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons, Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immunol* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic vital diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al. Cellular Biology* 15:141-151, 1995; Keller *et al., Mol. Cell. Biol.* 13:473-486, 1993; McClanahan *et al., Blood* 81:2903-2915, 1993.

10 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al., Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al., Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *al., In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, et al.,* (eds.) Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.,* (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

25 A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

30 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*, eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruberet *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,
10 antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenberg *et al.*, *J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gi4691395jemb CAB41562.1 - (AL049727) putative large secreted protein (Streptomyces coelicolor)		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gi2625003ipg77 359JSUOC.MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264699, 264638, 264567
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636,
4	82018837 (7, 8)			UNCLASSIFIED	264691, 264907, 264692, 264629
5	79970035 (9, 10)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
6	79842462 (11, 12)			UNCLASSIFIED	22275002, 264583
7	85515576 (13, 14)	Novel Protein sim. GBank gi4415926ipj A020157 - (AC006282) unknown protein (Arabidopsis thaliana)	Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/zinc family	UNCLASSIFIED	264908
8	56924278 (15, 16)	Novel Protein sim. GBank gi365962ipj O6458INR.R_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	20281089, 33696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264395, 264396, 264758, 264603, 264604, 264760, 264762, 264683, 264768, 264767, 264689, 35695917, 264628, 264682, 264693, 33857109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
9	79394457 (17, 18)			UNCLASSIFIED	264907
10	79596458 (19, 20)			UNCLASSIFIED	265007, 265019, 263972
11	20414027 (21, 22)			UNCLASSIFIED	264908
12	94141210 (23, 24)	Novel Protein sim. GBank gi3878145jemb CAA99871 - (Z75543) similar to potassium channel protein (Caenorhabditis elegans)		misc_channel	264605, 264250, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gi2832781jemb CAA12845 - (A-225805) inward potassium channel alpha subunit [Egna densa]	Contains protein domain (PF00023) - Anky repeat	UNCLASSIFIED potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gi1710791ipj Q1024PRT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	UNCLASSIFIED rbsomaiprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank glt114849ipP4439[URE1_HAEN_UREASE ALPHA SUBUNIT_UREA AMIDOHYDROLASE]	Contains protein domain (PF00449) - Urease		264600
18	60246804 (35, 36)	Novel Protein sim. GBank glt281102 (AC002333) - SF16 isoalg [Arabisopsis italiana]			29331927, 264495, 264557, 264638, 264558
19	80076824 (37, 38)	Novel Protein sim. GBank glt266112ipP4367[NUO-ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN NUO]		UNCLASSIFIED transport	22278996, 264497, 2644910, 264600, 264693
20	20724958 (39, 40)	Novel Protein sim. GBank glt1730203ipP50442[CATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE) GLYCINE AMIDINOTRANSFERASE] (TRANSAMINASE) (AT)]		UNCLASSIFIED	22278995, 264496, 265008, 265010, 265011, 264602, 264603, 264766, 264686, 21906194, 264691, 18108376, 264636, 18108397, 264466
22	11705858 (43, 44)	Novel Protein sim. GBank glt187329ipP408077[1- (Z8771)1] deE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase		264655
23	80419176 (45, 46)				264603, 264605, 264662, 264766, 32633986, 264600
24	20291697 (47, 48)				264593
25	80235774 (49, 50)			UNCLASSIFIED	22278995, 58192435, 265018, 264566
26	80235394 (51, 52)			ribosomal prot	18108370, 39599423, 264635, 264555
27	80235795 (53, 54)	Novel Protein sim. GBank glt480336ipP4842783.1[1- (A049841) putative 30S ribosomal protein S14 (Streptomyces coelicolor)]	Contains protein domain (PF00253) - Ribosomal protein S14p/S2be		
28	79483561 (55, 56)	Novel Protein sim. GBank glt3122290ipP008333[K6PF_STROCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]	Contains protein domain (PF00369) - Phosphofructokinase	UNCLASSIFIED	264638
29	82448765 (57, 58)			kinase	264601, 264762, 264766, 264769, 264636
30	79198333 (59, 60)			UNCLASSIFIED	264608, 265019, 264687, 21906764, 21905706
31	19848158 (61, 62)			UNCLASSIFIED	264534
32	82439495 (63, 64)	Novel Protein sim. GBank glt3560504 (AF027770) - unknown [Mycobacterium smegmatis]		UNCLASSIFIED	264905, 264605, 264762, 264766, 264687, 264689
33	79582628 (65, 66)	Novel Protein sim. GBank glt212003ipP1G04507 - hypothetical protein MJ1665 - Methanococcus jannaschii		UNCLASSIFIED	264687
34	87467657 (67, 68)			UNCLASSIFIED	60432289, 264600, 264602, 264760, 18108357, 264769, 265020, 264691
35	95005170 (69, 70)	Novel Protein sim. GBank glt420387ipP4048679.1[1- (A243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264600, 264687, 264658, 264639
36	19642042 (71, 72)	Novel Protein sim. GBank glt3287739ipP73538[BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]		UNCLASSIFIED	
37	20369215 (73, 74)	Novel Protein sim. GBank glt231313ipP4A007126.1[1- (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase (Helicobacter pylori 26695)]		synthase	264566
				dehydrogenase	264603

38	20466334 (75, 76)	Novel Protein sim. GBank gji305970[embj CAA06231] - (AJO04933) periplasmic nitrate reductase, large subunit (Rhodospirillum rubrum sp.)		reductase	264605
39	94300715 (77, 78)	Novel Protein sim. GBank gji1928449 (L6354-3) - endodermin (Xenopus laevis)	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 6672502, 264908, 264909, 264911, 265009, 264910, 5381209, 264756, 265011, 264762, 264682, 264763, 264764, 264766, 265022, 264693, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482
40	20635625 (79, 80)	Novel Protein sim. GBank gji654065[embj CAA58337] - (X63413) U88 (Human herpesvirus 8)		UNCLASSIFIED	264592
41	86023287 (81, 82)	Novel Protein sim. GBank gji3920584 (AF06791) - carbamoylphosphate synthetase large subunit (Zymomonas mobilis)	Contains protein domain (PF00950) - GMP synthase C terminal domain	UNCLASSIFIED	264591, 35665917
42	20724566 (83, 84)	Novel Protein sim. GBank gji2494764[sp G50729 CUAA, MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264602
43	20487069 (85, 86)	Novel Protein sim. GBank gji1881738 (U0668) - myosin-I binding protein Acan125 (Acetabularia castellanii)		synthase	264605
44	13085297 (87, 88)	Novel Protein sim. GBank gji2494764[sp G50729 CUAA, MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264769, 264636
45	39384711 (89, 90)	Novel Protein sim. GBank gji1881738 (U0668) - myosin-I binding protein Acan125 (Acetabularia castellanii)		UNCLASSIFIED	264769, 264410, 264408
46	95003398 (91, 92)	Novel Protein sim. GBank gji3914992[sp Q26264 SM1_1, HEMPU - 41 KD SP/CULE MATRIX PROTEIN PRECURSOR (HSM1_1) (HPSMC)		prol	264656
47	11698624 (93, 94)	Novel Protein sim. GBank gji3914992[sp Q26264 SM1_1, HEMPU - 41 KD SP/CULE MATRIX PROTEIN PRECURSOR (HSM1_1) (HPSMC)		UNCLASSIFIED	264660
48	79407216 (95, 96)	Novel Protein sim. GBank gji3960411 (AC004561) - putative proline-rich protein (Arabidopsis thaliana)		UNCLASSIFIED	18108385, 264635, 264823
49	21638444 (97, 98)	Novel Protein sim. GBank gji3411177 (AF076240) - MccC (Rhizobium leguminosarum bv. viciae)		UNCLASSIFIED	264603, 264603, 264769, 264689, 264636, 264606, 264603, 264769, 264689, 264636
50	80503996 (99, 100)	Novel Protein sim. GBank gji3411177 (AF076240) - MccC (Rhizobium leguminosarum bv. viciae)		UNCLASSIFIED	264558, 264466
51	80255569 (101, 102)	Novel Protein sim. GBank gji3411177 (AF076240) - MccC (Rhizobium leguminosarum bv. viciae)		UNCLASSIFIED	204593, 18108387
52	79208528 (103, 104)	Novel Protein sim. GBank gji3914992[sp Q26264 SM1_1, HEMPU - 41 KD SP/CULE MATRIX PROTEIN PRECURSOR (HSM1_1) (HPSMC)		strut	264634
53	36996970 (105, 106)	Novel Protein sim. GBank gji3960411 (AC004561) - putative proline-rich protein (Arabidopsis thaliana)		UNCLASSIFIED	264762
54	79570897 (107, 108)	Novel Protein sim. GBank gji1633572 (J52064) - Herpesvirus saimiri ORF73 homolog [kaposa's sarcoma-associated herpes-like virus]		UNCLASSIFIED	264630, 264909, 264766
55	80202703 (109, 110)	Novel Protein sim. GBank gji3321580[sp AA015785] - (AF050114) alginate lyase (Pseudomonas sp. W7)		UNCLASSIFIED	29331824, 264102, 265018, 18108376
56	8759408 (111, 112)	Novel Protein sim. GBank gji3321580[sp AA015785] - (AF050114) alginate lyase (Pseudomonas sp. W7)	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264604
57	11223386 (113, 114)	Novel Protein sim. GBank gji3321580[sp AA015785] - (AF050114) alginate lyase (Pseudomonas sp. W7)		UNCLASSIFIED	264557

58	91227506 (115, 116)	Novel Protein sim. GBank gi5516074 gb AA045616.1 AT091934 - (AT091943) protease- derived STE20-like kinase PSK (Homo sapiens)	Contains protein domain (PF00056) Eukaryotic protein kinase domain	kinase	58152575, 264259, 60433049, 35596052, 60712502, 264209, 265008, 265010, 265011, 264601, 264674, 35595917, 60710615, 264681, 264692, 264693, 10106374, 35595943, 58152575, 60433113 264600, 264689, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gi1172920 sp P4830 PFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHAN- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00953) Glycosyl transferase	transferase	
60	12958341 (119, 120)	Novel Protein sim. GBank			264589
81	80426806 (121, 122)	Novel Protein sim. GBank gi11710216 (U79260) - unknown [Homo sapiens]		glycoprotein	264766
62	13504966 (123, 124)				264630
63	16474553 (125, 126)			UNCLASSIFIED	265519
64	20724578 (127, 128)			UNCLASSIFIED	264602
65	79326308 (129, 130)	Novel Protein sim. GBank gi3122312 sp O08134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) Pyruvate kinase	kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gi3328723 emb CAA222191 - (A034355) Putative ABC transporter [Streptomyces coelicolor]		transport	22278986, 264558
67	76952543 (133, 134)	Novel Protein sim. GBank gi231985 sp P70224 DMA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	265021
68	79817382 (135, 136)				264609
69	79841784 (137, 138)			UNCLASSIFIED	264908
70	79871329 (139, 140)			UNCLASSIFIED	264903, 264908
71	65897458 (141, 142)			UNCLASSIFIED	264002, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gi4415928 gb A0201571 - (A006282) unknown protein [Paratubops italiana]		UNCLASSIFIED	264468, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264736, 87108474, 264682, 264766, 264689, 35595917, 265021, 60710615, 264691, 33857023, 264682, 264693, 264629, 264631, 264639, 22279000
73	80025241 (145, 146)			UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 19108387
74	20377419 (147, 148)			UNCLASSIFIED	264605
75	11819932 (149, 150)	Novel Protein sim. GBank gi285309 emb CAA169141 - (A021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gi4468811 emb CAB382121 - (A035603) putative protein [Paratubops italiana]		UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gi85406 emb CAA036331 - (263413) U98 [Human herpesvirus 6]		UNCLASSIFIED	264563
78	87582358 (155, 156)			UNCLASSIFIED	264604

79	94140190 (157, 158)	Novel Protein sim: GBank g 1568943 n j BAA3010.1 - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	35689286, 22278998, 29331822, 29331824, 29331825, 29331827, 294905, 294906, 294907, 66712502, 294908, 294909, 295008, 295009, 294910, 60170831, 55812038, 31099554, 295017, 295018, 294288, 294768, 56181582, 21906755, 21906769, 29148784, 295020, 294680, 294691, 294682, 294683, 60431528, 35698423, 294631, 294632, 294634, 294635, 294639, 83373044, 294564, 294566, 294567
80	82314840 (159, 160)		UNCLASSIFIED	294769, 294801, 295006, 294910, 294804, 294605, 294634, 294635, 294905, 294762, 294637, 294592, 294628, 294907, 294691, 294908, 294587, 294909, 294766, 294605
81	20467247 (161, 162)	Novel Protein sim: GBank g 1723442 p Q10288 YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C56F8.10 IN CHROMOSOME 1	UNCLASSIFIED	294567
82	16331388 (163, 164)	Novel Protein sim: GBank g 2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]	reductase	
83	94741180 (165, 166)	Novel Protein sim: GBank g 3402673 (AC004697) - unknown protein [Arabidopsis thaliana]	dehydrogenase	
84	80355375 (167, 168)	Novel Protein sim: GBank g 1173384 p P45389 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) [SULFATE/CARBONATE ANTIporter]	UNCLASSIFIED	284488, 294508, 294509, 294905, 294908, 294909, 294511, 294591, 294593, 294594, 294595, 294596, 294758, 294603, 294760, 294681, 18108351, 294762, 294682, 294764, 294684, 294766, 294688, 294632, 294637, 294557, 294638, 294639, 18108395, 294566
85	80499600 (169, 170)	Novel Protein sim: GBank g 2120998 p JST0682 - glycosyltransferase homolog - Bordetella pertussis	transport	294508, 294906, 294907, 294908, 294909, 294910, 294760, 294763, 294764, 294768, 294768, 294769, 35695855, 294636, 294637
86	39559043 (171, 172)	Novel Protein sim: GBank g 3256023 emb CAA17228.1 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]	transferase	294605, 294762, 294687, 294769, 18108374, 294636, 294486
87	13856808 (173, 174)		UNCLASSIFIED	294910, 294766, 294769, 35695855, 294636, 294637, 294605

88	95344718 (175, 176)	Novel Protein sim. GBank glij59703dbj BA040752j - (C038549) ha1025 is new [humo sapiens]			52644507, 52646365, 18108398, 65274572, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35698052, 35656970, 264105, 264508, 264905, 264906, 264907, 264908, 29331830, 56712502, 52644045, 56182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 2106754, 52646317, 33109554, 52644296, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 264288, 264766, 52644229, 21906766, 21906767, 21906768, 21906769, 55811957, 35659517, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27488261, 27486294, 33657149, 35659763, 264628, 263972, 18108374, 55810764, 35699423, 55811576, 65274791, 35659555, 69431850, 264636, 52644332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526466, 87168518, 60432113, 22279000, 22279002, 264482, 264594, 264486, 264600
89	50077389 (177, 178)	Novel Protein sim. GBank glij10393ip P46359 RPX, 9ACSU - PROBABLE INTEGRASE/RECOMBINASE RPX		UNCLASSIFIED	264760
90	52115595 (179, 180)			protease	265006
91	76906550 (181, 182)	Novel Protein sim. GBank glij49899ip P716403 VEQ, ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION		UNCLASSIFIED	264691
92	79554871 (183, 184)	Novel Protein sim. GBank glij336775 em C2A20079 - (A031155) hypothetical protein SC3A7.16 (Streptomyces coelicolor)			
93	50496778 (185, 186)	Novel Protein sim. GBank glij2865095 (AF011337) - putative EL2 ATPase [Mts musculus]		ATPase-associated	264307, 264308, 264910, 265009, 264605, 264769
94	79646845 (187, 188)	Novel Protein sim. GBank glij1719ip P46920 OPUA, BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUA	Contains protein domain (PF00571) - transport		264308
95	11090238 (189, 190)				264594

96	94322125 (191, 192)	Novel Protein sim. GBank gll158550glj BAA76602.1 - (AB023175) KIAA0958 protein [Homo sapiens]	UNCLASSIFIED	22278995, 264259, 29331822, 29331826, 35696032, 29146499, 264509, 264906, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21906785, 21906787, 21906789, 265020, 264692, 33857182, 35695763, 264638, 264639, 18108379, 264631, 264636, 18108391, 264559, 18108382, 83373044, 22279002, 264508
97	79605200 (193, 194)	Novel Protein sim. GBank gll1583559j emj CAB40384.1 - (AJ005255) OxyR [Erwinia chrysanthemi]	UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gll1001693glj BAA10430 - (D64002) hypotheical protein [Synchytrium sp.]	UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gll1169479slp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	264605
100	79640113 (199, 200)	Novel Protein sim. GBank gll1800897 pwj S37485 - gene	UNCLASSIFIED	264693
101	80203298 (201, 202)	msg1 protein - mouse	UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gll2894186j emj CAA11773.1 - (AJ223988) PCZA381.18 [Amycolopsis orientalis]	synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gll173104slp P4509 QHH_BACSU - HYPOTHEICAL HELICASE IN SINI-GCVT INTERGENIC REGION	helicase	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gll1854065j emj CAA58337 - (X3413) U88 Human herpesvirus 6	UNCLASSIFIED	264591, 264595, 264602
105	79605208 (209, 210)	Novel Protein sim. GBank gll1685117 (U07070) - furrowed	complement	264508
106	28342058 (211, 212)	[Drosophila melanogaster]	UNCLASSIFIED	264511, 265009
107	80057781 (213, 214)	Novel Protein sim. GBank gll1705505slp P54729 BS4_MOUSE - BS4 PROTEIN	ATPase-associated	29331824, 264591, 21906754, 265016
108	80237938 (215, 216)	Novel Protein sim. GBank gll488729glj AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus] (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	transport	18108374, 35695917, 22278996, 264113, 264600, 264602, 264603, 265017, 264910, 264906, 264636, 264766
109	95194148 (217, 218)	Novel Protein sim. GBank gll233079j emj CAB11269 - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	264758, 264603, 264630, 264636, 264637
110	79582823 (219, 220)			264687
111	39565458 (221, 222)			264564
112	79856038 (223, 224)		UNCLASSIFIED	264908
113	17959439 (225, 226)		UNCLASSIFIED	265007
114	80502101 (227, 228)		UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gji2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	UNCLASSIFIED	52645196, 52645080, 33656970, 264562, 21906754, 27486284, 18108379, 35696423, 264635, 52644332, 18108382
116	81298889 (231, 232)			284905, 284906, 284907, 284908, 284909, 284910, 284755, 265010, 284763, 284682, 284764, 284765, 284685, 284686, 284768, 284769, 33857023, 284683, 33857105, 284628, 18108374, 284631, 284632, 284634, 284636, 284637, 284638, 284639, 96326466, 284355, 284566
117	79636695 (233, 234)		Contains protein domain (PF00170) - bZIP transcription factor	284639, 284693
118	80222170 (235, 236)		UNCLASSIFIED	263974
119	91013071 (237, 238)	Novel Protein sim. GBank gji32526 (U22327) - alpha2(V) collagen [Caenorhabditis elegans]	UNCLASSIFIED	22278986, 29331824, 60432289, 285007, 6043438, 284603, 284605, 18108351, 284769, 284689, 265020, 284534, 27486281, 284358, 83373044, 18108385, 284564
120	8756491 (239, 240)	Novel Protein sim. GBank gji2131219pji[S50157] - cyclin-dependent kinase chain SRB10 - yeast [Saccharomyces cerevisiae]	kinase	284603
121	80026153 (241, 242)			284395
122	20457620 (243, 244)	Novel Protein sim. GBank gji0052147jmb[CAB08137] - (Z94742) ksaA [Mycobacterium tuberculosis]	transferase	284605
123	8758278 (245, 246)			284604
124	79104017 (247, 248)	Novel Protein sim. GBank gji2833385jpiQ43134[UGST_SORBI - GRANULE-BOUND GLYCOSYL (STARCH) SYNTHASE PRECURSOR	synthase	18108394, 18108397, 265005, 265007, 265008, 265010, 265011, 18108395, 18108379, 18108380, 18108384
125	87797968 (249, 250)	Novel Protein sim. GBank gji75542 (U08235) - glutamate receptor delta-1 subunit [Rattus norvegicus]	misc_channel	284505, 284905, 265005, 284596, 22278002
126	56701283 (251, 252)	Novel Protein sim. GBank gji5102785jmb[CAB45200.1] - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]		264511
127	20467267 (253, 254)			284605
128	80248473 (255, 256)	Novel Protein sim. GBank gji130120jpi23620[PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	UNCLASSIFIED phosphatase	284603, 284605, 284910, 284600, 264601, 264607, 284605, 18108351, 284693, 284537
129	95290543 (257, 258)	Novel Protein sim. GBank gji2506493jpi38093[GCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	UNCLASSIFIED	35996423, 35695855, 284600, 284602, 284603, 284604, 284605, 284508, 284906, 284564, 284628, 284687, 284685, 284693
130	80085593 (259, 260)	Novel Protein sim. GBank gji55065jmb[CA93937] - (X83413) U88 [Human herpesvirus 6]		284634
131	94995022 (261, 262)	Novel Protein sim. GBank gji1076038pji[SC4860 - ABC transporter Psc-2 chain - Mycobacterium tuberculosis]	transport	18108376, 284769, 29331826, 284689, 22278986, 265021, 284600, 284511, 284601, 284602, 284605, 284606, 284636

132	10857692 (263, 264)	Novel Protein sim. GBank g1187340[emb]CAB07068 - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264636 264605, 264689
133	94630883 (265, 266)	Novel Protein sim. GBank g1458583[emb]CAB40932.1 - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264605, 264605, 265021
134	79834660 (267, 268)	Novel Protein sim. GBank g11460074[emb]CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
135	19885057 (269, 270)	Novel Protein sim. GBank g1212686[emb]CAA73511 - (Y13070) polyphosphatase synthase [Streptomyces coelicolor]		synthase	264608
136	79946083 (271, 272)	Novel Protein sim. GBank g1212686[emb]CAA73511 - (Y13070) polyphosphatase synthase [Streptomyces coelicolor]			264608
137	79619770 (273, 274)	Novel Protein sim. GBank g15420387[emb]CAB46679.1 - (A1243459) proteophosphoglycan [Leishmania major]			264683, 264685, 264686, 264691, 264692, 264693
138	79635971 (275, 276)	Novel Protein sim. GBank g1568912[emb]CAB52075.1 - (AL108732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	UNCLASSIFIED - dehydrogenase	18108374, 18108385, 33657109, 33657182, 265010, 22278988, 265006, 265007, 265008, 265009, 264693
139	86688076 (277, 278)	Novel Protein sim. GBank g1568912[emb]CAB52075.1 - (AL108732) putative mutase [Streptomyces coelicolor A3(2)]			22278986, 265007, 264910, 60433356, 265010, 264602, 264605, 264768, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	79825759 (279, 280)	Novel Protein sim. GBank g13581916[emb]CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schistosoma caracasensis]		UNCLASSIFIED	264600, 264601
141	20700094 (281, 282)	Novel Protein sim. GBank g13581916[emb]CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schistosoma caracasensis]		nuclease	264602, 265017
142	80028104 (283, 284)	Novel Protein sim. GBank g13581916[emb]CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schistosoma caracasensis]			264600
143	11072274 (285, 286)	Novel Protein sim. GBank g13581916[emb]CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schistosoma caracasensis]		UNCLASSIFIED	263978, 264600, 264910, 264632, 264508, 264563, 264684, 264591, 264556, 264908, 264629, 264639
144	95009102 (287, 288)	Novel Protein sim. GBank g13581916[emb]CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schistosoma caracasensis]			264600
145	80027058 (289, 290)	Novel Protein sim. GBank g13581916[emb]CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schistosoma caracasensis]		UNCLASSIFIED	22278986, 264602
146	13085662 (291, 292)	Novel Protein sim. GBank g1408071[emb]P24536[Y121, BURCE - INSERTION ELEMENT IS402] HYPOTHETICAL 24 KD PROTEIN [Mycobacterium tuberculosis]	Contains protein domain (PF01679) - Transposase		264687
147	94320366 (293, 294)	Novel Protein sim. GBank g1408071[emb]P24536[Y121, BURCE - INSERTION ELEMENT IS402] HYPOTHETICAL 24 KD PROTEIN [Mycobacterium tuberculosis]		helicase	264605, 264606, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108365, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank g12916947[emb]CAA17585 - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265009, 265010, 264680, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank g11723073sp10407081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01 (AJ224340) meliophosphorylase [Lactobacillus santifrancisco]	Contains protein domain (PF00003) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486265, 264636
150	20294748 (299, 300)	Novel Protein sim. GBank g10724125jemb[CAAI1803] - (AJ224340) meliophosphorylase [Lactobacillus santifrancisco]			264600
151	20726398 (301, 302)	Novel Protein sim. GBank g17293125sp107651DEOB_ECOLI - PHOSPHOTRANSFERASE [PHOSPHODEOXYRIBOMUTASE]	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank g10497982sp1P55667Y4TM_RHNS - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	264602
153	80256655 (305, 306)	Novel Protein sim. GBank g10123021sp1090508VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	264593
154	82305666 (307, 308)	Novel Protein sim. GBank g1119697jpr1JN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	264510, 264762, 264691, 264634, 264605
155	20429659 (309, 310)	Novel Protein sim. GBank g1028710jpr1S41739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	264565
156	39564742 (311, 312)	Novel Protein sim. GBank g103695013 (AF052586) - CtrA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/NifX family	hydrolase	264691
157	10358687 (313, 314)	Novel Protein sim. GBank g1073021jpr1C55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	264605
158	78761936 (315, 316)	Novel Protein sim. GBank g1073021jpr1C55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	265008, 264605
159	78890376 (317, 318)	Novel Protein sim. GBank g1173021jpr1P4789PL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, C-beta repeat		
160	11075119 (319, 320)	Novel Protein sim. GBank g1173021jpr1P4789PL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Ribosomal protein L30pL7e	ribosomal prot	22478996, 264600, 264603, 35695917, 32833986, 35696423, 264636
161	80055007 (321, 322)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	264112, 264532, 22279002
162	80016371 (323, 324)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]			
163	11692306 (325, 326)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	264639
164	80077902 (327, 328)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	264605, 264807, 264600
165	10856067 (329, 330)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	264691
166	80095003 (331, 332)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	264605, 264486
167	16395460 (333, 334)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	265010
168	80079362 (335, 336)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	264600
169	80239481 (337, 338)	Novel Protein sim. GBank g10316855 dJ963K23.2 (novel protein) [Homo sapiens]			264556, 264657, 264558, 264559

170	79612364 (339, 340)	Novel Protein sim. GBank glt14088a p27184 TYGK_ECOLI - HYPOTHETICAL 15.4 KC PROTEIN IN RECO-PLD8 INTERGENIC REGION	Contains protein domain (PF01810) - LysE type translocator		264506 264595, 264604
171	95203073 (341, 342)	(P138) Novel Protein sim. GBank gik4210805 p AAD12048.11 - (AP04609) AgIC (Spirillum mellei)	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264769
172	37797007 (343, 344)	Novel Protein sim. GBank gik4210805 p AAD12048.11 - (AP04609) AgIC (Spirillum mellei)	Contains protein domain (PF00181) - Ribosomal Proteins L2	ribosomal prot	264769
173	57520660 (345, 346)	Novel Protein sim. GBank gll132854 p P2238 RL2_ECOLI -SIS RIBOSOMAL PROTEIN L2	Contains protein domain (PF01810) - LysE type translocator	transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
174	95293078 (347, 348)	Novel Protein sim. GBank gll1811350 p BAA119371 - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTIN IN STREPTOMYCES COELICOLOR (Bacillus pastorius)	Contains protein domain (PF00181) - Ribosomal Proteins L2	transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
175	78756270 (349, 350)	Novel Protein sim. GBank gll207272 p h CAB083261 - (Z05121) manA (Mycobacterium tuberculosis)	Contains protein domain (PF01810) - LysE type translocator	isomerase	264565
176	80066898 (351, 352)	Novel Protein sim. GBank gll1055198 (340187) - similar to PIP-A41174 chicken LD (limb deformity) gene product and to form, also P-rich region similar to collagen (Cysteine-rich)	Contains protein domain (PF01810) - LysE type translocator	UNCLASSIFIED	264407, 264910, 264681, 264558
177	86684852 (353, 354)	Novel Protein sim. GBank gll2328738 p h CAB109521 - (Z042869) hypothetical protein RV1695 (Mycobacterium tuberculosis)	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264768, 60424179, 264687, 264688, 264769, 26531828, 60433289, 18103796, 264689, 18103837, 32833986, 22278998, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264906, 264564, 264637, 264638, 264466, 60433398, 264768
178	79559526 (355, 356)	Novel Protein sim. GBank gll1906596 (L81788) - kinesin-73 (Drosophila melanogaster)	Contains protein domain (PF01513) - Domain of unknown function	strud	264693, 33657109, 264635
179	20263112 (357, 358)	Novel Protein sim. GBank gll169387 p P4259 ONAB_HAEN - REPLICATIVE DNA HELICASE	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264583
180	80488956 (359, 360)	Novel Protein sim. GBank gll169387 p P4259 ONAB_HAEN - REPLICATIVE DNA HELICASE	Contains protein domain (PF01513) - Domain of unknown function	helicase	264769
181	79585366 (361, 362)	Novel Protein sim. GBank gll13710615 (AF059465) - DOC4 (Mus musculus)	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	21906767, 264693, 264639, 18108384
182	80577895 (363, 364)	Novel Protein sim. GBank gll1076627 p h S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264566 264690
183	11614017 (365, 366)	Novel Protein sim. GBank gll1076627 p h S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264566 264690
184	10174167 (367, 368)	Novel Protein sim. GBank gik4371280 p AAD10138 - (AC066265) hypothetical protein (Arabidopsis thaliana)	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264510

185	21600822 (365, 370)	Novel Protein sim. GBank gll3006178[emb]CAA18398.1] - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]	UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gll282902[sp]P94408[YCLF_53.3 KD PROTEIN IN SFP-GERA INTERGENIC REGION]	transport	264595
187	80186611 (373, 374)	Novel Protein sim. GBank gll315026[emb]CAA19179j - (AL023634) cyclin [Schizosaccharomyces pombe]	UNCLASSIFIED	264369
188	20465942 (375, 376)	Novel Protein sim. GBank gll214583[jin]S72838 - hMX protein - Mycobacterium leprae	Kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gll1861244[dbj]BAA192711 - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE [Bacillus subtilis]	UNCLASSIFIED	35966052, 264602, 264605, 264762, 264689, 35985917, 16108370, 16108372, 264638, 264565
190	80066821 (379, 380)	Novel Protein sim. GBank gll10226[ep]P2825fKBP_STRCH - FK506-BINDING PROTEIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE [PPIASE] [ROTAMASE]	synthase	264563
191	86095012 (381, 382)	Novel Protein sim. GBank gll4980882[gb]AAD35474.1(AE001711 - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]	isomerase	264508, 264604, 264605, 264765, 264555
192	16333379 (383, 384)	Novel Protein sim. GBank gll1705461[sp]P3656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELAGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]	transport	264567
193	79910127 (385, 386)	Novel Protein sim. GBank gll3122305[sp]Q2778[KGPF_SCMA - 6- (PHOSPHOHEXOKINASE)]		264608, 264693
194	20464949 (387, 388)	Novel Protein sim. GBank gll781203[emb]CA0606119i - (Z93859) gnd [Mycobacterium tuberculosis]		264605
195	13318389 (389, 390)	Novel Protein sim. GBank gll284379[emb]CAA1481.1i - (Y14573) mg finger protein [Hordeum vulgare]	transport	264638
196	95005569 (391, 392)	Novel Protein sim. GBank gll781203[emb]CA0606119i - (Z93859) gnd [Mycobacterium tuberculosis]	gaba	264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gll781203[emb]CA0606119i - (Z93859) gnd [Mycobacterium tuberculosis]	kinase	264602, 264682, 264692, 16108374
198	79165835 (395, 396)	Novel Protein sim. GBank gll284379[emb]CAA1481.1i - (Y14573) mg finger protein [Hordeum vulgare]		264636
199	76890715 (397, 398)	Novel Protein sim. GBank gll284379[emb]CAA1481.1i - (Y14573) mg finger protein [Hordeum vulgare]		265006
200	79413849 (399, 400)	Novel Protein sim. GBank gll284379[emb]CAA1481.1i - (Y14573) mg finger protein [Hordeum vulgare]	UNCLASSIFIED	264595, 264596
201	86945924 (401, 402)	Novel Protein sim. GBank gll284379[emb]CAA1481.1i - (Y14573) mg finger protein [Hordeum vulgare]	UNCLASSIFIED	26331626, 265007, 264512, 33857402, 264596, 265017, 16108351, 264682, 264683, 264761, 264620, 58810764, 264634, 264635, 56182323, 60432113, 22279000

202	79590046 (403, 404)	Novel Protein sim. GBank g1231772p2609ICH51.1USTMA - CHITIN SYNTHASE 1 CHITIN UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3)	Contains protein domain (PF01644) Chitin synthase	synthase	264600
203	79643927 (405, 406)	Novel Protein sim. GBank g1504042p0b[BAA13220] - (D86984) similar to yeast adenylate cyclase (S36776) [Homo sapiens]			22276995, 29331822, 29331825, 29331827, 264906, 21906754, 264983, 21906766, 21906769, 3569423, 264556
204	79655186 (407, 408)	Novel Protein sim. GBank g1253380jenn[CAB13310] - (Z39911) similar to hypothetical proteins [Bacillus subtilis]		UNCLASSIFIED transport	264909
205	10090583 (409, 410)	Novel Protein sim. GBank g1213438 [prij]S06078 - polybromo 1 protein - chicken		UNCLASSIFIED	264604
206	8758473 (411, 412)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]		UNCLASSIFIED	264556
207	20754622 (413, 414)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]		UNCLASSIFIED	264605
208	20782621 (415, 416)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]		UNCLASSIFIED	264605, 264689
209	80071069 (417, 418)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]		UNCLASSIFIED	264605, 264689
210	80166800 (419, 420)	Novel Protein sim. GBank g15031809jenn[NP_005536, 1p]SLR - Immunoglobulin heavy chain containing leucine-rich repeat		UNCLASSIFIED	264905, 264907, 264908, 264766, 264987, 264991, 264629, 18108374, 264639
211	80034539 (421, 422)	Novel Protein sim. GBank g15031809jenn[NP_005536, 1p]SLR - Immunoglobulin heavy chain containing leucine-rich repeat		UNCLASSIFIED	263978
212	82442476 (423, 424)	Novel Protein sim. GBank g15122594p033123LEU2_MYCLE - 3 - ISOPROPYL-MALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYL-MALATE ISOMERASE) (ALPHA-IPM ISOMERASE) [PFM]	Contains protein domain (PF00330) Aconitase family (aconitate hydratase)	isomerase	264503, 264905, 264906, 264907, 264908, 264909, 264762, 264534, 264632, 264634, 264635, 264638, 264486
213	80248562 (425, 426)	Novel Protein sim. GBank g15122594p033123LEU2_MYCLE - 3 - ISOPROPYL-MALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYL-MALATE ISOMERASE) (ALPHA-IPM ISOMERASE) [PFM]	Contains protein domain (PF00330) Aconitase family (aconitate hydratase)	isomerase	22276996, 264908, 264909, 264600, 264602, 264603, 264605, 33657023, 264965, 264486
214	80079381 (427, 428)	Novel Protein sim. GBank g11523639p119421C460_COXBU - 60 KD CHAPERONIN 1 (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN 5)	Contains protein domain (PF00118) - TCP-1/Cpn60 chaperonin family	- eph	264600, 264693
215	14673283 (429, 430)	Novel Protein sim. GBank g13417287 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00696) Zinc finger, C2H2 type	UNCLASSIFIED dna_ma_bind	264629
216	80177716 (431, 432)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]			264448
217	79603634 (433, 434)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]			264508
218	80258476 (435, 436)	Novel Protein sim. GBank g11173288p03810PSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		mapolymerase	264494
219	20438797 (437, 438)	Novel Protein sim. GBank g11761097jenn[CAB06231] - (Z33854) gite [Mycobacterium tuberculosis]		synthase	264604
220	13499572 (439, 440)	Novel Protein sim. GBank g12561040p004914KSP - MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LGASE) [PROKS]		nucleasenhb	264689
221	11287468 (441, 442)	Novel Protein sim. GBank g14587313p0b[BAA16709.1] - unknown [Tetrahymena cruzi]		UNCLASSIFIED	264555

222	79862802 (443, 444)	Novel Protein sim. GBank glij1877265[emb]CAB070491 - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]	UNCLASSIFIED	264605, 264769, 3568423
223	63053960 (445, 446)		UNCLASSIFIED	264005, 264007, 264603
224	79557920 (447, 448)		UNCLASSIFIED	264684, 264693
225	79559541 (449, 450)		UNCLASSIFIED	264692
226	79172397 (451, 452)	Novel Protein sim. GBank glij2274851[dbj]BA215151 - (D64159) 3.7 gene product [Homo sapiens]	UNCLASSIFIED	22276998, 264112, 33657033, 263981
227	61777196 (453, 454)	Novel Protein sim. GBank glij669245 (U23488) C56C10.7 gene product [Caenorhabditis elegans]	UNCLASSIFIED	36695017, 264636, 264607
228	79872285 (455, 456)		UNCLASSIFIED	264768, 264607, 264906, 264692, 264693, 264633
229	79638266 (457, 458)		UNCLASSIFIED	264906, 264910
230	11013209 (459, 460)		UNCLASSIFIED	264631
231	20622207 (461, 462)	Novel Protein sim. GBank glij1835114[emb]CA4717331 - (Y10744) homoserine O-acetyltransferase [Leptospira mayot]	UNCLASSIFIED	264906, 264600, 264603, 264692
232	60055035 (463, 464)		UNCLASSIFIED	264600, 264603, 264605, 264687, 264769
233	60063054 (465, 466)	Novel Protein sim. GBank glij2642340 (AF032970) - indazole propionate hydrolase [Pseudomonas putida]	hydrolase	264604
234	7523998 (467, 468)	Novel Protein sim. GBank glij3510505 (AF030851) - polypeptide [Fugu subsp.]	UNCLASSIFIED	264369
235	60203671 (469, 470)	Novel Protein sim. GBank glij2104609[emb]CAB086051 - (Z95398) PcdA [Mycobacterium leprae]	UNCLASSIFIED	264106
236	78940001 (471, 472)		UNCLASSIFIED	264005
237	11755273 (473, 474)		UNCLASSIFIED	264681
238	79461407 (475, 476)		UNCLASSIFIED	264681
239	62435190 (477, 478)	Novel Protein sim. GBank glij2485617[sp]Q57252YDU_HAEIN - HYPOTHETICAL PROTEIN H1163	transport	264259, 264769
240	21635575 (479, 480)	Novel Protein sim. GBank glij183456[sp]71576YVLA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLA	UNCLASSIFIED	264639
241	60377307 (481, 482)	Novel Protein sim. GBank glij3875920[emb]CAB041111 - (Z41503) predicted using GeneFinder, similar to collagen, cDNA EST EMBL D85450 comes from this gene; cDNA EST EMBL D86868 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264908, 264909, 264764, 264639
242	62148454 (483, 484)		UNCLASSIFIED	264488, 264907, 264908, 264511, 264760, 264764, 264692, 264635, 264637
243	79633207 (485, 486)	Novel Protein sim. GBank glij2624302[emb]CA4155751 - (AL008967) ald [Mycobacterium tuberculosis]	UNCLASSIFIED	264906
244	60246662 (487, 488)		UNCLASSIFIED	264906
245	79683543 (489, 490)	Novel Protein sim. GBank glij2620625 (AF044459) - vgrE protein [Escherichia coli]	UNCLASSIFIED	264907, 264768
246	79162920 (491, 492)	Novel Protein sim. GBank glij5420387[emb]CAB4657911 - (A1243459) prothymosin [Lentivirus major]	UNCLASSIFIED	264637, 16108361, 16108367, 264655

247	7973185 (493, 494)	Novel Protein sim. GBank gII183005[emb]CA066481 - (Z55982) aegB [Mycobacterium tuberculosis]		kinase	264905, 264691, 35696423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gII168574[sp]P42464[ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35696286, 264607, 264511, 264602, 264768, 264666, 265021, 35695935, 18109385
249	79764645 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264636
250	79619860 (499, 500)			UNCLASSIFIED	21906768, 264692
251	84359469 (501, 502)			UNCLASSIFIED	26345156, 29331822, 29331824, 52644045, 263016, 21906765, 21906768, 265020, 27466261, 27468265, 35695763, 18108376, 264556, 264559, 264955
252	79737756 (503, 504)	Novel Protein sim. GBank gII327166[db]BA3316511 - (AB014576) KIAA0576 protein [Homo sapiens]		helicase	264685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gII003680[db]NC04185131 - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]			264604
254	80027421 (507, 508)	Novel Protein sim. GBank gII3915488[sp]P43158COA_BACSU - HYPOTHETICAL SYMPTONER IN COIT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264906, 264602, 264687, 265021, 264466
255	11398313 (509, 510)	Novel Protein sim. GBank gII1665720[db]BA041341 - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gII465781[sp]P4422YL31 CAELI - HYPOTHETICAL B6.0 KD PROTEIN F4489.1 IN CHROMOSOME III	Contains protein domain (PF00328) Prolyl oligopeptidase family	peptidase	264602, 264692
257	20286282 (513, 514)	Novel Protein sim. GBank gII172039[sp]P43158COA_BACSU - PROBABLE SUCCINYL-COA-3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA-3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gII3127836[emb]CA4189021 - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79910152 (517, 518)			collagen	
260	20379437 (519, 520)			UNCLASSIFIED	264681, 264686, 264692
261	20236585 (521, 522)	Novel Protein sim. GBank gII132761[sp]P42421[HUTL_STRGR - HISTIDINE AMMONIALLYASE (HISTIDASE)]	Contains protein domain (PF00221) Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264909
263	86095045 (525, 526)	Novel Protein sim. GBank gII3924708[emb]CA4845461 - (Z55597) Weak similarity with the zymogen precursor protein (blastp score 71); cDNA EST EMBL102689 comes from this gene; cDNA EST EMBL076135 comes from this gene; cDNA EST EMBL073147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264936, 264904, 265019, 264910, 264760, 18108351, 264763, 264764, 264628, 264766, 264768, 264769, 264931, 264932, 264933, 264628, 264634, 264635, 264635, 264636, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank gII3043734[db]BA235531 - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) Immunoglobulin domain	protease	264239, 264908, 21906754, 265018, 265019, 265020

265	95355646 (529, 530)	Novel Protein sim. GBank g14589624(b0)BA76834.11 - (AB023207) KIAA0990 protein [Homo sapiens]	kinase	264488, 36568286, 29331824, 56182181, 35696032, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264736, 264596, 55811386, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264691, 33857023, 33657109, 33857162, 264628, 35694423, 35695935, 264630, 264631, 264632, 264634, 264635, 264636, 264535, 264638, 5337304, 56526468, 67105518, 264564, 264566, 264486, 264600
266	79588075 (531, 532)		UNCLASSIFIED	264488
267	11362222 (533, 534)		UNCLASSIFIED	264628
268	79909566 (535, 536)		UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)		UNCLASSIFIED	264602
270	84381144 (539, 540)	Novel Protein sim. GBank g14507367(re)NP_003182.1lpTARS - threonyl-rRNA synthetase	UNCLASSIFIED	264693
271	79552301 (541, 542)	Novel Protein sim. GBank g14980738(gb)AAD35331.1(AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]	UNCLASSIFIED	264909, 264693
272	9874778 (543, 544)	Novel Protein sim. GBank g11168224(isp)P44569JNTD_HAEIN - PROBABLE 5' NUCLEOTIDASE PRECURSOR	synthase	264908
273	12840894 (545, 546)		UNCLASSIFIED	264686
274	39524246 (547, 548)	Novel Protein sim. GBank g13253159 (AF005335) - translation initiation factor eIF2C [Drosophila melanogaster]	UNCLASSIFIED	264564
275	82781041 (549, 550)	Novel Protein sim. GBank g1134920(isp)P21197/ISSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	UNCLASSIFIED	264907, 264908, 264909, 264766, 264768, 264991, 264532, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank g1172402(isp)P20964IQBG_BACSU - SPOOB-ASSOCIATED GTP-BINDING PROTEIN		265006, 60432229
277	90079735 (553, 554)	Novel Protein sim. GBank g1179639(prj)S03812 - wrb protein - Micrococcus luteus	ribosomal prot	264600, 18108387
278	12866947 (555, 556)	Novel Protein sim. GBank g13123160(isp)Q18964IYL2_CAEEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II	UNCLASSIFIED	264688
279	95292718 (557, 558)		nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603617 (559, 560)			264259
281	80249599 (561, 562)			18108392, 264634, 264535, 264556, 264557, 264558
282	18598662 (563, 564)		UNCLASSIFIED	265019
283	120614211 (565, 566)		UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim GBank gl 2429094 (U58632) - acetyl xylan esterase, AexA [Thermotoga neapolitana]	Contains protein domain (PF00300) Phosphoglycerate mutase family	UNCLASSIFIED	35696032, 29331828, 264508, 264905, 264600, 264602, 264603, 264602, 264764, 36161562, 21908704, 16108376, 264636, 264539, 19108387
285	6757940 (569, 570)	Novel Protein sim GBank gl 2072674 (emj)[CA106305] - (Z95120) rHE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) DEAD/DEAH box helicase	UNCLASSIFIED	264603
286	80503233 (571, 572)	Novel Protein sim GBank gl 765323 [hbs]157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]		UNCLASSIFIED	264689
287	12145521 (573, 574)	Novel Protein sim GBank gl 181000 [emj][CA106305] - (Z95120) rHE [Mycobacterium tuberculosis]		UNCLASSIFIED	264557
288	20756502 (575, 576)	Novel Protein sim GBank gl 765323 [hbs]157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]		UNCLASSIFIED	264557
289	80043804 (577, 578)	Novel Protein sim GBank gl 181000 [emj][CA106305] - (Z95120) rHE [Mycobacterium tuberculosis]	Contains protein domain (PF00440) Bacterial regulatory proteins, tetr family	UNCLASSIFIED	264593, 264600
290	80430175 (579, 580)	Novel Protein sim GBank gl 256664 [emj][P40120] YDCG, ECOLI - 59.4 PROTEIN IN TRG-RNASE INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim GBank gl 825182 [L30019] mitochondrial glutamyl-HRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim GBank gl 825182 [L30019] mitochondrial glutamyl-HRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim GBank gl 171605 [emj][P53528] UVRO_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	Helicase	UNCLASSIFIED	264909, 264605, 264687, 264689, 264692
294	79530303 (587, 588)	Novel Protein sim GBank gl 117422 [emj][P10040] CRB_DROME - CRUMBS PROTEIN PRECURSOR (95%)	Contains protein domain (PF00008) EGF-like domain	UNCLASSIFIED	35696032, 264906, 265011, 264628, 53811576
295	79444180 (589, 590)	Novel Protein sim GBank gl 1161519 [emj][BA111585] - (D82384) a variant of TSC-22 [Gallus gallus]		UNCLASSIFIED	52844507, 26331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim GBank gl 5646786 [emj][BA133403] - (A8012228) SecA [Vibrio anguillarum]	Synthase	UNCLASSIFIED	264508
297	79531297 (593, 594)	Novel Protein sim GBank gl 565997 [emj][CA106305] - (A1106463) putative membrane protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	UNCLASSIFIED	264905, 264687, 264639
298	80418898 (595, 596)	Novel Protein sim GBank gl 565997 [emj][CA106305] - (A1106463) putative membrane protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	UNCLASSIFIED	264905, 264689, 264639, 264766

299	95233298 (597, 598)	Novel Protein sim. GBank gll1220837d[gljBA00147]- (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	264488, 263894, 5694075, 22278937, 22278936, 22278999, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265006, 264910, 264995, 264596, 264758, 33857084, 87168559, 265018, 265019, 264764, 264288, 264766, 264687, 56181562, 264769, 21906705, 21906768, 21906769, 33657023, 264692, 33657109, 27466281, 18108370, 264628, 264629, 59811576, 35695855, 264631, 264634, 264635, 264638, 264639, 83373044, 18108397, 87168518, 22278900, 22279502, 264365, 264566, 264567
300	20711340 (598, 600)	Novel Protein sim. GBank gll145922 (A25981) - iron deficient transport protein precursor [Escherichia coli]	UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gll145922 (A25981) - iron deficient transport protein precursor [Escherichia coli]	transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gll174681[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)		264908
303	79574865 (605, 606)	Novel Protein sim. GBank gll6795[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)		264908
304	20711342 (607, 608)	Novel Protein sim. GBank gll6795[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)	helicase	264689 264602
305	80412520 (609, 610)	Novel Protein sim. GBank gll28867[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gll6795[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)	UNCLASSIFIED	263978
307	80222901 (613, 614)	Novel Protein sim. GBank gll28867[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)	UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80064305 (615, 616)	Novel Protein sim. GBank gll174681[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)	Contains protein domain (PF01351) - Ribonuclease HI	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504136 (617, 618)	Novel Protein sim. GBank gll54203[gljBA45M1CT]-HAEIN-QUEUINE TRNA- RIBOSYL TRANSFERASE (TRNA-QUININE TRANSLOCASE) (GUANINE INSERTION ENZYME)		264769
310	8053818 (619, 620)	Novel Protein sim. GBank gll145522 (A34957) - phosphoribosylaminimidazole succinyl-CoA synthetase [Mycobacterium tuberculosis]	synthase	264603 264602
311	11090659 (621, 622)	Novel Protein sim. GBank gll145522 (A34957) - phosphoribosylaminimidazole succinyl-CoA synthetase [Mycobacterium tuberculosis]		
312	80054347 (623, 624)	Novel Protein sim. GBank gll145522 (A34957) - phosphoribosylaminimidazole succinyl-CoA synthetase [Mycobacterium tuberculosis]	UNCLASSIFIED	264566
313	80046168 (625, 626)	Novel Protein sim. GBank gll145522 (A34957) - phosphoribosylaminimidazole succinyl-CoA synthetase [Mycobacterium tuberculosis]	UNCLASSIFIED	264603, 264567

314	87645112 (627, 628)	Novel Protein sim. G.Bank gji18661583 (AF092175) - <i>karos</i> [Danio rerio]	Contains protein domain (PF00320) GATA zinc finger	264259, 2643289, 26431828, 264605, 264606, 264608, 264609, 265008, 264910, 264911, 265017, 264603, 265018, 264984, 264766, 264692, 3565763, 264628, 264629, 264639, 60170394, 22279002, 264565
315	82356091 (629, 630)	Novel Protein sim. G.Bank gji1652620(bj)BAAT75407 - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synchocystis sp.]		264508, 264600, 264762, 264687, 264768, 2644229, 264769, 264689, 264635, 264638, 264486
316	79811077 (631, 632)	Novel Protein sim. G.Bank gji11824459(p24178)DAPE_ECOLI - SUCCINYL-DIAMINOPIPELATE DESUCCINYLASE [SDAP]	UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. G.Bank gji14680229(bj)AA027583.1(AFI1827.4) DNB-5 [Homo sapiens]	UNCLASSIFIED	264605
318	94141636 (635, 636)	Novel Protein sim. G.Bank gji1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]	transport	264508, 264600, 264910, 264693, 264594, 264760, 264288, 264768, 264769, 21907769, 264691, 264693, 264628, 63274791, 264635, 264638, 264638, 83373044, 22279002, 264558, 265018
319	17289360 (637, 638)	Novel Protein sim. G.Bank gji1149693(emj)CAA60220 - (X86499) rbsC [Clostridium perfringens]	transport	264508, 264600, 264910, 264693, 264594, 264760, 264288, 264768, 264769, 21907769, 264691, 264693, 264628, 63274791, 264635, 264638, 264638, 83373044, 22279002, 264558, 265018
320	13327672 (639, 640)	Novel Protein sim. G.Bank gji2811033(sp)O05314(GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)	synthase	264488, 265009, 264533, 264628, 264635, 264687, 264693
321	94134387 (641, 642)	Novel Protein sim. G.Bank gji1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]	synthase	264488, 265009, 264533, 264628, 264635, 264687, 264693
322	66489053 (643, 644)	Novel Protein sim. G.Bank gji1160335 (U30358) - UNC-89 [Caenorhabditis elegans]	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
323	94653725 (645, 646)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
324	79174393 (647, 648)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
325	79662591 (649, 650)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
326	28774974 (651, 652)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
327	79776267 (653, 654)	Novel Protein sim. G.Bank gji151544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]	UNCLASSIFIED	264488, 264905, 264609, 264910, 264592, 264510, 264508
328	80253202 (655, 656)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
329	10173821 (657, 658)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
330	86597767 (659, 660)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
331	79748888 (661, 662)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
332	80071440 (663, 664)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693
333	13009555 (665, 666)	Novel Protein sim. G.Bank gji1714393 (647, 648)	UNCLASSIFIED	264488, 265009, 264533, 264628, 264635, 264687, 264693

334	60230771 (667, 668)	Novel Protein sim. GBank glij22228[gljS32227 - glutamate dehydrogenase (NADP+)] (EC 1.1.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00209) - Glutamate succinate/Phenylalanine/Valine dehydrogenase	dehydrogenase	264905, 264800, 264604, 264486
335	60057026 (666, 670)	Novel Protein sim. GBank glij2193938[emjCA090602] - (Z96800) glpQ2 [Mycobacterium tuberculosis]	line dehydrogenase	esterase	264907, 264603, 264693, 18108374, 264636, 18108387
336	60414319 (671, 672)	Novel Protein sim. GBank		UNCLASSIFIED	264602
337	11080629 (673, 674)	Novel Protein sim. GBank		nuc_rept	264568, 18108397, 22278956, 29331822, 20251099, 25331824, 56182181, 68174117, 29331825, 35696052, 29331828, 264508, 264509, 264605, 264606, 264607, 264608, 264609, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87188559, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264682, 264764, 264766, 264685, 264686, 35895917, 264682, 264683, 264628, 18108370, 18108374, 55811578, 35696423, 35695855, 264635, 264555, 264638, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87188518, 60432113
338	95413134 (675, 676)	Novel Protein sim. GBank glij54074[efpNP_005303.1]pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain		264593
339	11398513 (677, 678)	Novel Protein sim. GBank glij4001713[dbjBA435087.1] - (AB015879) Dnak [Pseudomonas gingivalis]		eph	264905, 265018, 264766, 18108374
340	80504146 (679, 680)	Novel Protein sim. GBank glij2842699[epQ92333]UBPC - SCHPO - PUTATIVE (UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C5G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	
341	11075198 (681, 682)	Novel Protein sim. GBank glij268580 (45001166) - conserved hypothetical protein (Borelia burgdorferi)	Contains protein domain (PF00260) - Trypophan synthase alpha chain	isomerase	264605
342	80054193 (683, 684)	Novel Protein sim. GBank glij1684738[emjCA470601] - (Y09452) YedJ [hypothetical protein (Pseudomonas syringae)]			264603, 264604
343	20465792 (685, 686)	Novel Protein sim. GBank glij217275[emjCA09104] - (Z95618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
344	80428870 (687, 688)	Novel Protein sim. GBank glij217275[emjCA09104] - (Z95618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]			264600, 264605, 264766, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank glij0233171[RP148053]APHA - MYCBA - ACET-POLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank glij2329787[emjCA475437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00209) - Glutamate succinate/Phenylalanine/Valine dehydrogenase	dehydrogenase	264905

347	79158195 (693, 694)	Novel Protein sim. GBank g1371675ispP2879SYH4. YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NM2D INTERGENIC REGION protein - Escherichia coli	UNCLASSIFIED	265006, 265008, 265010, 265018, 263987, 263991
348	80020208 (695, 696)	Novel Protein sim. GBank g11073610jpi[SJ7672 - ogp8 protein - Escherichia coli	transport	264602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank g13261599amp[CAB0091 7]- (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]	nuclease	265007 265008, 264766, 264689, 18108370
350	80502370 (699, 700)	Novel Protein sim. GBank g12949367jemb[C4A1782 1]- (A1022117) hypothetical protein [Schistosoma haematophy- sum]	glycoprotein	264766, 264905, 264908
351	80501805 (701, 702)	Novel Protein sim. GBank g14416302gblAA020307 - (AF105716) copolymer polypeptide [Zea mays]	protease	264595
352	11611585 (703, 704)	Novel Protein sim. GBank g11174887spP42873URE1, STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	UNCLASSIFIED	264604
353	80061653 (705, 706)	Novel Protein sim. GBank g11174887spP42873URE1, STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) Urease	264595
354	56026132 (707, 708)	Novel Protein sim. GBank g1115157ispP16574BVGA, BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	UNCLASSIFIED	264628
355	80046344 (709, 710)	Novel Protein sim. GBank g1115157ispP16574BVGA, BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) Response regulator receiver domain	264505, 264595, 264683, 22279602 264503, 264591, 264592
356	80043835 (711, 712)	Novel Protein sim. GBank g1497637 (J03939) - cytochrome oxidase d subunit 1 [Escherichia coli]	oxidase	264605
357	80070566 (713, 714)	Novel Protein sim. GBank g12200990 (AF006000) - Bgl I [Bordetella pertussis]	UNCLASSIFIED	264768
358	37032756 (715, 716)	Novel Protein sim. GBank g13510639 (AF049344) - UDP- GALNAc:polysaccharide N-acetylglucosaminyltransferase T5 [Rattus norvegicus]	UNCLASSIFIED	264604, 264769
359	80501485 (717, 718)	Novel Protein sim. GBank g113764ispP25718AMY1, ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	UNCLASSIFIED	264594
360	80026745 (719, 720)	Novel Protein sim. GBank g113764ispP25718AMY1, ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	transferase	22278996, 264259, 29331822, 29331824, 264605, 59811957, 265022
361	80584075 (721, 722)	Novel Protein sim. GBank g113764ispP25718AMY1, ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	amylase	264688
362	13089485 (723, 724)	Novel Protein sim. GBank g12829816ispP95171NLUOK, MYCTU - NADH DEHYDROGENASE I CHAIN K NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11 (NADH11)	dehydrogenase	264566 264769, 264602, 264604, 264508, 264762, 264638, 264486
363	79750145 (725, 726)	Novel Protein sim. GBank g12829816ispP95171NLUOK, MYCTU - NADH DEHYDROGENASE I CHAIN K NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11 (NADH11)		
364	82443593 (727, 728)	Novel Protein sim. GBank g12829816ispP95171NLUOK, MYCTU - NADH DEHYDROGENASE I CHAIN K NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11 (NADH11)		

365	68040288 (729, 730)	Novel Protein sim. GBank gji492928[sp]AD033924.11 - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264468, 21906765, 21906767, 55811576, 21906769, 29148639, 22278994, 22278995, 22278996, 265002, 265002, 264634, 264691, 2645893, 33657023, 33657402, 264693, 264639, 264594, 26331824, 264758, 18108385, 26331827, 87166559, 265018, 22279000, 265019, 264482, 264761, 264681, 18108351, 265017, 264157
366	81821838 (731, 732)	Novel Protein sim. GBank gji4503843[sp]NP_003908.1pG240 - UNKNOWN	Contains protein domain (PF01602) - Adaplin N terminal region	60424176, 65274572, 58182575, 22278994, 56994075, 22278998, 264259, 26331822, 26331824, 56182181, 80424269, 66714117, 26331825, 60432289, 26331826, 26331827, 26331828, 264905, 264828, 58182435, 26331829, 265008, 264591, 55812038, 55811386, 265010, 87166559, 265017, 265018, 264604, 265019, 55811150, 264448, 264369, 264388, 264688, 264769, 56181582, 21906768, 21906769, 55811957, 35695917, 265022, 60170815, 33657023, 65274620, 18108385, 263967, 33657109, 33657349, 35695763, 264628, 18108376, 55811576, 65274791, 35695855, 56182323, 83373044, 60432113, 264583, 264584, 264587, 264569
368	79607265 (735, 736)	Novel Protein sim. GBank gji3913029[sp]P94967[ALR_MYCSM - ALANINE RACEMASE]	UNCLASSIFIED	264508, 264604, 264605, 264636
370	88090966 (738, 740)	Novel Protein sim. GBank gji3249559 (AF018251) - EH domain binding protein Ensin [Rattus norvegicus]		264905, 264902, 264605, 264766, 264691
371	95282598 (741, 742)	Novel Protein sim. GBank gji595399[em]C4A183291 - (A1022288) putative tRNA dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01715) - tRNA dehydratase	264905, 264906, 264510, 264600, 264601, 264602, 264603, 265018, 264604, 264605, 265021, 264692, 264636, 264564
372	80021107 (743, 744)	Novel Protein sim. GBank gji2506383[sp]P31576[FX - ECOLI - FERREDOXIN LIKE PROTEIN]		264564
373	79683765 (745, 746)	Novel Protein sim. GBank gji3341640[em]C4A131641 - (A231122) s61 [Vibrio cholerae]	UNCLASSIFIED	264909
374	79683766 (747, 748)	Novel Protein sim. GBank gji5458934[sp]A403716.11 - (AF152322) proto-cadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	264905, 264906
375	91230181 (749, 750)	Novel Protein sim. GBank gji1805408[sp]B408970 - (D50453) homologues to nitrite hydratase region 3' - hypothetical protein P47K of P. chlorophis [Bacillus subtilis]	cadherin	65274572, 264259, 26331826, 56182435, 6043356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33657023, 264769
376	800505214 (751, 752)	Novel Protein sim. GBank gji1805408[sp]B408970 - (D50453) homologues to nitrite hydratase region 3' - hypothetical protein P47K of P. chlorophis [Bacillus subtilis]	UNCLASSIFIED	
377	10339083 (753, 754)			264906

378	80056153 (755, 756)	Novel Protein sim. GBank gl 076013 gl A49020_cnrB (fragment)	Contains protein domain (PF00289): Carboxymyophosphate synthase (C2-Sase)	UNCLASSIFIED	265008, 264555
379	80503337 (757, 758)	protein homolog - Mycobacterium bovis (strain BCG) (D12651) glucide dehydrogenase [Escherichia coli]	Contains protein domain (PF01011): POO enzyme repeat	dehydrogenase	264768
380	80060937 (759, 760)				264604
381	11766927 (761, 762)	Novel Protein sim. GBank gl 3327136 gl BA31636 - (AB014567) KIAA0661 protein [Homo sapiens]		UNCLASSIFIED	264684
382	80043377 (763, 764)				264592
383	83236025 (765, 766)			UNCLASSIFIED	264559, 26331822, 60432289, 26331827, 264288, 264766, 263967, 65274791, 35658455, 263981, 83373044, 264557
384	95314325 (767, 768)				264692
385	10237676 (769, 770)	Novel Protein sim. GBank gl 0734456 gl S47610 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465): Iron-containing alcohol dehydrogenase	dehydrogenase	264595, 265017, 265021, 264638, 87168518, 22276902
386	76633434 (771, 772)				264966
387	17960637 (773, 774)	Novel Protein sim. GBank gl 460074 gl CAB01049 - (Z7250) hypothetical protein Rv2586 [Mycobacterium tuberculosis]	Contains protein domain (PF01841): Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gl 420159 gl BA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00846): F-box domain.	homeobox	35686288, 264905, 66712502, 60432228, 264493, 60433358, 264688, 264688, 21098736, 264681, 22270000, 264482
389	76316697 (777, 778)			UNCLASSIFIED	11018394, 22278956, 264630, 264556, 22276902
390	80079949 (779, 780)	Novel Protein sim. GBank gl 854055 gl C4A58337 - (X2413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264690
391	7657302 (781, 782)				264482
392	76766056 (783, 784)	Novel Protein sim. GBank gl 3378523 gl C4A08867 - (A009832) cytomalate dehydrogenase		UNCLASSIFIED	264690
393	33206031 (785, 786)	(Thermoplasma neapolitana)		UNCLASSIFIED	264690
394	10104463 (787, 788)			UNCLASSIFIED	264690
395	80229010 (789, 790)	Novel Protein sim. GBank gl 6777780 (U03327) - unknown (Pteropus poliocephalus)		UNCLASSIFIED	264690
396	20436224 (791, 792)	Novel Protein sim. GBank gl 6777780 (U03327) - unknown (Pteropus poliocephalus)	Contains protein domain (PF00047): Immunoglobulin domain	UNCLASSIFIED	264690
397	80417014 (793, 794)	Novel Protein sim. GBank gl 6777780 (U03327) - unknown (Pteropus poliocephalus)		UNCLASSIFIED	264690
398	91230517 (795, 796)	Novel Protein sim. GBank gl 1518456 (U45988) - syndrome (eczema-thrombocytopenia) mitochondrial single carrier (Ochrocerca voluulus)	Contains protein domain (PF00153): Mitochondrial carrier proteins	transport	265007, 265009, 264608, 264556, 264629, 264766
					18108388, 22278959, 22278956, 56894075, 22278959, 264239, 26331824, 28331820, 264905, 264906, 265007, 265008, 21098734, 35657084, 265017, 264446, 264288, 264766, 21906765, 21906766, 21906767, 265020, 265021, 35657023, 35657108, 264628, 35686423, 35686555, 264952, 18108386, 264587, 18108391

399	80055278 (797, 798)	Novel Protein sim. G.Bank gij3360091dbj[BA431995] - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) kinase FGCG family of carbohydrate	kinase	264592, 264595
400	94117490 (799, 800)	Novel Protein sim. G.Bank gij728635sep[P39192]ALUS_HUMAN - III ALU SUBFAMILY SC WARNING ENTRY III	Contains protein domain (PF00560) Leucine Rich Repeat	cadherin	18108394, 56162575, 22276995, 22276997, 22276999, 264259, 29331824, 265006, 265007, 265009, 60432229, 33657402, 21906754, 265010, 265017, 265018, 265019, 18103351, 18108337, 21906765, 265021, 265022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 90170394, 56192323
401	11397497 (801, 802)	Novel Protein sim. G.Bank gij4928292dbjAA033527 - 1AF13211 - (AF132117) FhuA [Staphylococcus aureus]	Contains protein domain (PF00017) Src homology domain 2	transport	264594
402	95420294 (803, 804)	Novel Protein sim. G.Bank gij566847dbj[BA483027] - (AG028998) KAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) Src homology domain 2	phosphatase	65274572, 56162575, 35666286, 22276996, 22276998, 264093, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 264907, 264909, 265006, 264511, 265007, 265008, 264910, 264591, 33657402, 60433386, 60433436, 264596, 21906754, 55844286, 265010, 265011, 87188559, 265017, 265018, 265019, 284681, 18103351, 284682, 284448, 284288, 264684, 264766, 264787, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264690, 264693, 65274620, 3565763, 264628, 18103370, 264629, 18103379, 35696423, 55811576, 264635, 264636, 264537, 264639, 18108385, 22279002, 264553, 264584, 264585, 264586, 264768, 264632, 264639, 264593
403	80439913 (805, 806)			UNCLASSIFIED	264632
404	11609655 (807, 808)			polymerase	265009, 264682
405	79471260 (809, 810)	Novel Protein sim. G.Bank gij265164jemb[CA415759] - (AL009198) dnaE2 [Mycobacterium tuberculosis]	Contains protein domain (PF00159) Pancreatic hormone peptides	UNCLASSIFIED	18108337, 264693
406	79634172 (811, 812)			UNCLASSIFIED	264769
407	80478229 (813, 814)			UNCLASSIFIED	264600
408	80079965 (815, 816)			UNCLASSIFIED	264259
409	5640527 (817, 818)	Novel Protein sim. G.Bank gij3047117 (AF058919) - similar to ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	

410	95357498 (619, 820)	Novel Protein sim. GBank gll47501gjbj006184; - (D29801) Unknown [Mus musculus]	UNCLASSIFIED	264489, 52646385, 52646842, 56181688, 35696286, 52645080, 29331822, 29331824, 56182181, 29331825, 60424269, 35696052, 33656970, 264506, 264509, 264605, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52646317, 55811386, 265010, 265011, 265017, 264604, 285018, 58811150, 264762, 264764, 264766, 264687, 264768, 264769, 52644229, 21906786, 265020, 285021, 264534, 52644150, 264692, 33657023, 65274620, 33857109, 33857182, 27486281, 35695763, 264628, 264629, 60431528, 18108376, 263978, 35696423, 35695955, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22278902, 284583, 264585, 264486
411	80501670 (821, 822)		UNCLASSIFIED	264769
412	80241862 (823, 824)	Novel Protein sim. GBank gll3261784jembjCA008971; - (Z95558) htpx [Mycobacterium tuberculosis]		264607, 264910, 263973, 22278902
413	11078446 (825, 826)	Novel Protein sim. GBank gll129039jlp20707j0001_AZ0V1 - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)	dehydrogenase	18108374, 264760, 264769, 264602, 264603, 264638, 264605, 264909, 264805
414	82050554 (827, 828)	Novel Protein sim. GBank gll4688350jg0AA031273_1jAF 13202 - (AF 132025) rhophilin [Drosophila melanogaster]	UNCLASSIFIED	264908, 87108518
415	84453144 (829, 830)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]	kinase	264488, 264600, 264602, 264764, 264636
416	80402775 (831, 832)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		264605
417	20153797 (833, 834)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		
418	94125841 (835, 836)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		
419	95314272 (837, 838)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		
420	37036349 (839, 840)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		
421	95292942 (841, 842)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		
422	79471293 (843, 844)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		
423	79604942 (845, 846)	Novel Protein sim. GBank gll2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		

424	7896557 (847, 848)	Novel Protein sm. GBank gJ14928514feipNP_004977.1lpCTN1 - kinesin 1 (kinesin superfamily)				265019
425	80431450 (848, 850)	Novel Protein sm. GBank gJ17037013bml76462 - KPSs-kinesin-related protein (pals, testes, Peptide Partial, 167 aa)	Contains protein domain (PF00223) - kinesin motor domain	-struct		264909, 265007, 55811386, 264768, 55810764
426	80064522 (851, 852)	Novel Protein sm. GBank				264605, 264559
427	80057232 (853, 854)	Novel Protein sm. GBank gJ231829lpjP29929COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED		264603, 264636
428	7948798 (855, 856)	Novel Protein sm. GBank gJ1826lpjS22897 - extensin - Vohox coded (fm domain)		UNCLASSIFIED		264683
429	80091252 (857, 858)	Novel Protein sm. GBank gJ1805154jenuCAB064511 - (Z84959) hypothetical protein Rv0638 [Mycobacterium tuberculosis]		UNCLASSIFIED		264554, 264762
430	80504192 (859, 860)	Novel Protein sm. GBank gJ1826lpjS22897 - extensin - Vohox coded (fm domain)		reductase		264508, 264905, 264509, 264900, 264900, 264900, 264508, 264900, 264887, 264769, 264689, 264636, 264639, 1810895, 264486
431	20524249 (861, 862)	Novel Protein sm. GBank gJ132552jenuCXA186091 - (A1022578) dJ93P12.2 (hypothetical) Promote-100 protein				264596
432	16525372 (863, 864)	Novel Protein sm. GBank K1A0259 (LKE) [Homo sapiens]				265020
433	81494303 (865, 866)	Novel Protein sm. GBank gJ2465272lpjQ8595CDX2_HUMAN - HOMEOROX PROTEIN CDX-2 (CAUDAL-TYPE HOMEOROX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED		264907, 264908, 264900, 264910, 264952, 264955, 264758, 264604, 264760, 264762, 264763, 264638, 264637, 22279002
434	94326323 (867, 868)	Novel Protein sm. GBank gJ114105lpjP04532ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH				53812038, 56182181, 55811562, 29331828, 35896052, 55810764, 55811576, 85274791, 35895855, 60432113, 55811150, 264636, 264766
435	80502738 (869, 870)	Novel Protein sm. GBank		transport		264955, 264769
436						
437	41055953 (871, 872)			UNCLASSIFIED		265020, 22279002
438	11395201 (873, 874)			UNCLASSIFIED		264593
439	11716335 (875, 876)			UNCLASSIFIED		264686
439	80014495 (877, 878)	Novel Protein sm. GBank gJ3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]				264905, 264600, 264602, 264604
440	79841082 (879, 880)	Novel Protein sm. GBank gJ23222jgplAA65351.1 - (AF016427) Contains similarity to Ham domain, PF00004 (AAA), Score=268.1, E-value=3.7e-77, N=1 (Caenorhabditis elegans)	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)	-ATPase _associated		35896052, 264905, 264908, 264809, 265011, 35896423
441	20396935 (881, 882)	Novel Protein sm. GBank gJ553946lpjP04532ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH				264605
442	85281058 (883, 884)	Novel Protein sm. GBank gJ1184790 (U46068) - von Ebner primary gland protein [Mus musculus]		UNCLASSIFIED		29331830, 264909
443	82456427 (885, 886)	Novel Protein sm. GBank gJ553946lpjP04532ARAH_ECOLI - (A110732) putative ATP-binding RNA helicase		UNCLASSIFIED		35896052, 264908, 264906, 264906, 264912, 264604, 264762, 264769, 264689, 264636
444	11395597 (887, 888)	Novel Protein sm. GBank gJ1733249lpjP04532ARAH_ECOLI - (D33029) homologous to citrate-sodium symport (citrate transporters), [Dydimetrical] [Bacillus subtilis]		UNCLASSIFIED		264591

445	70542709 (889, 890)	Novel Protein sim. GBank gll5531272jemb(CAB50897.1) - (A24360D) XSCA homologue (Myxeromyces acid)		UNCLASSIFIED	264693
446	78610337 (891, 892)	Novel Protein sim. GBank gll5361915 (L36319) - zinc finger			264509
447	80433888 (893, 894)	Novel Protein sim. GBank gll542914jemb(CAB02185) - (Z00108) [Myxeromyces acid]	Contains protein domain (PF00096): Zinc finger, C2H2 type	transcription factor	264768, 55811576
448	80233810 (895, 896)	Novel Protein sim. GBank gll542914jemb(CAB02185) - (Z00108) [Myxeromyces acid]	Contains protein domain (PF00051): Family transferase	dehydrogenase	264508, 264600, 264603, 264605, 264682, 264768, 18103382, 264634, 18103387
449	20460334 (897, 898)	Novel Protein sim. GBank gll187046jpt0443JDP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264605, 264559
450	94631210 (899, 900)	Novel Protein sim. GBank gll4589505jbjBAAT7675.1) - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481): Protein phosphatase 2C	phosphatase	65274572, 22278898, 26331824, 26331826, 264906, 264910, 264932, 35846317, 265017, 21908707, 55811957, 36526486, 22779002
451	21433503 (901, 902)			UNCLASSIFIED	264486
452	10287216 (903, 904)			UNCLASSIFIED	264992
453	52560056 (905, 906)	Novel Protein sim. GBank gll2650614 (AE001104) - conserved hypothetical protein [Aeromonas hydrophila]		UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gll246300jgq09490SCOT_CAEEL - PROBABLE SUCCINYL-COA-3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOXOIC COA-TRANSFERASE)		transferase	264603
455	13096892 (909, 910)			UNCLASSIFIED	264687
456	78563081 (911, 912)	Novel Protein sim. GBank gll4468609jemb(CAB38153.1) - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264691
457	78931273 (913, 914)	Novel Protein sim. GBank gll3411033 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]		UNCLASSIFIED	264905
458	78481227 (915, 916)	Novel Protein sim. GBank gll4589505jbjBAAT7675.1) - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00595): PDZ domain (Also known as DHR or GLGF)	kinase	55812038, 265010, 265018, 264681
459	80567355 (917, 918)	Novel Protein sim. GBank gll4589505jbjBAAT7675.1) - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00130): Phosphoesterase/glycosyl binding domain (C1 domain)	kinase	22278897, 264258, 26331828, 265018, 264448, 264369, 21908705, 35866423
460	78245806 (919, 920)	Novel Protein sim. GBank gll1131595jpt2516ACG1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDROLYASE 1) (ACONITASE 1)		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gll1048741jpt4246JATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33587023, 264559

462	79605589 (923, 924)	Novel Protein sim. GBank gjl13468911apP45597jTf1_XANCP... MILTIPOSPHOXYL TRANSFER PROTEIN CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM ENZYME II) PHOSPHOCARRIER PROTEIN HPR PROTEIN H) PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT	Contains protein domain (PF00381) - PEP-utilizing enzymes	UNCLASSIFIED	264807
463	79786417 (925, 926)	Novel Protein sim. GBank gjl8540651emb(CA58337) - (X834.13) U88 [Human herpesvirus 6]		UNCLASSIFIED	264805, 264806, 264808, 264909, 264910, 264591, 264595, 265011, 264832, 264635, 264636, 264637, 264638, 264639
464	82340151 (927, 928)	Novel Protein sim. GBank gjl5689776jmb(CAB82137.1) - (A1242332) calpain (Homo sapiens)	Contains protein domain (PF00648) Calpain family cysteine protease	UNCLASSIFIED	265017, 21904764, 265020
465	83005730 (929, 930)	Novel Protein sim. GBank gjl1806175jmb(CAB06470) - (ZK4395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain	UNCLASSIFIED	264605, 264559
466	20460945 (931, 932)	Novel Protein sim. GBank gjl547051apP38949jRESB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	264764
467	80406035 (933, 934)	Novel Protein sim. GBank gjl2114024jmb(CAB08957) - (ZK45589) gpcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	264692
468	52562208 (935, 936)	Novel Protein sim. GBank gjl2039459jmb(CAA17347) - (AL021929) coqQ [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
469	19520527 (937, 938)	Novel Protein sim. GBank gjl149211HP174jBRET_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		UNCLASSIFIED	264602, 264769
470	80502756 (939, 940)	Novel Protein sim. GBank gjl149211HP174jBRET_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		UNCLASSIFIED	265019
471	17937351 (941, 942)	Novel Protein sim. GBank gjl862343 (L10908) - Grap1 gene product [Mus musculus]		UNCLASSIFIED	264598, 264683, 264557
472	80047458 (943, 944)	Novel Protein sim. GBank gjl862343 (L10908) - Grap1 gene product [Mus musculus]		UNCLASSIFIED	264368
473	20558793 (945, 946)	Novel Protein sim. GBank gjl862343 (L10908) - Grap1 gene product [Mus musculus]		UNCLASSIFIED	22278997, 264692, 264288
474	80533363 (947, 948)	Novel Protein sim. GBank gjl862343 (L10908) - Grap1 gene product [Mus musculus]		UNCLASSIFIED	264607, 264508, 264511, 265009, 264762, 264448, 264638, 264638
475	82454665 (949, 950)	Novel Protein sim. GBank gjl862343 (L10908) - Grap1 gene product [Mus musculus]		UNCLASSIFIED	65274572, 60432049, 264259, 264508, 2644045, 55812038, 264758, 265011, 264284, 264666, 52644229, 65274791, 264638, 264566
476	94143857 (951, 952)	Novel Protein sim. GBank gjl545656jrefNP_008229.1pCAC1 - gioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00569) Leucine Rich Repeat	UNCLASSIFIED	264638
477	79175833 (953, 954)	Novel Protein sim. GBank gjl127551 (U18939) - orf2 [Batrachococcus balatensis]		UNCLASSIFIED	264693
478	79533483 (955, 956)	Novel Protein sim. GBank gjl127551 (U18939) - orf2 [Batrachococcus balatensis]		UNCLASSIFIED	264686, 35859555, 265008, 264831, 264910, 264632, 264638, 265018, 264599, 264909
479	80168746 (957, 958)	Novel Protein sim. GBank gjl127551 (U18939) - orf2 [Batrachococcus balatensis]		UNCLASSIFIED	264369
480	79390729 (959, 960)	Novel Protein sim. GBank gjl127551 (U18939) - orf2 [Batrachococcus balatensis]		UNCLASSIFIED	264693
481	79624578 (961, 962)	Novel Protein sim. GBank gjl4063042 (AF088085) - GP900; mucin-like glycoprotein (Cyrtosporidium parvum)		UNCLASSIFIED	264909, 264696, 264764, 264693, 55811576, 55182233, 18108395
482	83050611 (963, 964)	Novel Protein sim. GBank gjl4063042 (AF088085) - GP900; mucin-like glycoprotein (Cyrtosporidium parvum)		UNCLASSIFIED	

483	20293306 (965, 966)	Novel Protein sim. GBank gl 21043303[emb] (A008632) - (Z95387) hypothetical protein RV2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00634) - Glycosyl transferases group 1	264600
484	11618046 (967, 968)	Novel Protein sim. GBank gl 3450883 (AF083334) - Ibroin [Antheraea pernyi]	UNCLASSIFIED	264594
485	80191234 (969, 970)	Novel Protein sim. GBank gl 5042272[emb] (CA944526.1) - (A078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	UNCLASSIFIED	264604
486	80056042 (971, 972)	Novel Protein sim. GBank gl 5042272[emb] (CA944526.1) - (A078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase	264604
487	11813339 (973, 974)	Novel Protein sim. GBank gl 574778[emb] (KAC53522.2) - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain	264638
488	91222383 (975, 976)	Novel Protein sim. GBank gl 574778[emb] (KAC53522.2) - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain	264638
489	10867710 (977, 978)	Novel Protein sim. GBank gl 3882223[emb] (BA344471.1) - (AB018294) KIAA0751 protein [Homo sapiens]	kinase	264639
490	95381124 (979, 980)	Novel Protein sim. GBank gl 82091[emb] (A25494) - hydroxyproline-rich glycoprotein - tomato (fragment)	collagen	264639
491	80495412 (981, 982)	Novel Protein sim. GBank gl 2894205[emb] (CAA17072) - (AL021840) hypothetical protein RV3258c [Mycobacterium tuberculosis]	collagen	264639
492	87421264 (983, 984)	Novel Protein sim. GBank gl 5262605[emb] (CAB46743.1) - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264600
493	11659242 (985, 986)	Novel Protein sim. GBank gl 5262605[emb] (CAB46743.1) - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264638
494	87726604 (987, 988)	Novel Protein sim. GBank gl 5262605[emb] (CAB46743.1) - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264638
495	80025599 (989, 990)	Novel Protein sim. GBank gl 2791517[emb] (CAA16054) - (AL021840) hypothetical protein RV2477c [Mycobacterium tuberculosis]	transport	264638
496	76984624 (991, 992)	Novel Protein sim. GBank gl 230281[emb] (R59) - 434 Repressor (Amino-Terminal Domain) (R1-69)	ABC transporter	264602, 264682, 264638
497	76948661 (993, 994)	Novel Protein sim. GBank gl 129736[sp]P28225[PDH, EC001 - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMIP OXIDASE)]	Contains protein domain (PF01381) - Helix-turn-helix	264601, 265021
			oxidase	265006

488	88095488 (995, 996)	Novel Protein sim. GBank gII1145789 (U41662) - neuroigin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	264259, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264591, 33657402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264784, 264766, 264767, 264768, 264687, 264789, 21906787, 33657023, 264693, 264628, 264625, 35696423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264564, 264565, 264566, 264567
489	20438222 (997, 998)	Novel Protein sim. GBank gII97480[gII19739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (999, 1000)	Novel Protein sim. GBank gII6782250[embjCAB52363.1] - (AL109747) putative integral membrane protein		UNCLASSIFIED	264605
501	13418034 (1001, 1002)	Streptomyces coelicolor A3(2)		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gII4468678[embjCAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278896, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)	Novel Protein sim. GBank gII4033509[gP02598]CALM - TETPY - CALMODULIN		UNCLASSIFIED	264564
504	10887321 (1007, 1008)	Novel Protein sim. GBank gII2501069[gP046127]SYW, CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)	Contains protein domain (PF00036) - EF hand	UNCLASSIFIED	264687
505	95003068 (1009, 1010)	Novel Protein sim. GBank gII466068[gP134618]Y082 CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264369
506	16454292 (1011, 1012)			UNCLASSIFIED	265010
507	20451598 (1013, 1014)			UNCLASSIFIED	264604
508	76841424 (1015, 1016)			UNCLASSIFIED	264908
509	11776386 (1017, 1018)			UNCLASSIFIED	264638
510	83373465 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16252578 (1021, 1022)			UNCLASSIFIED	265007
512	20399484 (1023, 1024)			UNCLASSIFIED	264565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gII2497419[gP15635]Y4RB, RHIN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB			
514	79913805 (1027, 1028)	Novel Protein sim. GBank gII1278687 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - cyclin Cyclin	cyclin	264683, 264688, 35696423, 264639
515	79462591 (1029, 1030)	Novel Protein sim. GBank gII1184730 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264609
516	9862020 (1031, 1032)	Novel Protein sim. GBank gII2274400[gP1565770 - maltoliposylfuranolase trehalohydrolase - Arthrobacter sp. (strain Q36)		amylase	22278999, 264690
					264910

517	95202994 (1033, 1034)	Novel Protein sim. GBank gl293605 (AE00729) - ribose 5 phosphate isomerase B [<i>Quilax zeolitus</i>]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gl83403jemlCAA563371 - (K23413) Ube [<i>Human herpesvirus 6</i>]		UNCLASSIFIED	264487
519	91677688 (1037, 1038)	Novel Protein sim. GBank gl5689595j6lAA63073.11 - (A0024075) 1120 [<i>Homo sapiens</i>]	Contains protein domain (PF01388) ARD DNA binding domain	-dna_mg_bind	52644507, 22276997, 22276986, 60432048, 264259, 52645060, 29331824, 66714117, 60424269, 29331826, 35696052, 264905, 29331830, 66712502, 264511, 265007, 264591, 60432228, 33657402, 60433438, 21906754, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21906765, 21906766, 21906767, 21906769, 265021, 80170615, 33657023, 264692, 52645128, 33657109, 27486262, 27486264, 35695763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56526486, 60432113
520	79669188 (1039, 1040)	Novel Protein sim. GBank			264769
521	11076821 (1041, 1042)	gl1189126lp46839CITPA_MYCLE - CATION-TRANSPORTING CBTPE ATPASE A		transport	264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gl1172669lp4432jBRSK_HAEIN - RIBOKINASE	Contains protein domain (PF00294) PKB family carbohydrate kinase	-kinase	264905, 264768
523	183556013 (1045, 1046)	Novel Protein sim. GBank gl2132243ipr1561028 - hypothetical protein YP_2336c - yeast [<i>Saccharomyces cerevisiae</i>]		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gl4033608dbjAA351581 - (AB012308) B2HC [<i>Anthracinus crassipalpis</i>]		ATPase-associated	264092, 264596, 265011
525	79810046 (1049, 1050)	Novel Protein sim. GBank gl4106610jemlCAA213651 - (A021866) ORF42, 600-389 aa, similarity to an phosphotransferase, in P9397 <i>Sulfolobus solfataricus</i> , (401 aa), 33, 1% identity in 393 aa overlap, Pstia scores: 94-488, E(1) 8.5e-24, in Q64602 <i>R. norvegicus</i> (425 aa), 28.8% ident...		UNCLASSIFIED	264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gl10869lp24219JUXA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	264758
527	80504728 (1053, 1054)	Novel Protein sim. GBank		UNCLASSIFIED	264769
528	85484134 (1055, 1056)	Novel Protein sim. GBank gl42144jemlCAA252001 - (X00313) NusA protein (nusA) [<i>Escherichia coli</i>]		UNCLASSIFIED hydrolase	56182575, 265017, 265018, 265019
529	17795810 (1057, 1058)	Novel Protein sim. GBank		UNCLASSIFIED	264687
530	10887338 (1059, 1060)	gl7310869lp24219JUXA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
531	80726576 (1061, 1062)	Novel Protein sim. GBank gl42144jemlCAA252001 - (X00313) NusA protein (nusA) [<i>Escherichia coli</i>]		UNCLASSIFIED	264488, 264490, 264491, 264492, 264760, 265021, 264690, 263976, 264558
532	80533444 (1063, 1064)	Novel Protein sim. GBank gl5262640jemlCAA45758.11 - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00692) SPRY domain	UNCLASSIFIED	

533	876175133 (1065, 1066)	Novel Protein sim. GBank gi44833336p AAD31593.1 AF11229 - (AF11229) integral nucleon membrane protein MAAT1 [Homo sapiens]			284907, 284909, 284766, 35695917, 2846330, 2846955
534	82368264 (1087, 1088)	Novel Protein sim. GBank gi23953522p rm CA04066.1 - AJ001205 PEP1 [Streptomyces coelicolor]		UNCLASSIFIED	284905, 285011, 284601, 284602, 284605, 284762, 284766, 285020, 284693, 284636 284906
535	79641850 (1068, 1070)	Novel Protein sim. GBank gi3976536p rm CAA88653.1 (249123) similar to cAMP-dependent protein kinase cDNA EST iEMBL1100719 comes from this gene; cDNA EST YK46508.3 comes from this gene; cDNA EST YK46508.5 comes from this gene; cDNA EST YK49214.3 comes from this gene; cDNA EST Y...	Contains protein domain (PF00689) Eukaryotic protein kinase domain	ATPase-associated	
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi24956282p sp 55737 YOH_L SERMA - HYPOTHETICAL 10.1 K D PROTEIN IN BIOA 5 REGION		reductase	18108376, 284905, 284906, 284907, 284909
537	94147448 (1073, 1074)	Novel Protein sim. GBank			285000, 284605, 65274781
538	87821963 (1075, 1076)	gi134920p sp P1987 ISSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 182 (SSG 185)	Contains protein domain (PF00599). PDZ domain (Also known as DHR or GLGF).	collagen	293331822, 29331824, 29331825, 29331826, 293331827, 284908, 52640405, 33657402, 285017, 284762, 284693, 284288, 284685, 21906765, 35985763, 284558, 60170394, 284559, 22279002
539	28396266 (1077, 1078)	Novel Protein sim. GBank gi2498433p Q1234 1HAT1_YEAST - HISTONE ACETYLTRANSFERASE		histone	284602, 285019
540	76837077 (1079, 1080)	Novel Protein sim. GBank gi3882241p BAX34480.1 - (Novel)	Contains protein domain (PF00069). Zinc finger, C2H2 type	transcript factor	284693
541	87763268 (1081, 1082)	gi1803033 KIAA07650 protein [Homo sapiens]			18108394, 22278997, 22278998, 264239, 284112, 285009, 33657402, 5812038, 52646317, 285017, 21906765, 284693, 55911576, 284635, 56528486, 284589
542	95285838 (1083, 1084)	Novel Protein sim. GBank gi5042272p rm CAB44528.1 - (AL078618) ruoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	284910, 285018, 284669, 284639, 284486
543	79786290 (1085, 1086)	Novel Protein sim. GBank gi2791398p rm CAA15994.1 (AL021184) hypothetical protein Rv1484 [Mycobacterium tuberculosis]		UNCLASSIFIED	284602, 284908
544	20437191 (1087, 1088)	Novel Protein sim. GBank		UNCLASSIFIED	284605
545	80434504 (1089, 1090)	Novel Protein sim. GBank			284769, 284634, 284907, 284592, 284909
546	80249016 (1091, 1092)	gi488721 pbp AAD32237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]			284600, 284602, 21906765
547	11075663 (1093, 1094)	Novel Protein sim. GBank gi1350855p P19176 PPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT)		mapolymerase	284604
548	82114936 (1095, 1096)	Novel Protein sim. GBank gi3230021 AF1019205 - knoxin- related protein, KRP-Cest2a2 [Drosophila melanogaster]		UNCLASSIFIED	284488, 284908, 52640405, 284760, 284693, 284639, 284583, 284564

549	95421904 (1097, 1098)	Novel Protein sim. GBank g14337460jg AAD18133 - (AF026195) neuroblastoma-amplified protein [Homo sapiens]	UNCLASSIFIED	284488, 55274572, 18108388, 22278995, 22278996, 22278997, 22278998, 22278999, 284259, 29331824, 66714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 284592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 284764, 284369, 284288, 284766, 284688, 284688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52645129, 33657109, 27486281, 27486262, 27486264, 33657349, 55811576, 18108387, 60432113, 22279002
550	10866616 (1099, 1100)	Novel Protein sim. GBank	UNCLASSIFIED	284688
551	80439990 (1101, 1102)	g13122833p P49851SYFB_MYCTU - PHENYLALANINE--TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PIERS)	UNCLASSIFIED	284908, 264909, 264768
552	94573870 (1103, 1104)	Novel Protein sim. GBank	UNCLASSIFIED	284689, 284639, 264563
553	80106002 (1105, 1106)	Novel Protein sim. GBank protein Drosophila melanogaster	glycoprotein	55811957, 284628
554	78619378 (1107, 1108)	g1501971jg AAD37857_1 AF13326 - (AF13326) histidine protein kinase-response regulator hybrid protein CysSY [Pseudomonas syringae pv. syringae]	kinase	284906
555	78965347 (1109, 1110)	Novel Protein sim. GBank g1131515p P29089 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	transport	284762
556	20457127 (1111, 1112)	Novel Protein sim. GBank g13914014p P4390JMPD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	transcription factor	284508, 264602, 264559
557	19523408 (1113, 1114)	Novel Protein sim. GBank g1502273j em CAG444827.1 - (AL076818) nuc. NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase	284488
558	20724429 (1115, 1116)	Novel Protein sim. GBank g11709339p P45331 METE_HAEIN - 5-METHYLTHIAHYDROPTEROYLTRIGLYCINAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)	UNCLASSIFIED	284602
559	80084353 (1117, 1118)	Novel Protein sim. GBank g14980567jg AAD35173_1 AE00169 - (AE00169) iron(III) ABC transporter, permease protein [Thermotoga maritima]	UNCLASSIFIED	284634

560	80066533 (1119, 1120)	Novel Protein sim. GBank glt492595p[Q5193]Y41TR, RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y41TR	Contains protein domain (PF00003) - ABC transporter	transport	18108396, 264906, 264602, 264604, 19103374
561	20293187 (1121, 1122)			UNCLASSIFIED	264600
562	11689161 (1123, 1124)			UNCLASSIFIED	264603
563	79761420 (1125, 1126)	Novel Protein sim. GBank glt404925 (AF042276) - poly(hydroxycarboxylate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	264910, 264691
564	56716390 (1127, 1128)	Novel Protein sim. GBank glt792310 (AF040570) - unknown [Amycolatopsis mediterranei]	dehydrogenase		264592
565	56465616 (1129, 1130)	Novel Protein sim. GBank glt449294p[gb]BA32462 - [AB011532] MEGF8 [Rattus norvegicus]	Contains protein domain (PF00009) - EGF-like domain	synthase	265010
566	94323886 (1131, 1132)	Novel Protein sim. GBank glt453958p[gb]CA33487.1] - (A1035636) putative helicase [Streptomyces coelicolor]		helicase	264908, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264605, 264768, 264687, 264689, 36695917, 264693, 55274620, 264446
567	79560955 (1133, 1134)	Novel Protein sim. GBank glt100506p[gl]S17455 - Melate dehydrogenase (oxalacetate-decarboxylating) (NADP+)	Contains protein domain (PF00390) - Malic enzyme	UNCLASSIFIED	264689
568	94681793 (1135, 1136)	Novel Protein sim. GBank glt915843p[Q31212]RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	dehydrogenase	264689
569	39506897 (1137, 1138)	Novel Protein sim. GBank glt115122p[gl]P21627BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		ribosomal prot.	264565
570	78757827 (1139, 1140)	Novel Protein sim. GBank glt115122p[gl]P21627BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		UNCLASSIFIED	18108376, 18108387, 264585
571	79793961 (1141, 1142)			transport	264907, 264909
572	36566638 (1143, 1144)	Novel Protein sim. GBank glt453923p[gb]CA539881.1] - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	264762
573	20715521 (1145, 1146)			UNCLASSIFIED	265007, 264601
574	13521592 (1147, 1148)	Novel Protein sim. GBank glt118794p[gl]P10443JOP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN			
575	13076416 (1149, 1150)			polymerase	264636 264657
576	20482246 (1151, 1152)	Novel Protein sim. GBank glt545762p[gb]CA549116.1] - (AJ248283) PAB2227 [Pyrococcus abyssi]			264605
577	86727102 (1153, 1154)	Novel Protein sim. GBank glt504227p[gb]CA544528.1] - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 kd subunit	dehydrogenase	35696052, 264636
578	11804477 (1155, 1156)	Novel Protein sim. GBank glt723081p[gl]Q11046[Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	264638
579	11794723 (1157, 1158)				264682, 264556

580	80059417 (1159, 1160)				2227899, 3669052, 264555, 264556, 264558
581	79230833 (1161, 1162)	Novel Protein sim. GBank gl 23243131 (AF045777) - Ilin	Contains protein domain (PF00047)	UNCLASSIFIED	
582	80048617 (1163, 1164)	Novel Protein sim. GBank gl 25011825 (P77726)VAR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CTOE INTERGENIC REGION	Immunoglobulin domain	struct	265008, 264564
583	79321392 (1165, 1166)	Novel Protein sim. GBank gl 3882221 (dbj BA34470.1) - (AB018293) KIAA0735 protein (Homo sapiens)		transport	264594
584	76944024 (1167, 1168)	Novel Protein sim. GBank gl 4487250 (emb CA83757) - (AF035669) probable obu-RNA Gm amidotransferase		UNCLASSIFIED	264485, 264906, 264766, 264687, 36690423
585	79581454 (1169, 1170)	Novel Protein sim. GBank gl 5608519 (dbj BA33043.1) - (AB023014) KUA1091 protein (Homo sapiens)		UNCLASSIFIED	265015, 264684, 21906769
586	36277486 (1171, 1172)	Novel Protein sim. GBank gl 4487250 (emb CA83757) - (AF035669) probable obu-RNA Gm amidotransferase		UNCLASSIFIED	264905, 265007
587	80497359 (1173, 1174)	Novel Protein sim. GBank gl 5608519 (dbj BA33043.1) - (AB023014) KUA1091 protein (Homo sapiens)		hydrolase	264600, 264602, 264605, 264766, 264690, 264557
588	79557238 (1175, 1176)			UNCLASSIFIED	265020, 264692
589	79005828 (1177, 1178)			UNCLASSIFIED	2227899, 264907, 264909, 264510, 265009, 265010, 264687, 264766, 36695917, 18108376, 264634, 264638, 264838
590	79515628 (1179, 1180)	Novel Protein sim. GBank gl 2143293 (emb CA809390) - (Z95972) p98b [Mycobacterium tuberculosis]		UNCLASSIFIED	264906, 264909
591	10313540 (1181, 1182)	Novel Protein sim. GBank gl 2143293 (emb CA809390) - (Z95972) p98b [Mycobacterium tuberculosis]		mapolymerase	264691
592	13389763 (1183, 1184)	Novel Protein sim. GBank gl 4511983 (gb AA021543.1) - (AF08896) electrotransfer ubiquinone oxidoreductase			
593	82248659 (1185, 1186)	Novel Protein sim. GBank gl 2172388 (U51896) - LgE [Cymodons modis]		MHC	263972
594	20212392 (1187, 1188)	Novel Protein sim. GBank gl 2172388 (U51896) - LgE [Vibrio parahaemolyticus]		dehydrogenase	264511, 264762, 264766, 264488
595	10064064 (1189, 1190)	Novel Protein sim. GBank gl 131460 (p 20869)PTB_ECOLI - PTS SYSTEM, (FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)		UNCLASSIFIED	264605
596	13085178 (1191, 1192)				264769
597	80259023 (1193, 1194)				
598	34140026 (1195, 1196)				
599	20385137 (1197, 1198)	Novel Protein sim. GBank gl 125329 (p P04910)SB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) [CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE] (CKS)		UNCLASSIFIED	264636
600	10357663 (1199, 1200)			UNCLASSIFIED	264592
601	79610044 (1201, 1202)	Novel Protein sim. GBank gl 217414 (p P150064 - Hypothetical protein 2 - Corynebacterium glutamicum		UNCLASSIFIED	264755, 59810764, 264555, 264556, 264637, 83373044
				UNCLASSIFIED	264603
				UNCLASSIFIED	264606
				UNCLASSIFIED	264510

602	78250602 (1203, 1204)	Novel Protein sim. GBank gll3522961gblAAC3424.11 - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	265007
603	11466067 (1205, 1206)			UNCLASSIFIED	264595
604	81675420 (1207, 1208)			UNCLASSIFIED	264758
605	20436657 (1209, 1210)	Novel Protein sim. GBank gll1753221gplP4917V883_HAEIN - HYPOTHETICAL PROTEIN H10883		UNCLASSIFIED	264605
606	80334382 (1211, 1212)	Novel Protein sim. GBank gll5020264lgb/AAD38043.1AF15138 - (AF151383) Cdb42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264764
607	95361506 (1213, 1214)	Novel Protein sim. GBank gll188864 (MTA027) - mucin [Homo sapiens]		UNCLASSIFIED	264608, 264906, 86585542, 264682, 264687, 264689, 264534, 18103376, 35968423, 264636, 264555, 264638
608	11810888 (1215, 1216)	Novel Protein sim. GBank gll2496701gplP5552Y4LL_RHSIN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605
609	80064775 (1217, 1218)			UNCLASSIFIED	264682
610	79629413 (1219, 1220)			UNCLASSIFIED	264682
611	87588205 (1221, 1222)			UNCLASSIFIED	264605
612	95287851 (1223, 1224)	Novel Protein sim. GBank gll1877386jmb/CAB07118 - (Z0272) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264600, 264601, 264604, 264769, 264558, 264565
613	7523475 (1225, 1226)	Novel Protein sim. GBank gll5114231gblAAD40238.1AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		UNCLASSIFIED	264359
614	79869348 (1227, 1228)	Novel Protein sim. GBank gll1339650jdb/BAAT2741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boyanum]		kinase	18100372, 264563
615	39286996 (1229, 1230)	Novel Protein sim. GBank gll5443671gplP35673GALE_ERVAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gll2498097gplQ80769TNF3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	isomerase	264605
617	81227222 (1233, 1234)			Inf	52645156, 21906765, 35969423, 21906768, 21906769, 22278994, 35969286, 22278996, 285020, 265021, 265007, 265008, 264636, 52644150, 33657023, 264692, 264693, 29331822, 29331824, 59812038, 83373044, 56182181, 60424269, 66714117, 29331825, 33657108, 29331826, 33657182, 29331827, 35696052, 29331828, 21486262, 33657349, 56526486, 265018, 265019, 22279002, 264482, 264448, 29331930, 66712502, 264609

618	20632843 (1235, 1236)	Novel Protein sim. GBank g 1545938 emb CAB50746.1 - (AL06639) putative aminotransferase (Streptomyces coelicolor)		isomerase	264603
619	91227224 (1237, 1238)				56984075, 29331826, 33556970, 265008, 33657402, 33109594, 87165599, 264448, 18108374, 83373844, 23140488, 264736, 264369, 2914627
620	81183143 (1239, 1240)	Novel Protein sim. GBank g 464335 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	
621	80239251 (1241, 1242)	Novel Protein sim. GBank g 2633357 emb CAB13069 - (Z59110) yJcf [Bacillus subtilis]		UNCLASSIFIED	264556, 264558, 264639
622	20455427 (1243, 1244)	Novel Protein sim. GBank g 1857710 gb AA048432 - (U87224) contactin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) Laminin G domain	UNCLASSIFIED	264605
623	10131796 (1245, 1246)	Novel Protein sim. GBank g 1705703 sp P2225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCCK		laminin	264606
624	19534127 (1247, 1248)	Novel Protein sim. GBank g 1705703 sp P2225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCCK		cytochrome	264596
625	13084619 (1249, 1250)	Novel Protein sim. GBank g 2684252 emb CAA17114.1 - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688
626	88062603 (1251, 1252)	Novel Protein sim. GBank g 165923 sp P32323 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264605, 264906, 33657023, 33657109, 264936
627	80255457 (1253, 1254)	Novel Protein sim. GBank g 1008418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635
628	80077096 (1255, 1256)	Novel Protein sim. GBank g 1711543 sp P05296 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) Eukaryotic protein kinase domain	kinase	264600
629	79851602 (1257, 1258)	Novel Protein sim. GBank g 1143294 (U34305) - ORF2. Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264606, 264607
630	39565156 (1259, 1260)	Novel Protein sim. GBank g 3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490
631	20598718 (1261, 1262)	Novel Protein sim. GBank g 140687 sp P11666 YSGB_ECQL - HYPOTHETICAL 30.9 KD PROTEIN IN SBM.FBA INTERGENIC REGION (ORF 4) (F286)			263978
632	27843890 (1263, 1264)			UNCLASSIFIED	264606, 264600, 264605, 264769, 264699, 264486
633	80477772 (1265, 1266)			UNCLASSIFIED	264769
634	17938906 (1267, 1268)			UNCLASSIFIED	265019
635	79574506 (1269, 1270)			UNCLASSIFIED	264689
636	79910981 (1271, 1272)			UNCLASSIFIED	264596, 264762, 264693

637	82455796 (1273, 1274)	Novel Protein sim. GBank g[i]2326739[mbiCAB10953] - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264782, 264766, 264687, 264769, 264689, 35695917, 264683, 264634, 264638, 264559, 18108395, 264636
638	14997457 (1275, 1276)	Novel Protein sim. GBank g[i]4678662[mbiCAB41074.1] - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]		struct	264112, 263974
639	80204210 (1277, 1278)	Novel Protein sim. GBank g[i]4586628[biBA76836.1] - (AB023209) KIAA0992 protein [Homo sapiens]		transpolymerase	265009, 265010
640	17929579 (1279, 1280)	Novel Protein sim. GBank g[i]1432083 (U60951) - homolog to Skp1p, an evolutionarily conserved klotochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	UNCLASSIFIED	264693
641	79635398 (1281, 1282)			UNCLASSIFIED	264693
642	19888737 (1283, 1284)			UNCLASSIFIED	264693
643	81516220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264564
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	95010807 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069683 (1291, 1292)			UNCLASSIFIED	264595, 264566
647	80257085 (1293, 1294)	Novel Protein sim. GBank g[i]507613[ecfNP_003738.1]TNKS - TANKYASE	Contains protein domain (PF00023) - Ank repeat	transcript factor	264909, 264581
648	80077428 (1295, 1296)	Novel Protein sim. GBank g[i]1044963[bsb169646 - protamine [Monodelphis domestica, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank g[i]1346916[spP12863]PURA, ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)		UNCLASSIFIED	264602, 264638
652	85516704 (1303, 1304)	Novel Protein sim. GBank g[i]130327[spP26647]PLSC, ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)		UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)	Novel Protein sim. GBank g[i]172971[spP10638]O3C, MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278986, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	95010589 (1307, 1308)	Novel Protein sim. GBank g[i]130327[spP26647]PLSC, ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - Acyltransferase	UNCLASSIFIED	264906, 264595, 264632
655	79320692 (1309, 1310)			transerase	264592
656	80416739 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264766, 264681
657	20611010 (1313, 1314)			UNCLASSIFIED	264557, 264558

658	87716151 (1315, 1316)	Novel Protein sim. GBank gji5589493[dbj BA83030.1] - (A0209001) KIAA1078 protein [Homo sapiens]		UNCLASSIFIED	22278696, 60432049, 29331822, 29331824, 29331843, 265007, 265009, 33657402, 33657084, 265017, 264448, 21900765, 21900766, 263967, 20281149, 16108370, 16108374, 264482
659	87716665 (1317, 1318)	Novel Protein sim. GBank gji2137972[dbj A8724 - zinc finger protein PZF - mouse	Contains protein domain (PF00056) Zinc finger, C2H2 type	transcript/factor	22278899, 60432049, 66714117, 29331827, 265007, 264166, 56161562, 16108359, 16108365, 16108370, 16108381
660	81897922 (1319, 1320)	Novel Protein sim. GBank gji134180[dbj F1401]SACY, BACSU - LEVANSUCRASE	Contains protein domain (PF00874)	UNCLASSIFIED	284737
661	80026923 (1321, 1322)	Novel Protein sim. GBank gji1652848[dbj BA317766] - ANTIMETABOLITE	Transcriptional antiemulator ovg family	UNCLASSIFIED	284604, 284605, 33833985, 16108376, 284636, 16108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gji4545229[dbj A022450, j1AF11618 - (AF116183) SecA homolog [Acetobacterium aceti] (complanatum)		UNCLASSIFIED	284605
663	20626860 (1325, 1326)	Novel Protein sim. GBank gji5589250[dbj BA828431.1] - (A024335) similar to orf5 [Comamonas testaceorum]		dehydrogenase	284605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gji1652848[dbj BA317766] - (D09059) DNA photolyase [Synecococcus sp.]		UNCLASSIFIED	284769
665	80079053 (1329, 1330)	Novel Protein sim. GBank gji11684156[dbj P21640]COBL PSEDE - PRECORIN-3B C17 METHYLTRANSFERASE (PRECORIN-3 METHYLTRANSFERASE) (PRECORIN-3 METHYLASE)		isomerase	284600
666	79603142 (1331, 1332)	Novel Protein sim. GBank gji3261339[dbj CAB109271 - (298250) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	284907, 265507
667	94631002 (1333, 1334)	Novel Protein sim. GBank gji5588851[dbj BA82702.1] - (A017438) Odf5 [Stegomyia albopictus]		UNCLASSIFIED	284686, 284602, 284593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gji3581853[dbj CAA2009 - (A031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) Ribosomal protein L20		284605, 284906, 284908, 284600, 284601, 284603, 284605, 284760, 284689, 284636, 284638, 284639
669	12967154 (1337, 1338)	Novel Protein sim. GBank gji2583251 (AF026444) 2- isopropylmalate synthase [Streptomyces coelicolor]		UNCLASSIFIED	284637
670	80238549 (1339, 1340)	Novel Protein sim. GBank gji2114430 (U82703) - Olf1 (EBF- like-3 transcription factor) [Mus musculus]	Contains protein domain (PF00023) Atk repeat	synthase	284905, 284906, 284908, 284601, 284762, 284766, 284689, 284638, 16108385, 284485
671	79601368 (1341, 1342)	Novel Protein sim. GBank gji1652848[dbj BA317766] - (D09059) DNA photolyase [Synecococcus sp.]	Contains protein domain (PF00023) Atk repeat	UNCLASSIFIED	284690, 284692, 284693, 284636, 16108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gji2114430 (U82703) - Olf1 (EBF- like-3 transcription factor) [Mus musculus]		transcript/factor	284910, 265017
673	822865708 (1345, 1346)	Novel Protein sim. GBank gji4589250[dbj A022450, j1AF11618 - (AF116183) SecA homolog [Acetobacterium aceti] (complanatum)			284769
674	79199259 (1347, 1348)	Novel Protein sim. GBank gji1652848[dbj BA317766] - (D09059) DNA photolyase [Synecococcus sp.]		UNCLASSIFIED	284629

675	87895970 (1349, 1350)	Novel Protein sim. GBank glf6980759ip1A0D3547, j1AE00170 - (AE001708) D- alanine-D alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) D-alanine D-alanine ligase	UNCLASSIFIED	264488, 2227899, 6571417, 264508 264511, 265008, 60433438, 264600, 264601, 264602, 264603, 264604, 264605, 264762, 264687, 264769, 60431602, 18108374, 264636, 264638 265010
676	78896007 (1351, 1352)	Novel Protein sim. GBank glf723566ip101479VDF7, SC-PRO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07		ATPase-associated	264591, 264632
677	21644312 (1353, 1354)	Novel Protein sim. GBank glf87208 (U03976) - dynein heavy chain isoform SC [Tropuseta spalis]		laminin	264758, 264682, 264557
678	84225200 (1355, 1356)	Novel Protein sim. GBank glf1586274ip12203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) Laminin EGF-like (Domains III and V)	UNCLASSIFIED	22278996, 264693
679	7988855 (1357, 1358)	Novel Protein sim. GBank glf3928723emb1CA222191 - (A1034355) putative ABC transporter [Streptomyces coelicolor]			264600, 264602 264702, 264707, 264908, 265006, 264693, 263972, 83370044, 264588
680	20726424 (1359, 1360)	Novel Protein sim. GBank glf1574493ipNP_006050.1p1A-MC - laminin, gamma 3	Contains protein domain (PF00053) Laminin EGF-like (Domains III and V)	UNCLASSIFIED	264595 264634
681	94322017 (1361, 1362)	Novel Protein sim. GBank glf7542028ipNP_004081.1pDUSP - dual specificity phosphatase 3 (vacuolar virus phosphatase V11-related)	Contains protein domain (PF00782) Dual specificity phosphatase, catalytic domain	UNCLASSIFIED	264605
682	11392478 (1363, 1364)	Novel Protein sim. GBank glf420337emb1CA1846679.11 - (A12343459) proteophosphoglycan [Leishmania major]			264909, 263967, 263981 264631 264693, 264635 264907, 264638
683	8003860 (1365, 1366)	Novel Protein sim. GBank glf54056ip101479VDF7, SC-PRO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07		peptidase	264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
684	20465367 (1367, 1368)	Novel Protein sim. GBank glf2688962 (AF027768) - LspA (Scorcia microscopum)	Contains protein domain (PF00076) RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
685	80246735 (1369, 1370)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
686	8058529 (1371, 1372)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
687	8058529 (1371, 1372)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
688	78533412 (1373, 1374)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
689	80064256 (1377, 1378)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
690	8038756 (1379, 1380)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
691	8154392 (1381, 1382)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
692	8350835 (1383, 1384)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
693	79586116 (1385, 1386)	Novel Protein sim. GBank glf3046931 (AF040330) - PPAR gamma coactivator [Mus musculus]			264905, 264907, 265007, 265009, 60433438, 2198574, 264760, 11010388, 2198576, 2198579, 265021, 18108381, 263974, 18108379, 26457, 18108385, 22279002 264510, 264511, 264764, 264769
694	82455983 (1387, 1388)	Novel Protein sim. GBank glf2673275ip101479VDF7, SC-PRO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07	Contains protein domain (PF00097) Zinc finger, C2H2 type (RING finger)	UNCLASSIFIED	22278996, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94177849 (1389, 1390)	Novel Protein sim. GBank gji4648339[emb](CAB30059.1) - (A.010901) MUCA [Homo sapiens]	Contains protein domain (PF000994) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264905, 264907, 264910, 264908, 264909, 264511, 265007, 264910, 264758, 264754, 264286, 55274791, 264905, 264595
696	79830982 (1391, 1392)	Novel Protein sim. GBank gji2549950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) (Pseudomonas fluorescens)	Contains protein domain (PF00005) - ABC transporter	transport	
697	17577880 (1393, 1394)	Novel Protein sim. GBank gji1731343[gen](G8941Y25_MYCTU - HYPOTHETICAL 2.4 KD PROTEIN C149.25)	Contains protein domain (PF01039) - Transposase	UNCLASSIFIED	264682
698	66695682 (1395, 1396)				264688, 35695917
699	79582558 (1397, 1398)				264682
700	79630698 (1399, 1400)				264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gji001226[gb](BA110471) - (D34003) hypothetical protein (Synchocystis sp.)	UNCLASSIFIED		264468, 264510, 264511, 264602, 264605, 264609
702	79814789 (1403, 1404)	Novel Protein sim. GBank gji24468220 (1403, 1404)	UNCLASSIFIED	oxidase	264604
703	20446820 (1405, 1406)	Novel Protein sim. GBank gji498953[gb](C4333[SOXG_CORSP - SARCOSINE OXIDASE GALLIMIA SUBUNIT])			
704	94312224 (1407, 1408)	Novel Protein sim. GBank gji0159513 (AF067219) - contains similarity to the kelch/MiRP family (Caenorhabditis elegans)	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264628, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gji421091[gb](S30730 - hypothetical protein G238 - Escherichia coli)	UNCLASSIFIED		265006
706	20238692 (1411, 1412)	Novel Protein sim. GBank gji3024872[gb](Q37351[074_SVNY3 - HYPOTHETICAL 82.8 KD PROTEIN SLR0074])			264600
707	20836065 (1413, 1414)	Novel Protein sim. GBank gji424260[gb](AAC31907.1) - (A073709) ABC transporter ATP-binding subunit (Pseudomonas putida)	transport		264603
708	20708282 (1415, 1416)	Novel Protein sim. GBank gji3540741[emb](CAA03985) - (A000281) mucin [Homo sapiens]	struct		264601, 264682
709	98001439 (1417, 1418)	Novel Protein sim. GBank gji380425[emb](CAA18744.1) - (A022604) putative protein (Arabidopsis thaliana)			18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)				264389
711	17931418 (1421, 1422)	Novel Protein sim. GBank gji475869[gb](NP_002223.1)[gb]RP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	apolipoprotein		385019
712	80236164 (1423, 1424)		Contains protein domain (PF00059) - Low-density lipoprotein receptor repeat class B		264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gji1703269[gb](Q11059)AM2_MYCTU - PUTATIVE AMIDASE C130.19C	hydrolase		264906, 264907
714	27847851 (1427, 1428)	Novel Protein sim. GBank gji4502351[gb](NP_001692.1)[gb]BAAT - bile acid Coenzyme A: amino acid N-acetyltransferase, glycine N-choyltransferase			264508, 264555

715	76639423 (1429, 1430)	Novel Protein sim. GBank g11789035 (AE000332) - ori. hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907
716	76559072 (1431, 1432)	Novel Protein sim. GBank g12494074[sp]P56503[GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+)(SSDH)]		dehydrogenase	264692 264636
718	94319658 (1435, 1436)	Novel Protein sim. GBank g13873679[emb]CAA94860 - (Z11178) similar to pro-collagen domains: cDNA EST EMBL-D27978 comes from this gene; cDNA EST EMBL-D27977 comes from this gene; cDNA EST EMBL-D34199 comes from this gene; cDNA EST EMBL-D64392 comes from this gene; cDNA EST EMBL Novel Protein sim. GBank g12104302[emb]CAB086311 - (Z55387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18100392, 22278994, 22278998, 265008, 265018, 264681, 18100354, 264684, 264685, 264686, 264687, 264689, 21906769, 18100361, 264691, 264692, 55810764, 264635, 18100381, 18100382, 83373044, 18100388 265011
719	17679664 (1437, 1438)	(Z55387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	
720	76841684 (1439, 1440)	Novel Protein sim. GBank			264908
721	15020160 (1441, 1442)	g1123530[sp]P04928[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629
722	9662603 (1443, 1444)	Novel Protein sim. GBank g1498253 (U02372) - integrase [Vibrio cholerae]			264910
723	19755599 (1445, 1446)	Novel Protein sim. GBank g12253054[emb]CAB10705 - (Z57559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691
724	10126494 (1447, 1448)	Novel Protein sim. GBank g1063015 (AF083061) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264909
725	76978679 (1449, 1450)			UNCLASSIFIED	264805, 264907
726	13086282 (1451, 1452)			UNCLASSIFIED	264636
727	13522872 (1453, 1454)			UNCLASSIFIED	264634
728	20268471 (1455, 1456)	Novel Protein sim. GBank g13833910[emb]CAB13411 - (Z59112) similar to hypothetical proteins [Bacillus subtilis]			264567
729	11293753 (1457, 1458)	Novel Protein sim. GBank		UNCLASSIFIED	264480
730	19900373 (1459, 1460)	g12494860[sp]P045291[GALE_BRELA - UDP-GLUCOSE 4- EPIMERASE (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE)]		isomerase	264564
731	80098750 (1461, 1462)	Novel Protein sim. GBank g11146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605
732	80258175 (1463, 1464)	Novel Protein sim. GBank g111683396[sp]P46681[IAIP2_YEAST - ACTIN INTERACTING PROTEIN 2]		struct	264591, 264594, 264595
733	20446839 (1465, 1466)	Novel Protein sim. GBank g13184080[emb]CAA19336 - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
734	20435987 (1467, 1468)			ubiquitin	264604

735	11607959 (1469, 1470)	Novel Protein sim. GBank g14015821sp1274321ICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELIC INTERGENIC REGION				264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank g1400831sp131351POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - binding-protein-dependent transport systems inner membrane component	transport		264636
737	78945340 (1473, 1474)		Contains protein domain (PF00615) - Regulator of G protein signaling domain	UNCLASSIFIED		265020
738	17885353 (1475, 1476)	Novel Protein sim. GBank g12508867sp1332251TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) [TRIMETHYLAMINE OXIDE]		oxidase		265008 264910
740	19881557 (1479, 1480)					
741	79827273 (1481, 1482)	Novel Protein sim. GBank g13077494lem0(CAA08472.1) - (Z48583) ATP binding protein with similarity to the CDC48/PA51/SEC18 family; cDNA EST EMBL D68307 comes from this gene; cDNA EST EMBL D68340 comes from this gene; cDNA EST EMBL D68348 comes from this gene; cDNA EST EMBL D6845...	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED		264907, 264764, 264634, 264637 264689, 35696286, 264510, 264908, 18108362
742	82333795 (1483, 1484)	Novel Protein sim. GBank g13077494lem0(CAA08472.1) - (Z48583) ATP binding protein with similarity to the CDC48/PA51/SEC18 family; cDNA EST EMBL D68307 comes from this gene; cDNA EST EMBL D68340 comes from this gene; cDNA EST EMBL D68348 comes from this gene; cDNA EST EMBL D6845...	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED		264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264908, 265009, 265010, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264683, 18108370, 264639, 18108372, 264630, 264631, 264634, 264538, 18108385, 264482, 264584, 264587
743	82300051 (1485, 1486)	Novel Protein sim. GBank g11274202sp19088[MTBA_BACAR - MODIFICATION METHYLASE BAN] (CYTOSINE-SPECIFIC METHYLTRANSFERASE BAN) (M.BANI)				264638, 264932, 264639, 264766, 264906
744	80230421 (1487, 1488)			glycoprotein		
745	9841963 (1489, 1490)	Novel Protein sim. GBank g1178921[pi1504846 - UDP-N- acetyluracilamyl-D-glutaryl-2, 6-diaminopimelate-D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli				
746	11073229 (1491, 1492)	Novel Protein sim. GBank g13386354 (AF074705) - pyocitellin synthetase [Pseudomonas aeruginosa]		synthase		264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank g12887411[bb][AA24848] - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase		6871417, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264981, 264388, 264766, 264687, 264768, 264769, 21903768, 35696917, 264691, 264693, 264628, 264634, 264635, 264639, 36122323, 83373044
748	11617923 (1495, 1496)					264690

748	20469119 (1497, 1499)	Novel Protein sim. GBank gl1189277spIP4448/PPG. HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)	UNCLASSIFIED	284604 284600
750	20296427 (1499, 1500)	Novel Protein sim. GBank gl1390068(gi)AAD42851.1(AE15989) - (AF15989) serine/threonine kinase PKN3 (<i>Mycrococcus xanthus</i>)	- kinase Eukaryotic protein kinase domain	284605, 284559
751	21636169 (1501, 1502)	Novel Protein sim. GBank gl118862spIP44426/BIOA. HAEIN - ADENOSYLMETHIONINE-8-AMINO-2-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELAGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	UNCLASSIFIED	284508, 284907, 284510, 285011, 284762, 284689, 35695955, 284639, 18108387
752	82450366 (1503, 1504)	Novel Protein sim. GBank gl2851530spIP232399/YHGE. BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLT INTERGENIC REGION (ORF8)	UNCLASSIFIED	284909, 284600, 284602, 284604, 284760, 284769, 284634
753	80500718 (1505, 1506)	Novel Protein sim. GBank gl118862spIP44426/BIOA. HAEIN - ADENOSYLMETHIONINE-8-AMINO-2-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELAGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	UNCLASSIFIED	284508, 284906, 284907, 284908, 284909, 284759, 284602, 284764, 284769, 284628, 284629, 284630, 284632, 284634, 284635, 284637, 284638, 83373944, 18108385
754	85083741 (1507, 1508)	Novel Protein sim. GBank gl13449276(emb)CA3204201 - (AL031317) putative dehydrogenase (<i>Streptomyces coelicolor</i>)	UNCLASSIFIED	284769, 284689, 284639, 284639
755	80185448 (1509, 1510)	Novel Protein sim. GBank gl4580331(emb)CAB40107.11 - (AJ001206) putative glycosyl branching enzyme (<i>Streptomyces coelicolor</i>)	UNCLASSIFIED	284682, 284685
756	84031686 (1511, 1512)	Novel Protein sim. GBank gl2911858 (AF047659) - No definition line found (<i>Caenorhabditis elegans</i>)	UNCLASSIFIED	285007, 18108387, 285007, 18108387
757	79475667 (1517, 1518)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
758	78983176 (1515, 1516)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
759	78475667 (1517, 1518)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
760	87628888 (1519, 1520)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
761	79877965 (1521, 1522)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
762	80023953 (1523, 1524)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
763	20284813 (1525, 1526)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686
764	39515024 (1527, 1528)	Novel Protein sim. GBank gl13451312(emb)CA3204481 - (AL031324) membrane alase (<i>Schizosaccharomyces pombe</i>)	UNCLASSIFIED	284684, 284686

765	80023347 (1529, 1530)	Novel Protein sim. GBank gl3845093 (AE001371) - erythrocyte membrane protein PIEMP3 (Plasmodium falciparum)		struct	284905, 284906, 284594, 284666, 33657023
766	82417404 (1531, 1532)	Novel Protein sim. GBank gl541121 (pjlj1840827 - hypochlorite protein o300 - Escherichia coli)		UNCLASSIFIED	284605, 284762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gl541121 (pjlj1840827 - hypochlorite protein o300 - Escherichia coli)		UNCLASSIFIED	284907
768	79416080 (1535, 1536)	Novel Protein sim. GBank gl2982501 (embCA06164) - (AJ004532) neuroglycyl target esterase (Homo sapiens)		UNCLASSIFIED	284592, 284595
769	80063594 (1537, 1538)	Novel Protein sim. GBank gl283437 (pjlj527850) - hypochlorite protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	55810764, 284559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gl759004 (glAD29715) - (AF140598) ring box protein 1 (Homo sapiens)		UNCLASSIFIED	284905, 284907, 284826, 284909, 285010, 284766, 284628, 284629, 284634, 284638, 284555
771	95239508 (1541, 1542)	Novel Protein sim. GBank gl759004 (glAD29715) - (AF140598) ring box protein 1 (Homo sapiens)	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35696286, 284259, 68714117, 284107, 68712502, 56182435, 284112, 55812038, 87168559, 284288, 21906786, 33657023, 65274620, 65274791, 18108381
772	78971382 (1543, 1544)	Novel Protein sim. GBank gl553132 (embCA851045.1) - (AJ009578) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	284910
773	72845353 (1545, 1546)	Novel Protein sim. GBank gl553132 (embCA851045.1) - (AJ009578) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	285020
774	78655129 (1547, 1548)	Novel Protein sim. GBank gl553132 (embCA851045.1) - (AJ009578) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	284909
775	20520141 (1549, 1550)	Novel Protein sim. GBank gl553132 (embCA851045.1) - (AJ009578) putative alkane 1-monoxygenase (Pseudomonas fluorescens)		UNCLASSIFIED	284555
776	78942693 (1551, 1552)	Novel Protein sim. GBank gl553132 (embCA851045.1) - (AJ009578) putative alkane 1-monoxygenase (Pseudomonas fluorescens)	Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	285019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gl435046 (lirj1p_003624) - (p1NRPB - nuclear restricted protein, B1B domain-like brain)	Contains protein domain (PF01344) - Kelch motif	protease	21906754, 265020, 60170615, 284691
778	20891310 (1555, 1556)	Novel Protein sim. GBank gl435046 (lirj1p_003624) - (p1NRPB - nuclear restricted protein, B1B domain-like brain)		UNCLASSIFIED	284511
779	80050204 (1557, 1558)	Novel Protein sim. GBank gl435046 (lirj1p_003624) - (p1NRPB - nuclear restricted protein, B1B domain-like brain)		UNCLASSIFIED	284603
780	85288987 (1559, 1560)	Novel Protein sim. GBank gl11144520 (U34556) - phosphotransferase/glycylcholine synthase (Mycobacterium tuberculosis)		synthase	284907, 284600, 284601, 284602, 284603, 284604, 284605, 284486
781	80250049 (1561, 1562)	Novel Protein sim. GBank gl11144520 (U34556) - phosphotransferase/glycylcholine synthase (Mycobacterium tuberculosis)			284905, 284907, 285010, 284600, 284601, 18108362, 18108374, 284556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gl4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	284605
783	16410791 (1565, 1566)	Novel Protein sim. GBank gl4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	285020
784	80051197 (1567, 1568)	Novel Protein sim. GBank gl4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	284635, 33657023, 28331828, 285017, 284565, 284566
785	56073541 (1569, 1570)	Novel Protein sim. GBank gl3451335 (AC005525) - F22162.1 (Homo sapiens)	Contains protein domain (PF00047) - Immunoglobulin domain	struct	33696052, 284604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gl3451335 (AC005525) - F22162.1 (Homo sapiens)		transport	284603
787	80258364 (1573, 1574)	Novel Protein sim. GBank gl3451335 (AC005525) - F22162.1 (Homo sapiens)		UNCLASSIFIED	284593

788	80507844 (1575, 1576)	Novel Protein sim. GBank g12746079 (AF015310) - BTH1 [Brassica napus]		synthase	264909, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank g12351849 (U93337) - 40 Oa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank g150703780b [BAA83099.1] - (AB028118) MAL11 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87168599, 265016, 21906765, 21906767, 21906768, 21906769, 265020, 264892, 22279000, 264593
791	94651627 (1581, 1582)	Novel Protein sim. GBank g15689948 [CAB51985.1] - (AL10963) putative isoleucyl-RNA synthase [Streptomyces coelicolor A3(2)]		struc	264601, 264605, 264636
792	80086768 (1583, 1584)	Novel Protein sim. GBank g1333194 (J02379) - S-antigen [Plasmodium falciparum]		struc	265021, 264631, 264635, 264566
793	79638730 (1585, 1586)	Novel Protein sim. GBank g11345400b [BAA0546] - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00048) - Homeobox domain	homeobox	264693
794	81839294 (1587, 1588)	Novel Protein sim. GBank g11058849 [J524023] - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264906, 264939, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank g11877334 [emb] [CAB07082] - (Z82771) bfrA [Mycobacterium tuberculosis]		carboxylase	264488, 3668052, 264905, 264907, 265010, 36686423, 264636
796	86669451 (1591, 1592)	Novel Protein sim. GBank g123995447 [emb] [CAAT71519] - (Y10495) CDV-1R protein [Mus musculus]		struc	60432229, 59811150, 264630, 264637, 264495
797	87771781 (1593, 1594)	Novel Protein sim. GBank g123995447 [emb] [CAAT71519] - (Y10495) CDV-1R protein [Mus musculus]		struc	22278998, 264093, 264094, 66714117, 21906767, 21906769, 265020, 265022
798	79865209 (1595, 1596)	Novel Protein sim. GBank g14487250 [emb] [CAB3757] - (AL035569) probable Glu-RNA Gm amidotransferase subunit [Streptomyces coelicolor]		transcript factor	264687, 264768, 264693
799	79557618 (1597, 1598)	Novel Protein sim. GBank g14487250 [emb] [CAB3757] - (AL035569) probable Glu-RNA Gm amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264909, 264910, 264636, 264638
800	79970189 (1599, 1600)	Novel Protein sim. GBank g12791517 [emb] [CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
801	80499399 (1601, 1602)	Novel Protein sim. GBank g12791517 [emb] [CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		transport	264308, 264311, 265006, 265009, 264769, 264367, 264466
802	79834398 (1603, 1604)	Novel Protein sim. GBank g14487250 [emb] [CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264905, 264693
803	20467520 (1605, 1606)	Novel Protein sim. GBank g11176152 [p] [P44507] [YHAD_HAEIN - HYPOTHETICAL binding protein 1B [Pseudomonas aeruginosa]		struc	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank g11176152 [p] [P44507] [YHAD_HAEIN - HYPOTHETICAL binding protein 1B [Pseudomonas aeruginosa]		kinase	264510
805	79599993 (1609, 1610)	Novel Protein sim. GBank g12764612 [emb] [CAA04683] - (AJ01330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264508
806	80484113 (1611, 1612)	Novel Protein sim. GBank g12764612 [emb] [CAA04683] - (AJ01330) ornithine transcarbamoylase [Lactobacillus sakei]		transferase	264769
807	80381612 (1613, 1614)	Novel Protein sim. GBank g12633311 [sp] [Q21828] [YNF_D_CAEEL - HYPOTHETICAL 18.9 kD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi3913092[sp]Q46170[ARCD_CLOPE- ARGININE/ORNITHINE ANTI-PORTER		transport	264900, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi3913016[sp]P74309[ALF1_SVNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264606, 264609, 265007, 264810, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264466, 264369
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi401472[sp]30863YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPHALT INTERGENIC REGION	Contains protein domain (PF00248) Aldol/keto reductase family	reductase	
811	80076280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi146168 (j01617) - glutaminyl- RNA synthetase [Escherichia coli]		synthase	264005, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi1586632[db][BAA76848.1]- (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22778908, 22778909, 29331872, 29331824, 29331825, 29331827, 29331828, 29146499, 264805, 264908, 265007, 33657402, 60433368, 80433438, 264758, 265011, 265017, 265018, 265019, 264369, 264788, 264685, 21906765, 21906767, 265020, 285021, 264692, 85274620, 33857109, 264629, 18108378, 264635, 264638, 60170394, 56182323, 264584, 264600
816	19881910 (1631, 1632)	Novel Protein sim. GBank gi178114[emb]CA062541 - (Z83865) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264595
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi1477488 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22778909, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696243, 55811576, 264636
818	90938190 (1635, 1636)	Novel Protein sim. GBank gi1477488 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]		transport	264565
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi1001332[db][BAA10839]- (D64005) ABC transporter [Smechobrysis sp.]		UNCLASSIFIED	264600, 264602, 264604
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi568814[sp]P37484[YBYT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLCOTF INTERGENIC REGION			
821	79762590 (1641, 1642)	Novel Protein sim. GBank gi378400[emb]CA595281 - (Z71264) predicted using GeneFinder: Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL.D32742 comes from this gene; cDNA EST EMBL.D33617 comes from this gene; cDNA EST...		UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	264510, 264584, 264637
823	94989259 (1645, 1646)			UNCLASSIFIED	264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi137007[emb]CA4668871 - (X98235) type 1 [Drosophila melanogaster]	Contains protein domain (PF 01429) Methyl-CpG binding domain		264910, 264763, 264786, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank g 3025132 lp p77391YEAG_ECOLI - HYPOTHETICAL 74.5 KO PROTEIN IN GAP-RND INTERGENIC REGION				UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank g 324228 lcm CMA1668 - (A1021646) hypothetical protein Rv202c [Mycobacterium tuberculosis]					264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank g 3417424 lcm CJAA203121 - (A1031261) putative transport protein [Schistosoma mansoni]					264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank g 4336692 lp A017897 - (AF101361) Anomalous X segregation [Otophophila melanogaster]				UNCLASSIFIED	5264580, 264588, 264585, 264585, 264589, 264596, 264907, 264908, 264905, 264905, 264512, 264910, 264991, 264758, 264600, 264766, 264768, 21906768, 35695917, 264891, 264828, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264658, 264639, 83373044, 18108385, 264583, 264586, 264486
829	81742215 (1657, 1658)	Novel Protein sim. GBank g 3820539 (AF080002) - UDP-N- acetylmuramyl tripeptide synthetase MurC [Helicobacter modis]				UNCLASSIFIED	264756, 264634
830	20396091 (1659, 1660)					UNCLASSIFIED	264603
831	87112435 (1661, 1662)	Novel Protein sim. GBank g 1870004 lcm CAB06855 - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]				UNCLASSIFIED	66714117, 264810, 264639
832	19536322 (1663, 1664)					UNCLASSIFIED	264906
833	20726654 (1665, 1666)	Novel Protein sim. GBank g 2500056 lp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME				UNCLASSIFIED	264602
834	21426762 (1667, 1668)	Novel Protein sim. GBank g 248753 lp Q46078 PKYK_CORGL - PYRUVATE KINASE (PK)			Contains protein domain (PF00224) - Pyruvate kinase		264600, 264602, 264766, 264689, 264636
835	94104462 (1669, 1670)						264768, 263394, 21906767, 264810, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35696092, 22279002, 264508, 264905, 264906, 264448, 263972, 264909, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank g 659315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]				transport	35695917, 264457
837	79450450 (1673, 1674)	Novel Protein sim. GBank				UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank g 72867 lp P4082 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR				UNCLASSIFIED	264687
839	79841125 (1677, 1678)	Novel Protein sim. GBank g 2496533 lp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KO PROTEIN.CY1A1.08				UNCLASSIFIED	264906
840	80059851 (1679, 1680)	Novel Protein sim. GBank g 4557753 lp NP_000372_1 PM1D1 - midline 1 protein (fibrein)			Contains protein domain (PF00097) - Zinc finger, C3H4 type (RING finger)	interleukinrecept	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBANK glt138055p[0904]XFIN_XENLA_XFIN PROTEIN	Contains protein domain (PF00098) Zinc finger, C2H2 type	Transcript factor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBANK glt114321[09]BAJ200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) Zinc finger present in GyrA protein, CYP19A30	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264536
843	87002847 (1685, 1686)	Novel Protein sim. GBANK glt3882325[09]BAJ34522_11 - (A8018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) bZIP transcription factor	strut	264091, 29331825, 264906, 264768, 264583
844	17941439 (1687, 1688)	Novel Protein sim. GBANK glt22472_1[09]BAJ038441 - (A8002388) KIAA0380 [Homo sapiens]	Contains protein domain (PF00098) Zinc finger, C2H2 type	Transcript factor	265011
845	18346844 (1689, 1690)	Novel Protein sim. GBANK glt25879[09]A35929 - virulence regulatory protein VsrB : Pseudomonas solanaceum		kinase	264629, 264907
847	76895348 (1693, 1694)				264909
848	78489265 (1695, 1696)			UNCLASSIFIED	265020
849	79756367 (1697, 1698)			UNCLASSIFIED	264566
850	79817849 (1699, 1700)	Novel Protein sim. GBANK glp18245[09]P78061[VCJK_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	Contains protein domain (PF00120) Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBANK glt5454130[re]NP_005260.1[ptTLN] - talin	Contains protein domain (PF01608) - ILWEC domain		264488, 52644507, 264489, 18108398, 65274372, 56182575, 22278994, 22278995, 22278996, 35692866, 22278997, 22278998, 22278999, 20281171, 264490, 264295, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146488, 29146499, 264107, 264905, 264906, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433358, 33657402, 60433438, 264595, 264768, 264769, 21906754, 33109854, 56844286, 265010, 265011, 87188559, 265017, 265018, 265019, 264760, 264761, 264762, 264881, 18108351, 264763, 264448, 264682, 264764, 264853, 18108354, 264288, 264369, 264685, 264766, 264687, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29146527, 21906769, 29146529, 58811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 264692, 33657023, 264693, 263986, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281089, 264629, 18108374, 18108376, 55911576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	1302587 (1705, 1706)	Novel Protein sim. GBank glt5402836[emj]CA476082] - (Y16136) 2-shinole reductase [Moorilla thermococcal]	reductase	264636 264566
854	80052438 (1707, 1708)			
855	79541130 (1709, 1710)			
856	11594238 (1711, 1712)		UNCLASSIFIED	264692 264591
857	79210163 (1713, 1714)		UNCLASSIFIED	264630, 264634
858	80246910 (1715, 1716)			265008, 265009, 264601, 264602, 264603, 18108351
859	20296834 (1717, 1718)			264559
860	80041748 (1719, 1720)		UNCLASSIFIED	264489
861	85451745 (1721, 1722)		UNCLASSIFIED	33657023, 264630
862	80079463 (1723, 1724)		UNCLASSIFIED	264600
863	80079931 (1725, 1726)	Novel Protein sim. GBank glt2246532 (U33872) - ORF 73, contains large complex repeat CR 73 (Kaposi's sarcoma-associated herpesvirus)	UNCLASSIFIED	264488, 18108398, 33668286, 264259, 18108351, 264288, 265021
864	94539904 (1727, 1728)	Novel Protein sim. GBank glt568984[emj]CA832047.1] - (A1109132) hypothetical protein [Streptomyces coelicolor AS2]	UNCLASSIFIED	264259, 264112, 263974
865	80045310 (1729, 1730)	Novel Protein sim. GBank glt458767[emj]NP_000341.1]p4BCR - ATP binding cassette transporter	transport	264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank glt458767[emj]NP_000341.1]p4BCR - ATP binding cassette transporter		264288, 264557, 264558
867	80092402 (1733, 1734)			
868	10075384 (1735, 1736)		UNCLASSIFIED	264605
869	80092403 (1737, 1738)			
870	80249851 (1739, 1740)	Novel Protein sim. GBank glt286667[emj]S37755 - Adenyltransferase - Escherichia coli	transferase	264605, 264687, 18108374
871	20378294 (1741, 1742)	Novel Protein sim. GBank glt17001809[Q10602]HEMK_MYCTU - HEK1K PROTEIN HOMOLOG	UNCLASSIFIED	264601, 264636
872	95197114 (1743, 1744)	Novel Protein sim. GBank glt1545959[emj]CA487763] - (X95384) paladin [Mus musculus]		264603
873	20189728 (1745, 1746)	Novel Protein sim. GBank glt1156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	UNCLASSIFIED	33656296, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 36969052, 264509, 264506, 264508, 264507, 264508, 264509, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264991, 60433396, 264596, 52646317, 87168474, 265010, 264602, 264603, 265017, 265018, 264605, 18108351, 264784, 264786, 264788, 52644229, 264789, 21906785, 265021, 264534, 264691, 52645129, 264628, 264629, 36969423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22279000, 22279002, 264594

874	80077692 (1747, 1748)	Novel Protein sim. GBank gi134319 sp P07819 SCRB_BACSU_SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE) human (fragment)		UNCLASSIFIED	264600
875	86508446 (1749, 1750)	Novel Protein sim. GBank gi481000 pf S37594_mucin- human (fragment)			264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gi13728283 (AF010490) - iron(ii) dicarboxylate transport ATP-binding protein [Rhodococcus capsulatus]	Contains protein domain (PF00005) - transport ABC transporter		264907, 264601, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi137107 sp P40349 URB1_USTIVA_SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URB51	Contains protein domain (PF00320) - transcriptorfactor GATA zinc finger		22278988, 264809, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gi135161 sp Q094853 YAE2_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I (274030) predicted using GeneFinder: cDNA EST EMBL C07609 comes from this gene: cDNA EST EMBL C09023 comes from this gene: cDNA EST jk505e9.3 comes from this gene: cDNA EST jk489p9.3 comes from this gene: cDNA EST jk489p9.5 com...		ATPase-associated	264369, 264555
879	94328692 (1757, 1758)	Novel Protein sim. GBank gi397530 emb CA984341 - (274030) predicted using GeneFinder: cDNA EST EMBL C07609 comes from this gene: cDNA EST EMBL C09023 comes from this gene: cDNA EST jk505e9.3 comes from this gene: cDNA EST jk489p9.3 comes from this gene: cDNA EST jk489p9.5 com...			56182575, 29331824, 264508, 264006, 265018, 18108351, 264448, 264683, 21908768, 21908768, 60170515, 33657023, 65274620, 33657109, 18108374, 33658855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kingle domain		264508
881	11290122 (1761, 1762)	Novel Protein sim. GBank gi263209 emb CA756071 - (Y15513) Prodox protein [Drosophila melanogaster]		UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi115506 emb CA644251 - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264558
883	76542969 (1765, 1766)	Novel Protein sim. GBank gi115506 emb CA644251 - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi2078027 emb CA6084671 - (295208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264636
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi2695834 emb CA159041 - (AL021006) sucA [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108362
886	11685136 (1771, 1772)	Novel Protein sim. GBank gi568939 sp gb AA2381.11 - (AB024952) KIAA1029 protein [Homo sapiens]			264650
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi568939 sp gb AA2381.11 - (AB024952) KIAA1029 protein [Homo sapiens]		dehydrogenase	33595052, 264606, 264600, 264603, 33595917, 35995855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gi1381339 sp gb AA192651 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]		UNCLASSIFIED	264608
889	20385917 (1777, 1778)	Novel Protein sim. GBank gi1381339 sp gb AA192651 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]			264603
890	19904337 (1779, 1780)	Novel Protein sim. GBank gi852405 emb CA456371 - (X63413) U88 [Human herpesvirus 6]			264629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gil459396gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]	UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gil545526 bsl143833 - LBP- 1b-transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namalwa cells, Peptide, 541 aa]	transcription factor	22278996, 22278999, 29331828, 35696002, 264908, 264909, 265009, 265011, 264602, 265019, 264766, 21906765, 21906766, 21906769, 265020, 265021, 56526486 264689, 263967
893	76168037 (1785, 1786)	Novel Protein sim. GBank gil2829688 spP06086 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL-SERINE SULFHYDRYLASE) (O- ACETYL-SERINE (THIO-L)YLASE) (CSASE)	synthase	264689, 263967
894	11102240 (1787, 1788)			263978
895	80239668 (1789, 1790)		UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)			264632
897	94991923 (1793, 1794)		UNCLASSIFIED	264686, 29331828, 264511
898	87895109 (1795, 1796)			5618257, 60432289, 56182435, 60432229, 55811957, 22279000, 264486
899	11100463 (1797, 1798)			264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gil1750127 (U66480) - YmcC [Bacillus subtilis]	transport	264769, 284691, 264563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gil3122879 g O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) tRNA synthetases class II (A)	264907, 284602, 264605, 284769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gil33355701 emb CAA200011 - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) Aconitase family (aconitate hydratase)	264909, 265008, 284602, 284604, 284769, 264689, 264693
903	82060208 (1805, 1806)	Novel Protein sim. GBank gil2960120 emb CAA18018.1 - (AL022121) g pk [Mycobacterium tuberculosis]	Contains protein domain (PF00370) FGY family of carbohydrate kinases	35696052, 264905, 264510, 264511, 264512, 264605, 264760, 18108351, 264782, 264687, 264768, 264769, 284688, 21906784, 35695917, 27486282, 35695855, 264634, 264636, 264486 264604
904	20451078 (1807, 1808)	Novel Protein sim. GBank gil28887 sp P40906 ARGI_COCIM - ARGININASE	Contains protein domain (PF00481) Arginase family	264909
905	9398483 (1809, 1810)	Novel Protein sim. GBank gil4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264595, 264605
906	80052628 (1811, 1812)	Novel Protein sim. GBank gil3738200 emb CAA212021 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]		
907	87913201 (1813, 1814)			
908	11754482 (1815, 1816)		UNCLASSIFIED	60432289, 264601, 264690
909	20727907 (1817, 1818)	Novel Protein sim. GBank gil3668840 gb BAA342961 - (AB015054) Alg2 [Rhizomucor pusillus]	UNCLASSIFIED	264602
910	16776206 (1819, 1820)	Novel Protein sim. GBank gil4358726 db JAA17683.11 - (AB003137) DnaJ homologue protein [Salix glauca]	Contains protein domain (PF00694) DnaJ central domain (4 repeats)	265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P3585 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 80432113
912	20448663 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAO07921.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter Pylori 26865]		hydrolase	264559
913	20469357 (1825, 1826)	Novel Protein sim. GBank gi 477657 sp Q03604 IR1_ CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 568957 dbj BA03069.1 - (AB029040) KIAA1117 protein [Homo sapiens]		UNCLASSIFIED	264538 264595
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264605
917	20185985 (1833, 1834)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) pterophorin-S [Volvox carter]		synthase	264259, 29331826, 284908, 295019, 264448, 265020, 264635, 83273044
918	91226795 (1835, 1836)	Novel Protein sim. GBank gi 5689968 emb CA52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	265006, 264512, 284600, 284602, 284604, 284768, 18108370, 284653
920	79608095 (1839, 1840)	Novel Protein sim. GBank gi 186448 sp Q05413 JAMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYL-PROLINE AMINOPEPTIDASE I) (ALD033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21911.1 - (ALD033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	76862605 (1843, 1844)	Novel Protein sim. GBank gi 267079 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		UNCLASSIFIED	265019, 22779002
923	86695630 (1845, 1846)	Novel Protein sim. GBank gi 2497688 sp Q06963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		luciferin	264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)	Novel Protein sim. GBank gi 2497688 sp Q06963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264510 264603
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 3862325 dbj BA034522.1 - (AB018345) KIAA0802 protein [Homo sapiens]		UNCLASSIFIED	55811957, 263972, 284639
926	75397657 (1851, 1852)	Novel Protein sim. GBank gi 3862325 dbj BA034522.1 - (AB018345) KIAA0802 protein [Homo sapiens]		UNCLASSIFIED	264769
927	37036201 (1853, 1854)	Novel Protein sim. GBank gi 3862325 dbj BA034522.1 - (AB018345) KIAA0802 protein [Homo sapiens]		UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gll155146 (A33316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]	dehydrogenase	264605
929	20630336 (1857, 1858)	Novel Protein sim. GBank gll115936(gllA400346-1)- (AF118223) No definition found (Aradobryopsis balliana)	UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gll49069(jemA333042-1)- (A1133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	reductase	264239
931	10242731 (1861, 1862)	Novel Protein sim. GBank gll54939(jemA350754-1)- (A1069539) putative integral membrane transport protein [Streptomyces mellesii]	transport	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gll54939(jemA350754-1)- (A1069539) putative integral membrane transport protein [Streptomyces mellesii]	transport	264508, 264905, 264906, 264907, 264908, 264909, 264602, 264603, 264605, 264766, 264658, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gll5689523(jemA430345-1)- (A8029016) KIAA1093 protein (Homo sapiens)	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gll119111(jsp12379)EBN2_EBV EBNA-2 NUCLEAR PROTEIN		264369, 22279002
935	80063162 (1869, 1870)			
936	80026632 (1871, 1872)	Novel Protein sim. GBank gll845686 (A32103) - ORF-27 [Staphylococcus aureus]	UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
937	80250273 (1873, 1874)	Novel Protein sim. GBank gll1350656(per)CSHU1V - collagen alpha 1(V) chain (bovine)	UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
938	80026633 (1875, 1876)	Novel Protein sim. GBank gll228243(jemA3474531-1)- (Y14083) hypothetical protein [Bacillus subtilis]	synthase	263978
939	11071694 (1877, 1878)		UNCLASSIFIED	264602
940	94144252 (1879, 1880)	Novel Protein sim. GBank gll3550116(jemA3420678)- (A1031525) ubiquitin carboxy-terminal hydrolase [Schistosoma mansoni]	ubiquitin	264600
941	11398414 (1881, 1882)			264905, 264906, 264907, 264908, 264909, 264511, 264910, 264992, 33657402, 264586, 264758, 264760, 264983, 264768, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264656, 264636, 264639, 83373044, 18108385, 264585, 18108391
942	19484122 (1883, 1884)			264593
943	80080255 (1885, 1886)	Novel Protein sim. GBank gll033729 (A1038595) - isoprenoid N-acyltransferase [Pseudomonas aeruginosa]	UNCLASSIFIED	264760
944	80216098 (1887, 1888)	Novel Protein sim. GBank gll033729 (A1038595) - isoprenoid N-acyltransferase [Pseudomonas aeruginosa]	UNCLASSIFIED	264600, 264687, 264689, 264583
945	80052477 (1889, 1890)	Novel Protein sim. GBank gll2494754(jsp050729)GUA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) [GMP SYNTHETASE]	synthase	264511, 264603
946	78248402 (1891, 1892)	Novel Protein sim. GBank gll723535(jsp090606)WCH_BACSU - HYPOTHEICAL 35.6 KD PROTEIN IN G0X4-VPR INTERGENIC REGION	UNCLASSIFIED	264906, 264904, 264605, 265020, 18108387
				265017

947	18102699 (1893, 1894)	Novel Protein sim. GBank gl 289677 emb CAA17247 - (ALD1 899) hypothetical protein RV2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	18106394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264689, 264683
948	86165538 (1895, 1896)	Novel Protein sim. GBank gl 2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]	fgf	18106398, 56182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	86081786 (1897, 1898)	Novel Protein sim. GBank gl 4507395 (pNP_003427) - zinc finger protein 135 (clone pH2-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	29331825, 2106764, 27486261, 21906766, 52644296, 33657349, 27169518, 56994075, 265020, 265021, 87168559, 52944150, 264637
950	75485872 (1899, 1900)	Novel Protein sim. GBank gl 107946 (pS43865) - cycloratin 8, type II - poliovirus (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	264683, 18106361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gl 520387 (emb CA846679.1) - (A243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264604
952	75566954 (1903, 1904)	Novel Protein sim. GBank gl 5505702 (pAADM1775.1) (AF126866) - calpain-like protease [Mus musculus]	calpain	264910, 264681
953	10196003 (1905, 1906)	Novel Protein sim. GBank gl 2495842 (pC47143) (YH5, ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION	transport	264510
954	9863328 (1907, 1908)	Novel Protein sim. GBank gl 2360965 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]	dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gl 5454064 (pNP_008318.1) (pSP1) - SVT interacting protein	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264689, 264767, 264687, 264768, 264769, 264689, 264698, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108398, 264553, 264584
956	80064224 (1911, 1912)	Novel Protein sim. GBank gl 2052129 (emb CA808155) - (2947552) (nu) [Mycobacterium tuberculosis]		264685
957	80056206 (1913, 1914)	Novel Protein sim. GBank gl 1709767 (pC00465) (PRF_1_LYCES - 36.4 KD PROLINE-RICH PROTEIN	UNCLASSIFIED	264603, 18106362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gl 2131050 (emb CA808260) - (295844) (pcaA [Mycobacterium tuberculosis])	UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gl 2129479 (pJ551939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED	264602, 264682
960	37815406 (1919, 1920)	Novel Protein sim. GBank gl 2129479 (pJ551939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED	264259
961	20567383 (1921, 1922)			263978
962	11389318 (1923, 1924)			264593

963	80500374 (1925, 1926)					UNCLASSIFIED	264510, 264288, 264555, 264556, 264559, 264496
964	76832019 (1927, 1928)	Novel Protein sim. GBank gji4589622bjiBA76833.1i- (AB023206) KIAA0989 protein [Homo sapiens]				UNCLASSIFIED	264712, 264910, 264689
965	91229485 (1929, 1930)	Novel Protein sim. GBank gji5420387rmi(CA946679.1i- (A.243459) proteophosphoglycan [Leishmania major]				UNCLASSIFIED	264408, 264592, 264496, 264604, 264768, 21806784, 264692, 264693, 264623, 264636, 264638
966	95202815 (1931, 1932)					phosphatase	264760
967	79255708 (1933, 1934)	Novel Protein sim. GBank gji731207bjiD11158RGX3.MVCTU - SENSORY TRANSDUCTION PROTEIN RECD3			Contains protein domain (PF00072): Response regulator receiver domain		
968	79502569 (1935, 1936)	Novel Protein sim. GBank gji2681836rmb(CAA75187i- (Y14684) putative transport protein [Methylophilus methylotrophus]			transport		264693
969	78919470 (1937, 1938)	Novel Protein sim. GBank gji541987rmb(CAB46422.1i- (AL086747) hypothetical protein [Homo sapiens])			Contains protein domain (PF00096): Zinc finger, C2H2 type		
970	95059547 (1939, 1940)					UNCLASSIFIED	35689286, 264895, 264886, 35695917, 264692, 18108374, 264635
971	78919770 (1941, 1942)					UNCLASSIFIED	18108392, 18108394, 18108398, 18108398, 22276996, 22276998, 22276999, 29147620, 264628, 265006, 265007, 285008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21908767, 21906768, 18108370, 18108374, 18108377, 264630, 284635, 18108380, 83373044, 18108387, 18108388
972	20770704 (1943, 1944)	Novel Protein sim. GBank gji172319l9p(P53990)Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				UNCLASSIFIED	265007, 265020, 22279002
973	20370183 (1945, 1946)						264557
974	80037103 (1947, 1948)					UNCLASSIFIED	264504
975	10196018 (1949, 1950)					UNCLASSIFIED	264555
976	80205742 (1951, 1952)	Novel Protein sim. GBank gji3881459rmb(CAA9298.1i- (Z68753) predicted using Genefinder; Similarity to Yeast hypothetical protein YrkG (SW:YrkG, YEAST), cDNA EST EMBL D27680 comes from this gene; cDNA EST EMBL D27679 comes from this gene; cDNA EST EMBL D84477 comes from this ge...				UNCLASSIFIED	264510
977	10355349 (1953, 1954)	Novel Protein sim. GBank gji549456l9p(Q05335)XY53_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3				UNCLASSIFIED	264906
978	80025927 (1955, 1956)					UNCLASSIFIED	264906, 264902, 264903, 264904
979	80447820 (1957, 1958)	Novel Protein sim. GBank gji317190l9rmb(CAA75869i- (Y15908) DIA-12C protein [Homo sapiens])				UNCLASSIFIED	264767, 264768, 265006, 265007, 264906
980	80025928 (1959, 1960)					UNCLASSIFIED	264903
981	80098550 (1961, 1962)	Novel Protein sim. GBank gji359940 (AF017688) - facioscapular dysplasia protein 2 [Mus musculus]				UNCLASSIFIED	264902, 264555, 264558, 264559, 264559

982	80195670 (1983, 1964)	Novel Protein sim. GBank gl 2550220[emb CAA7157]. - [Y10545] fused-cdb [Escherichia coli]		UNCLASSIFIED	264404
983	90955041 (1965, 1966)	Novel Protein sim. GBank gl 476389[pi B43402. - myosin heavy chain-B, neuronal - chicken		struct	65274572, 5618275, 264908, 264909, 265007, 265008, 264755, 265010, 558111, 50, 33657023, 264534, 264557, 264558
984	20466876 (1967, 1968)			UNCLASSIFIED	264605
985	65461358 (1969, 1970)	Novel Protein sim. GBank gl 3451504[emb CAA07660.1] - (AJ007477) hypothetical protein BLPS1.21 [Bordetella bronchiseptica]	Glycosyl transferases group 1	transferase	56182435, 264600
986	87102868 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)			UNCLASSIFIED	264609
988	19855661 (1975, 1976)			UNCLASSIFIED	264600
989	88095328 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gl 5725506[gb AAD48080.1] (AF060152) METH protein [Homo sapiens]	Contains protein domain (PF01421) Reprolysin (M12B) family zinc metalloprotease	oxidase	264258, 264908, 265009, 264910, 264596, 264369, 264288, 264766, 264623, 264635, 264568
991	10106140 (1981, 1982)	Novel Protein sim. GBank gl 210504[emb CA088335] - (Z95438) hypothetical protein RV3645 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gl 3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)	Novel Protein sim. GBank gl 3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264907
994	11090590 (1987, 1988)	Novel Protein sim. GBank gl 5106572[gb AAD39760.1] (AF43946) transcriptional activator SRAP [Homo sapiens]	Contains protein domain (PF00176) SNF2 and others N-terminal domain		264602
995	94321811 (1989, 1990)			-helicase	18108398, 55274572, 22278996, 22278997, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432228, 60431735, 33657402, 264595, 264755, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906769, 55811957, 246892, 264693, 264629, 35696423, 55811576, 35695855, 264636, 264555, 264556, 264559, 83373044, 22279002, 264563
996	81013745 (1991, 1992)	Novel Protein sim. GBank gl 2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 2633978, 55811957, 56526486, 87166519, 264910, 264906, 264565, 264666, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gl 2649107 (AE001001) - ABC transporter, ATP-binding protein [Aerobacterium fujidus]	Contains protein domain (PF00005) ABC transporter	-transport	35696286, 22278997, 22278999, 264908, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gl 123503[sp P04929] (H-RP-X, PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	18108391, 264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2506597 sp 46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN H10188		UNCLASSIFIED	264682
1000	20272944 (1999, 2000)	Novel Protein sim. GBank gi 2224599 gb BAA20833 - (AB002377) KIAA0376 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264602
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 58612 sp P37709 TRHY_RABIT - TRICHOHYALIN		UNCLASSIFIED	26432049, 264909, 264511, 264603, 264683, 264684, 264687, 264689, 29148627, 21906769, 264692, 18108365, 22279000 2650009, 264369, 265020
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 58612 sp P37709 TRHY_RABIT - TRICHOHYALIN		UNCLASSIFIED	265019
1003	17933491 (2005, 2006)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X63413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264635
1004	16314987 (2007, 2008)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508
1005	79671144 (2009, 2010)	Novel Protein sim. GBank gi 4062979 gb BAA38210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	264259 264905
1006	37815429 (2011, 2012)	Novel Protein sim. GBank gi 280807 emb CAA04807.1 - (AJ001206) putative trihalase [Streptomyces coelicolor]		UNCLASSIFIED	265007, 264602, 264605, 264760, 264638
1007	78620871 (2013, 2014)	Novel Protein sim. GBank gi 36393077 AF050113 - ALMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF08595) - POZ domain (Also known as DHR or GLF)	UNCLASSIFIED	284102, 284288
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 (AF1616307) - possible NADH-dependent oxidase, may function as a demethylase [Strombococcus moutoni]		UNCLASSIFIED	264692
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 2342647 gi AA086591.1 - (U08653) DHRC-domain-containing cysteine-rich protein [Haptophyceae]		UNCLASSIFIED	35686032, 264905, 264784, 264768, 35695917, 264628
1012	952394456 (2023, 2024)	Novel Protein sim. GBank gi 341311 emb CAA302721 - (AL031231) putative phosphatase synthetase polyphosphonucleide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	35686032, 264905, 264600, 264601, 264602, 264605, 264762, 264766, 264768, 264689
1013	86095712 (2025, 2026)	Novel Protein sim. GBank gi 2506597 sp 46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN H10188		UNCLASSIFIED	264591, 21906768
1014	86608828 (2027, 2028)	Novel Protein sim. GBank gi 2506597 sp 46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN H10188		UNCLASSIFIED	29331924, 265019, 265020

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gi 4155995 (AF063085) - SELL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	- struct	22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331825, 29331828, 264907, 56182435, 2644510, 264591, 264593, 60433356, 264594, 55812038, 264758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33857182, 22833986, 18108370, 18108377, 55811576, 35696423, 264630, 22279000, 264565
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gi 2506969 (P41407) ACPQ - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	264686, 264693
1017	11068213 (2033, 2034)	Novel Protein sim. GBank gi 5103943 (QJBA79259.1) - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Acetopyrum pernix]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	- transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gi 4483973 (emb CA339032.1) - (AL034559) predicted using hexExon, MAL3P7.14 (PFC0925W). Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 29148627, 264563
1019	11703607 (2037, 2038)				264686
1020	80234432 (2039, 2040)			UNCLASSIFIED	264508, 264509, 264512, 264600, 264762, 264769, 264689, 18108370, 264636, 264638, 264486
1021	37038243 (2041, 2042)	Novel Protein sim. GBank gi 4533807 (gb AA028655.1) (AF127795) trehalase biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gi 1781230 (emb CA086277) - (238867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	- phosphatase	35595052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gi 3777495 (U92083) - calcium transporting ATPase [Pichia angustia]	Contains protein domain (PF00122) - E1-E2 ATPase	- ATPase, associated	264593
1024	80557129 (2047, 2048)			UNCLASSIFIED	52546842, 33657402, 33657021, 18108379, 55811576, 264631, 264556, 264557, 264559, 18108388, 264566
1025	79644200 (2049, 2050)	Novel Protein sim. GBank gi 3483045 (emb CAA0556) - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264683
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gi 174922 (p Q02322) UVRD - DNA HELICASE II [Streptomyces coelicolor]		helicase	264602
1027	17658234 (2053, 2054)	Novel Protein sim. GBank gi 475772 (p NP_004886.1) pAGTA - angiotensin vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20297928 (2055, 2056)	Novel Protein sim. GBank g12191409[emb][CAA16003] - (AL021184) aon [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Acetate family (acetylase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	86095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264602, 264630, 264634, 264638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank g14503995[ref][NP_000145, 1]GALK - galactokinase 1		UNCLASSIFIED	264689
1033	86484818 (2065, 2066)	Novel Protein sim. GBank g12982590 (AE000882) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35696052, 264906, 264510, 18108354, 18108357, 264769, 264689, 60431602, 18108385, 264486
1034	79245937 (2067, 2068)	Novel Protein sim. GBank g1455895 (U00007) - methionyl- tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	79956355 (2069, 2070)			UNCLASSIFIED	264682
1036	85804998 (2071, 2072)			UNCLASSIFIED	264905, 66712502, 264908, 264766
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264909, 60433438, 265019
1038	20481015 (2075, 2076)		Contains protein domain (PF01477) - PLATLH2 domain	UNCLASSIFIED	264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank g12605597 (AF030027) - 24 kidney disease-associated protein [Homo sapiens]		UNCLASSIFIED	264002, 264083, 264094, 264683, 264689, 265967
1040	80025840 (2079, 2080)	Novel Protein sim. GBank g12352095 (U97022) - DNA topoisomerase I [Eubacterium islandicum]		isomerase	264555
1041	10156682 (2081, 2082)	Novel Protein sim. GBank g13256533[db][BA29218.1] - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Xylococcus horkosii]		kinase	264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank g12058299[emb][CA466953] - (X99309) ARI protein [Diosaphia melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank g11870167[emb][CA470125] - (V08921) msK [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter		264565, 264567
1044	80025952 (2087, 2088)	Novel Protein sim. GBank g15689890[emb][CAB2053.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED		265008, 264602, 265017, 29331825, 264637
1045	52415482 (2089, 2090)				
1046	11754862 (2091, 2092)	Novel Protein sim. GBank g1854055[emb][CA458337] - (X83413) U88 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank g14210471[db][BA474535.1] - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2096)	Novel Protein sim. GBank g1341319[emb][CA420279] - (AL012332) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank g15051636[db][AAC38325.1]AF07372 - (AF073727) EH domain-binding inhibitory phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686

1051	80475471 (2101, 2102)			UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442662 (2103, 2104)	Novel Protein sim. GBank g1312327(isp)P35136ISERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF003389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank g15441319(emt)CAB671.11 - (ALQ34366) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]			264686, 18108374, 29331824, 83373044, 21900754, 52645156, 56182435, 264689, 29331827, 27466261, 35696052, 21900765, 35696423, 21900768, 56182575, 21900769, 55811957, 87168516, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 284766
1054	79580225 (2107, 2108)	Novel Protein sim. GBank g15052500(isp)AD38584.1(AF145609)	Contains protein domain (PF00270) - DEAD/IDEAH box helicase	UNCLASSIFIED	264686
1055	80594136 (2109, 2110)	BcDNA GH02833 [Drosophila melanogaster]		helicase	264907, 264602, 264681, 264288, 21900768, 33657109, 55810764, 35695955, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank g13021676(dh)BAA25358) - (D68033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]		mapolymerase	264906
1057	82667216 (2113, 2114)	Novel Protein sim. GBank g11262821 (U50308) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264682
1058	80376576 (2115, 2116)	Novel Protein sim. GBank g1170016(isp)P46808IGREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREY (TRANSCRIPTION FACTOR GREY)		transcriptfactor	264764
1059	84662754 (2117, 2118)	Novel Protein sim. GBank g12499087(isp)O09332UGGG_DROME - UDP- GLUCOSE GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	35696052, 35695955, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank g12499087(isp)O09332UGGG_DROME - UDP- GLUCOSE GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank g190254(isp)JAZ2334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		phosphatase	264634
1062	35657937 (2123, 2124)	Novel Protein sim. GBank g13334200(isp)O49954GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)		dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank g12499666(isp)Q41229IPSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI- A)			264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank g182654(isp)JAU0086 - 10k zein precursor - maize			265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. cBank gll120989[prl]S70682 - glycosyltransferase homolog. - Bordetella pertussis		transferase	264600, 264602, 264689
1066	17956879 (2131, 2132)	Novel Protein sim. cBank gll2506362[sp15042DNL] ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	265009
1067	10132178 (2133, 2134)	Novel Protein sim. cBank gll4007669[emb]CAA22355[- (ALD34443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) Aldoketo reductase family	- reductase	264909
1068	82052057 (2135, 2136)	Novel Protein sim. cBank gll4599484[dbi]BAAT6770.1[- (AB023143) KIAA0928 protein (Homo sapiens)]		UNCLASSIFIED	264688, 18108352, 264558, 264600, 264760
1069	83002954 (2137, 2138)	Novel Protein sim. cBank gll120304[sp15032F]LGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	264604
1070	82101992 (2139, 2140)	Novel Protein sim. cBank gll1750397 (U81281) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1071	20710589 (2141, 2142)	Novel Protein sim. cBank gll477532[prl]A48175 - Motif B protein - mouse (fragment)	Contains protein domain (PF00008) EGF-like domain	- synthase	264687, 264688, 21906784, 35695052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264505, 264690, 264906, 264762, 264828, 264768
1072	82356540 (2143, 2144)	Novel Protein sim. cBank gll3893109[emb]CAA76940[- (Y17820) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	264909
1073	79811400 (2145, 2146)	Novel Protein sim. cBank gll4033487[sp144472]UDL_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1074	80105982 (2147, 2148)	Novel Protein sim. cBank gll1175203[sp146442]YHMC ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (E375)		UNCLASSIFIED	264596, 265018, 265019, 264681, 264369, 264688, 265020, 18108364, 18108374
1075	81850293 (2149, 2150)	Novel Protein sim. cBank gll4033487[sp144472]UDL_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1076	80477264 (2151, 2152)	Novel Protein sim. cBank gll1175203[sp146442]YHMC ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (E375)		UNCLASSIFIED	264596, 265018, 265019, 264681, 264369, 264688, 265020, 18108364, 18108374
1077	79831334 (2153, 2154)	Novel Protein sim. cBank gll4033487[sp144472]UDL_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1078	20288874 (2155, 2156)	Novel Protein sim. cBank gll3413028[emb]CAA20296[- (ALD31260) hypothetical protein SC9A10.06 [Streptomyces coelicolor]		UNCLASSIFIED	264600
1079	80494516 (2157, 2158)	Novel Protein sim. cBank gll3413028[emb]CAA20296[- (ALD31260) hypothetical protein SC9A10.06 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 264769, 264634, 264636
1080	11767188 (2159, 2160)	Novel Protein sim. cBank gll3413028[emb]CAA20296[- (ALD31260) hypothetical protein SC9A10.06 [Streptomyces coelicolor]		UNCLASSIFIED	264684
1081	94741080 (2161, 2162)	Novel Protein sim. cBank gll3413028[emb]CAA20296[- (ALD31260) hypothetical protein SC9A10.06 [Streptomyces coelicolor]		UNCLASSIFIED	83373044, 265019, 22279002, 264482, 18108351, 264682, 264908, 264693, 264487
1082	11490656 (2163, 2164)	Novel Protein sim. cBank gll3413028[emb]CAA20296[- (ALD31260) hypothetical protein SC9A10.06 [Streptomyces coelicolor]		UNCLASSIFIED	264758, 264768, 264769, 21906787, 264511, 264910, 264634, 264635, 264905, 264636, 264906, 264637, 264907, 264908, 264764, 264638, 20281099, 264766, 264595

1003	87446717 (2185, 2186)	Novel Protein sim. GBank glt172945sq10523Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN C1427_23		UNCLASSIFIED	60421479, 264905, 264906, 264510, 60432229, 264759, 17168474, 264605, 264769, 264689, 16106364, 16106370, 35695955, 264636 264769
1004	37769306 (2187, 2188)	Novel Protein sim. GBank glt18344ep23057MCAL_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1005	86475368 (2189, 2170)	Novel Protein sim. GBank glt18344ep23057MCAL_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI	Contains protein domain (PF00118) - sph		60432229, 264687
1006	76003259 (2171, 2172)	Novel Protein sim. GBank glt117295sq1p46_76RL14_ACYXS - 50S RIBOSOMAL PROTEIN L14	TCF-1q2nd0 chapter family Contains protein domain (PF00238) - Ribosomal protein L14		264486
1007	76003979 (2173, 2174)	Novel Protein sim. GBank glt1450139lamb1CA115431 - (AL008593) 13227.16.3 (novel CHRONOXO family protein) (Homo sapiens)	Contains protein domain (PF00385) - chromo (CHRONOXO Organization Modifier) domain	helicase	29331827, 264693
1008	76854963 (2175, 2176)	Novel Protein sim. GBank glt2983155 (AE000893) - phosphoglucomutase/phosphomannomutase (Aquila aquilus)		UNCLASSIFIED	264905, 264601, 16106387
1009	80216600 (2177, 2178)	Novel Protein sim. GBank glt4981758sq1AD06500_1(AE00177) - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermoga margaritae]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 kDa subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264788, 264689, 21900764, 35695917, 265020, 32633986, 16106370, 35695955
1010	11083825 (2179, 2180)	Novel Protein sim. GBank glt4007560lamb1CA22366 - (AL034443) putative oxidoreductase (Streptomyces coelicolor)			264604
1011	12917471 (2181, 2182)	Novel Protein sim. GBank glt2495562sq1P7209YLCO_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264637
1012	80252266 (2183, 2184)	Novel Protein sim. GBank glt2600909lamb1CA117998_1 - (AL002121) adh (Mycobacterium tuberculosis)	Contains protein domain (PF00730) - Endonuclease III	nuclease	264568 264769, 35695917, 35695955, 264600, 264602, 264603, 264605, 16106351
1013	80496304 (2185, 2186)	Novel Protein sim. GBank glt1001642q1p4A_10373 - (064002) GTPase [Thermoplasma volcanum]	UNCLASSIFIED		264686
1014	10880972 (2187, 2188)	Novel Protein sim. GBank glt1001642q1p4A_10373 - (064002) GTPase [Thermoplasma volcanum]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deor family	nuclease	264905, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264786, 264769, 264636, 264558, 16106367, 60432113, 264482, 264496
1015	87457250 (2189, 2190)	Novel Protein sim. GBank glt4053537lamb1CA040685_1 - (AL049828) putative adenine glycosylase [Streptomyces coelicolor]		synthase	264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1016	80025977 (2191, 2192)	Novel Protein sim. GBank glt11500116p1P209JB0B_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		UNCLASSIFIED	265019 264687
1017	76239560 (2193, 2194)	Novel Protein sim. GBank glt114159p1P209JB0B_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		UNCLASSIFIED	
1018	76188424 (2185, 2186)	Novel Protein sim. GBank glt114159p1P209JB0B_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		UNCLASSIFIED	

1109	35523638 (2197, 2198)	Novel Protein sim. GBank gl3915144[spQ3307]TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (MTG- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gl3023255[spQ64420]ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FAITY ACID DESATURASE) (DELTA9-DESATURASE)		desaturase	264259, 264636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gl1174735[spQ43012]TOP1_JAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769
1102	79777614 (2203, 2204)	Novel Protein sim. GBank gl1906596 (U81768) - kinesin-73		UNCLASSIFIED	264910, 264909
1103	81897259 (2205, 2206)	[Drosophila melanogaster]		struct	264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gl2535448 (AF048970) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	26331822, 21006754, 264555, 264556, 264558, 22279002
1105	80255121 (2209, 2210)				264566
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 264369
1107	80470019 (2213, 2214)				264908, 264769
1108	80440818 (2215, 2216)	Novel Protein sim. GBank gl1173421[spQ43416]SECY_STRSC - PREPROTEIN TRANSLUCASE SECY SUBUNIT		transport	264907, 264510, 264511, 264600, 264602, 264605, 264768, 264769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gl2695310[emb]CAA18338] - (AL022286) putative ATP-dependent helicase (Streptomyces coelicolor]		helicase	264602, 264605, 264636
1110	80503554 (2218, 2220)				264908, 264583, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264636
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gl2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			18108370, 264557
1112	95010088 (2223, 2224)	Novel Protein sim. GBank gl321837[emb]CAA19628] - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	264908
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gl1083428[pm]J554876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	264600, 264602, 264604, 264605, 264762, 264769, 264585
1114	14998014 (2227, 2228)				264636
1115	11765583 (2229, 2230)			UNCLASSIFIED	264666
1116	79841152 (2231, 2232)				264908

1117	93050465 (2233, 2234)	Novel Protein sim. GBank glij255695jmb CA9440891- (Z70200) US snRNP-specific 200MD protein (Homo sapiens)	Contains protein domain (PF00270): DEAD/DEAH box helicase	Helicase	18108392, 264488, 263594, 264489, 18108398, 56162575, 22278995, 22278996, 3566286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696002, 33656970, 29146486, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264909, 52640445, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 56812038, 264596, 264758, 264759, 21987764, 33109854, 33657094, 265011, 87198559, 264600, 264601, 264602, 264603, 264760, 56811150, 264681, 264762, 264763, 264764, 264765, 264766, 264767, 264768, 264769, 264788, 264889, 264890, 264891, 264892, 264893, 264894, 264895, 264786, 264787, 264788, 264789, 264790, 264791, 264792, 264793, 264794, 264795, 264796, 264797, 264798, 264799, 264800, 264801, 264802, 264803, 264804, 264805, 264806, 264807, 264808, 264809, 264810, 264811, 264812, 264813, 264814, 264815, 264816, 264817, 264818, 264819, 264820, 264821, 264822, 264823, 264824, 264825, 264826, 264827, 264828, 264829, 264830, 264831, 264832, 264833, 264834, 264835, 264836, 264837, 264838, 264839, 264840, 264841, 264842, 264843, 264844, 264845, 264846, 264847, 264848, 264849, 264850, 264851, 264852, 264853, 264854, 264855, 264856, 264857, 264858, 264859, 264860, 264861, 264862, 264863, 264864, 264865, 264866, 264867, 264868, 264869, 264870, 264871, 264872, 264873, 264874, 264875, 264876, 264877, 264878, 264879, 264880, 264881, 264882, 264883, 264884, 264885, 264886, 264887, 264888, 264889, 264890, 264891, 264892, 264893, 264894, 264895, 264896, 264897, 264898, 264899, 264900, 264901, 264902, 264903, 264904, 264905, 264906, 264907, 264908, 264909, 264910, 264911, 264912, 264913, 264914, 264915, 264916, 264917, 264918, 264919, 264920, 264921, 264922, 264923, 264924, 264925, 264926, 264927, 264928, 264929, 264930, 264931, 264932, 264933, 264934, 264935, 264936, 264937, 264938, 264939, 264940, 264941, 264942, 264943, 264944, 264945, 264946, 264947, 264948, 264949, 264950, 264951, 264952, 264953, 264954, 264955, 264956, 264957, 264958, 264959, 264960, 264961, 264962, 264963, 264964, 264965, 264966, 264967, 264968, 264969, 264970, 264971, 264972, 264973, 264974, 264975, 264976, 264977, 264978, 264979, 264980, 264981, 264982, 264983, 264984, 264985, 264986, 264987, 264988, 264989, 264990, 264991, 264992, 264993, 264994, 264995, 264996, 264997, 264998, 264999, 265000, 265001, 265002, 265003, 265004, 265005, 265006, 265007, 265008, 265009, 265010, 265011, 265012, 265013, 265014, 265015, 265016, 265017, 265018, 265019, 265020, 265021, 265022, 265023, 265024, 265025, 265026, 265027, 265028, 265029, 265030, 265031, 265032, 265033, 265034, 265035, 265036, 265037, 265038, 265039, 265040, 265041, 265042, 265043, 265044, 265045, 265046, 265047, 265048, 265049, 265050, 265051, 265052, 265053, 265054, 265055, 265056, 265057, 265058, 265059, 265060, 265061, 265062, 265063, 265064, 265065, 265066, 265067, 265068, 265069, 265070, 265071, 265072, 265073, 265074, 265075, 265076, 265077, 265078, 265079, 265080, 265081, 265082, 265083, 265084, 265085, 265086, 265087, 265088, 265089, 265090, 265091, 265092, 265093, 265094, 265095, 265096, 265097, 265098, 265099, 265100, 265101, 265102, 265103, 265104, 265105, 265106, 265107, 265108, 265109, 265110, 265111, 265112, 265113, 265114, 265115, 265116, 265117, 265118, 265119, 265120, 265121, 265122, 265123, 265124, 265125, 265126, 265127, 265128, 265129, 265130, 265131, 265132, 265133, 265134, 265135, 265136, 265137, 265138, 265139, 265140, 265141, 265142, 265143, 265144, 265145, 265146, 265147, 265148, 265149, 265150, 265151, 265152, 265153, 265154, 265155, 265156, 265157, 265158, 265159, 265160, 265161, 265162, 265163, 265164, 265165, 265166, 265167, 265168, 265169, 265170, 265171, 265172, 265173, 265174, 265175, 265176, 265177, 265178, 265179, 265180, 265181, 265182, 265183, 265184, 265185, 265186, 265187, 265188, 26
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1129	60422480 (2257, 2258)	Novel Protein sim. GBank g[5689483]dbj AA30226.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank g[4981328]g AAD35881.1 AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055381 (2261, 2262)	Novel Protein sim. GBank g[1841552] (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank g[1841552] (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22276996, 264906, 265009, 264600, 264602, 264604, 264605, 264760, 32633986, 18106374
1133	17290437 (2265, 2266)	Novel Protein sim. GBank g[4982454]g AAD36931.1 AE00182 - (AE001823) ATP-dependent Protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	265018
1134	80235376 (2267, 2268)	Novel Protein sim. GBank g[4982454]g AAD34768.1 - (AF132180) unknown [Drosophila melanogaster]		UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank g[4982454]g AAD36931.1 AE00182 - (AE001823) ATP-dependent Protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264508, 264600, 264602, 264603, 18106376
1136	79842032 (2271, 2272)	Novel Protein sim. GBank g[4982454]g AAD36931.1 AE00182 - (AE001823) ATP-dependent Protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank g[4982454]g AAD34768.1 - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain		22276998, 22278999, 35696052, 264907, 265009, 60433356, 264596, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55811578, 35695855, 264631, 264632, 22275002
1138	78441163 (2275, 2276)	Novel Protein sim. GBank g[731807]sp P38739 YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT-1/RIM1 INTERGENIC REGION PRECURSOR	struct		264908
1139	76833561 (2277, 2278)	Novel Protein sim. GBank g[3650031] (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264693
1140	35480358 (2279, 2280)	Novel Protein sim. GBank g[3650031] (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264593
1141	79538019 (2281, 2282)	Novel Protein sim. GBank g[3650031] (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	265019, 264693
1142	15835848 (2283, 2284)	Novel Protein sim. GBank g[3650031] (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank g[328000]emb CA055880 - (AJ003125) procollagen 1 N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - oxidase		56182575, 264908, 264600, 264632, 87168518
1144	80089988 (2287, 2288)	Novel Protein sim. GBank g[328000]emb CA055880 - (AJ003125) procollagen 1 N-proteinase [Homo sapiens]	Thrombospondin type 1 domain		264635, 264636, 264907, 264593, 264908, 264596, 264909
1145	14610262 (2289, 2290)	Novel Protein sim. GBank g[249903]sp P76422 HID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)		UNCLASSIFIED	264112
1146	82062092 (2291, 2292)	Novel Protein sim. GBank g[249903]sp P76422 HID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)		UNCLASSIFIED	264769, 264689, 35696286, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)	Novel Protein sim. GBank g[249903]sp P76422 HID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank g[249903]sp P76422 HID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)		UNCLASSIFIED	264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank g[249903]sp P76422 HID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)		UNCLASSIFIED	264591

1150	8132507.4 (2329, 2300)	Novel Protein sim. GBank gl 2859505 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase associated	264488, 35696286, 264307, 264308, 264309, 264310, 264311, 264312, 264313, 264314, 264315, 264316, 264317, 264318, 264319, 264320, 264321, 264322, 264323, 264324, 264325, 264326, 264327, 264328, 264329, 264330, 264331, 264332, 264333, 264334, 264335, 264336, 264337, 264338, 264339, 264340, 264341, 264342, 264343, 264344, 264345, 264346, 264347, 264348, 264349, 264350, 264351, 264352, 264353, 264354, 264355, 264356, 264357, 264358, 264359, 264360, 264361, 264362, 264363, 264364, 264365, 264366, 264367, 264368, 264369, 264370, 264371, 264372, 264373, 264374, 264375, 264376, 264377, 264378, 264379, 264380, 264381, 264382, 264383, 264384, 264385, 264386, 264387, 264388, 264389, 264390, 264391, 264392, 264393, 264394, 264395, 264396, 264397, 264398, 264399, 264400, 264401, 264402, 264403, 264404, 264405, 264406, 264407, 264408, 264409, 264410, 264411, 264412, 264413, 264414, 264415, 264416, 264417, 264418, 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1151	8007087.4 (2301, 2302)	Novel Protein sim. GBank gl 4324655(gb AA016978) - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	264595
1152	8023554.7 (2303, 2304)	Novel Protein sim. GBank gl 3874275(emc CA07311.1) - (Z92825) predicted using Genefinder. Similarity to Yeast low affinity glucose transporter HXT4 (PS-32467). cDNA EST EMBL C12555 comes from this gene; cDNA EST YK04C10.3 comes from this gene; cDNA EST YK04C10.5 comes from this gene.		glycoprotein	264488, 22276998, 264905, 264628, 264486
1153	8002783 (2305, 2306)	Novel Protein sim. GBank gl 4240315(d BAA74336.1) - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557
1154	83002995 (2307, 2308)	Novel Protein sim. GBank gl 596655(p P37617 ATZN, ECOLI - ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLCATING P-TYPE ATPASE)	Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	265008
1155	79411098 (2309, 2310)	Novel Protein sim. GBank gl 184901(p P32139 YHR, ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION		UNCLASSIFIED	264689, 264638, 264666
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gl 2498481(p Q50724 YOS, MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		UNCLASSIFIED	264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gl 1136406(d BAA11490) - (D79995) similar to pig tubulin-lysine ligase. [Homo sapiens]		UNCLASSIFIED	264687
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gl 1741743 (2321, 2322)		UNCLASSIFIED	29331822, 29331824, 66714117, 29331828, 29331830, 29331832, 29331834, 29331836, 29331838, 29331840, 29331842, 29331844, 29331846, 29331848, 29331850, 29331852, 29331854, 29331856, 29331858, 29331860, 29331862, 29331864, 29331866, 29331868, 29331870, 29331872, 29331874, 29331876, 29331878, 29331880, 29331882, 29331884, 29331886, 29331888, 29331890, 29331892, 29331894, 29331896, 29331898, 29331900, 29331902, 29331904, 29331906, 29331908, 29331910, 29331912, 29331914, 29331916, 29331918, 29331920, 29331922, 29331924, 29331926, 29331928, 29331930, 29331932, 29331934, 29331936, 29331938, 29331940, 29331942, 29331944, 29331946, 29331948, 29331950, 29331952, 29331954, 29331956, 29331958, 29331960, 29331962, 29331964, 29331966, 29331968, 29331970, 29331972, 29331974, 29331976, 29331978, 29331980, 29331982, 29331984, 29331986, 29331988, 29331990, 29331992, 29331994, 29331996, 29331998, 29332000, 29332002, 29332004, 29332006, 29332008, 29332010, 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1167	79633962 (2333, 2334)	Novel Protein sim. G.Bank gji560433[dbj][AA23138] - (D76414) pGpp hydrolase (Staphylococcus aureus)			kinase	264488
1168	88094676 (2335, 2336)				UNCLASSIFIED	264259, 29331827, 56182435, 60434338, 265019, 33657023, 35695555, 264566
1169	11805403 (2337, 2338)				UNCLASSIFIED	264681
1170	21632244 (2339, 2340)				UNCLASSIFIED	264682
1171	20434582 (2341, 2342)	Novel Protein sim. G.Bank gji7727814 (AF029429) - procollagen D [Mytilus edulis]			UNCLASSIFIED	264556
1172	79610113 (2343, 2344)	Novel Protein sim. G.Bank gji4757846[refNP_004317, 1pBCL9 - b-cell CLL lymphoma 9]			UNCLASSIFIED	55810764, 35696052, 264634, 264486
1173	80235713 (2345, 2346)	Novel Protein sim. G.Bank gji564053[dbj][AA22946] - (A8007832) Bm trachealless (Bombyx mori)				264508, 264906, 264807, 264809, 264591, 264632, 264638, 264839
1174	20293077 (2347, 2348)	Novel Protein sim. G.Bank gji3911027[emb][CAAT1520] - (AL021958) mmsA [Mycobacterium tuberculosis]			dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. G.Bank gji118333[igpP23234]DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)			carboxylase	264601
1176	80252445 (2351, 2352)	Novel Protein sim. G.Bank gji1144520 (U34956) - phosphoribosylformylglycylamidine synthase [Mycobacterium tuberculosis]			synthase	264509, 264805, 264833, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. G.Bank gji119791[igpP28643]FABG_CURLA - 3-OXOACYL-ACYL-CARRIER PROTEIN REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)			reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. G.Bank gji031697[refNP_005594, 1pFC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)]			Contains protein domain (PF00368) - ATPase-associated E1-E2 ATPase	65274572, 18106398, 22278998, 22278999, 29331826, 264508, 264908, 264628, 33657402, 33109944, 264769, 21906765, 21906766, 21806768, 55811957, 33657023, 264629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22278000, 22279002
1179	80055275 (2357, 2358)	Novel Protein sim. G.Bank gji2960090[emb][CAAT7888, 1] - (AL022121) dppA [Mycobacterium tuberculosis]			transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. G.Bank gji2558614[emb][CAA04787] - (AJ001483) dehydroquinolate dehydratase [Streptomyces coelicolor]			Bacterial extracellular solute-binding proteins, family 5	264638
1181	17946362 (2361, 2362)	Novel Protein sim. G.Bank gji5420387[emb][CAB46678, 1] - (AJ243459) proteophosphylican [Leishmania major]			Contains protein domain (PF01220) - synthase	265017
1182	81494264 (2363, 2364)				Dehydroquinase class II	265007, 265009, 264584, 264909, 264693
1183	79574044 (2365, 2366)	Novel Protein sim. G.Bank gji4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]				264689, 35696423, 264638, 18105385
1184	52559933 (2367, 2368)	Novel Protein sim. G.Bank gji2128479[igf][S51939 - chitinase (EC 3.2.1.14) precursor - beet			UNCLASSIFIED	264602
1185	79491185 (2369, 2370)				glycoprotein	263967

1185	20224012 (2371, 2372)					264559
1187	79248834 (2373, 2374)					2631825, 265017, 16108351
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gi 2960039 (AF054526) - hypothetical protein [Synchococcus PCC7002]				264905, 264906
1189	79609367 (2377, 2378)					264692
1190	79830589 (2379, 2380)					265018
1191	80310105 (2381, 2382)					264600, 264605, 264764, 35695955, 264639, 264486
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMRF amide related peptide family			264636
1193	11103584 (2385, 2386)	Novel Protein sim. GBank gi 854055 (emb CA583371) - (X83413). U88 [human herpesvirus 6]				263978
1194	79893947 (2387, 2388)	Novel Protein sim. GBank gi 170277 (AE000459) - putative oxidoreductase [Escherichia coli]				265007, 265008
1195	20445442 (2389, 2390)					264605
1196	13000688 (2391, 2392)	Novel Protein sim. GBank gi 2497360 (sp Q50715) (MOH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)				264689
1197	11392317 (2393, 2394)		Contains protein domain (PF00571) - CBS domain			264594
1198	95290101 (2395, 2396)	Novel Protein sim. GBank gi 1709525 (sp P54673) (P3K1_DICDI - PHOSPHATIDYLINOSITOL 3-KINASE 1 (P13-KINASE) (PTDINS-3-KINASE) (P13K)				264603
1199	81882011 (2397, 2398)					264239, 264757, 3310954, 21906768
1200	9848860 (2399, 2400)	Novel Protein sim. GBank gi 2498877 (sp P70645) (BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)				264910
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 605342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]				264768, 264769
1202	80062633 (2403, 2404)					264600, 264558
1203	82125373 (2405, 2406)					264768, 264769, 35695917, 264910, 264760, 264906, 264907, 264629, 264905, 264909, 264766
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 (sp Q59912) (SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT				264905, 264769, 264636
1205	80053961 (2409, 2410)					264666
1206	80241965 (2411, 2412)					264556, 264557, 264558
1207	79941192 (2413, 2414)					26331824, 264907, 265021, 18108370
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2 related ovarian killer protein [Rattus norvegicus]				26331824, 26331825, 26331827, 265007, 264764, 264683, 264768, 264688, 264689

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gl117503[sp]p44398[Xyla_HAEN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)	Novel Protein sim. GBank gl3080[sp]p30688 - hypothetical protein o246 - Escherichia coli		UNCLASSIFIED	264907, 264693
1211	94665655 (2421, 2422)	Novel Protein sim. GBank gl3080[sp]p30688 - (293785) predicted using GeneFINDER, similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL:011692 comes from this gene; cDNA EST EMBL:0179923 comes from this gene; cDNA EST EMBL:027559 comes from this gene	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transferase	264591, 264592, 264595
1212	79167929 (2423, 2424)	Novel Protein sim. GBank gl3080[sp]p30688 - (293785) predicted using GeneFINDER, similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL:011692 comes from this gene; cDNA EST EMBL:0179923 comes from this gene; cDNA EST EMBL:027559 comes from this gene			264689, 263967
1213	79959633 (2425, 2426)	Novel Protein sim. GBank gl2262[sp]p1505375A - vr gene (Bordetella pertussis)		kinase	264909
1214	10143306 (2427, 2428)	Novel Protein sim. GBank gl572628[sp]p4048396.1[AF12616] (AF12616) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050106 (2429, 2430)	Novel Protein sim. GBank gl23267[sp]p10953[(29268) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	26438324 (2431, 2432)	Novel Protein sim. GBank gl417329[sp]p33038[MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYLPRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOYLPRUVYL TRANSFERASE) (EPT)]		transferase	264604
1217	95011344 (2433, 2434)				
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gl1805460[db][BAA09022] - (D50453) homologue of succinate semialdehyde dehydrogenase GdbD of E. coli [Bacillus subtilis]		UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564
1219	87126252 (2437, 2438)			dehydrogenase	264601
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gl4240315[db][BAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	55181686, 29331822, 60432289, 264601, 264692, 264629
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gl2143866[sp]p152223 - nucleoporin p62 homolog - rat (fragment)			52644507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gl73005[sp]p39683[SPHR_SYPN7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	UNCLASSIFIED	264788, 265020, 264906
1223	11615647 (2445, 2446)			phosphatase	264601
1224	86432845 (2447, 2448)	Novel Protein sim. GBank gl117502[sp]p46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)]	Contains protein domain (PF01472) - PLA domain	kinase	264593 264593, 264600, 264601, 264603, 264605, 264788, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gll12105650[eml]CA008336] - (Z95438) hypothetical protein R3044c [Mycobacterium tuberculosis]		polymerase	264768 264905, 264512, 264689
1226	80237518 (2451, 2452)	Novel Protein sim. GBank gll106768[pp98133]FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP240)		UNCLASSIFIED	264908, 264637, 264639
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gll1653501[pp]BAA188111 - Novel Protein sim. GBank gll1653501[pp]BAA188111 - (D90917) acriflavine resistance protein [Symbiodinium sp.]	Contains protein domain (PF00873) - Acridin/DNAcr family		264605, 264634
1228	79208027 (2455, 2456)	Novel Protein sim. GBank gll1653501[pp]BAA188111 - Novel Protein sim. GBank gll1653501[pp]BAA188111 - (D90917) acriflavine resistance protein [Symbiodinium sp.]	Contains protein domain (PF00118) - TCP-1/tpm60 chaperonin family		87168474, 265011, 87168556, 264681, 264689, 264693, 63274620, 18108374
1229	94329135 (2457, 2458)	Novel Protein sim. GBank gll1653501[pp]BAA188111 - Novel Protein sim. GBank gll1653501[pp]BAA188111 - (D90917) acriflavine resistance protein [Symbiodinium sp.]		-eph	264909, 264605, 18108398
1230	80048357 (2459, 2460)	Novel Protein sim. GBank gll1653501[pp]BAA188111 - Novel Protein sim. GBank gll1653501[pp]BAA188111 - (D90917) acriflavine resistance protein [Symbiodinium sp.]		UNCLASSIFIED	264908 264909
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gll1215733 (U48718) - OHC		UNCLASSIFIED	265017, 264654
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gll1215733 (U48718) - OHC		UNCLASSIFIED	265017, 264654
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gll1192398[pp]P20730C[HG, BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN IS PRECURSOR (HC-B 13).		UNCLASSIFIED	265017, 264654
1234	79422158 (2467, 2468)	Novel Protein sim. GBank gll1295671[pp]P40280[H2A, MAIZE - HISTONE H2A	Contains protein domain (PF00123) - Core histone H2A/H2B/H2H4	histone	265009, 265010, 18108381
1235	79914423 (2469, 2470)	Novel Protein sim. GBank gll1295671[pp]P40280[H2A, MAIZE - HISTONE H2A			264634, 264762
1236	81027147 (2471, 2472)	Novel Protein sim. GBank gll1295671[pp]P40280[H2A, MAIZE - HISTONE H2A		UNCLASSIFIED	265018, 55811150, 264855, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gll13875133[eml]CA04750] - (Z70750) similar to acid binding domain, CDNA EST EMBL D00093 comes from this gene, CDNA EST EMBL D34443 comes from this gene, CDNA EST EMBL D37508 comes from this gene, CDNA EST EMBL D84247 comes from this gene, CDNA EST EMBL... Novel Protein sim. GBank gll13875133[eml]CA04750] - G protein-coupled receptor LGR4 [Rattus norvegicus]			264756, 264801, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gll13875133[eml]CA04750] - (Z70750) similar to acid binding domain, CDNA EST EMBL D00093 comes from this gene, CDNA EST EMBL D34443 comes from this gene, CDNA EST EMBL D37508 comes from this gene, CDNA EST EMBL D84247 comes from this gene, CDNA EST EMBL... Novel Protein sim. GBank gll13875133[eml]CA04750] - G protein-coupled receptor LGR4 [Rattus norvegicus]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264255, 26331822, 26331824, 35686052, 264508, 264906, 52640445, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1239	82197448 (2477, 2478)	Novel Protein sim. GBank gll1007990[pp]AAC05339] - (AF084363) DOK protein [Mus musculus]		oncogene	264509, 264511, 264759, 264760, 264764, 264557
1240	80497255 (2479, 2480)	Novel Protein sim. GBank gll1176192[pp]P44520[HCD, ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLT-NANT INTERGENIC REGION PRECURSOR			264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gll121383[pp]P19809[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264801, 264804, 264638
1242	79759902 (2483, 2484)	Novel Protein sim. GBank gll121383[pp]P19809[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)			264906, 264807, 264808, 264634

1243	75779458 (2485, 2486)	Novel Protein sim. Gbank gi3355671[emb CAA11997.1] - (AL031124) branched-chain amino acid aminotransferase (Streptomyces coelicolor)		UNCLASSIFIED	18108374, 35695917, 35695955, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. Gbank gi2970946 (AF051949) - Xin (Mus musculus)		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. Gbank gi4586338[db BAA76357.1] - (AB016787) cytochrome c ubiquinol oxidase B (Pseudomonas putida)	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	- oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. Gbank gi3581848[emb CAA20805.1] - (AL031541) putative phenylalanyl-HRNA synthetase beta chain (Streptomyces coelicolor)		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. Gbank gi2621684 (AE000942) - adhesion protein (Methanobacterium thermoautotrophicum)			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. Gbank gi1352403[sp P09467.1F] - HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 26331825, 264106, 264508, 264907, 264828, 265009, 80433356, 264757, 264758, 21906754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. Gbank gi2791407[emb CAA18001.1] - (AL021184) hypothetical protein Rv1173 (Mycobacterium tuberculosis)		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2499, 2500)	Novel Protein sim. Gbank gi112765[sp P051003MG1.1] - ECOLI - DNA-3-METHYLADENINE GLYCOSYLASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)	Novel Protein sim. Gbank gi112765[sp P051003MG1.1] - ECOLI - DNA-3-METHYLADENINE GLYCOSYLASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)			264909
1252	79458087 (2503, 2504)	Novel Protein sim. Gbank gi112765[sp P051003MG1.1] - ECOLI - DNA-3-METHYLADENINE GLYCOSYLASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. Gbank gi5870178[db AAC46818.1] - (AF161317) NRAMP manganese transport protein MnA (Salmonella typhimurium)		glycoprotein	264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. Gbank gi103160[sp S22126.1] - finger protein untempl. - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906767, 55811957, 264592, 264556, 264639
1255	79169728 (2509, 2510)	Novel Protein sim. Gbank gi2995353[emb CAA04608.1] - (AD01206) pep2 (Streptomyces coelicolor)			264636
1256	87889508 (2511, 2512)	Novel Protein sim. Gbank gi3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB-AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27186265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. Gbank gi3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB-AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20709150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264908
1260	80084606 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gi5689511[dbj BAAC0309.1] - (A9028010) KIAA1087 protein (Homo sapiens)	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264905, 264765, 264769, 264689, 264693, 264639, 18108384, 264563
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gi95100[pir S21334] - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	264634
1263	20710997 (2525, 2526)	Novel Protein sim. GBank gi3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264602
1264	80083396 (2527, 2528)	Novel Protein sim. GBank gi1085002[pir S55056] - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans		struct	264602
1265	80253579 (2529, 2530)	Novel Protein sim. GBank gi1085002[pir S55056] - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264563
1266	79914604 (2531, 2532)	Novel Protein sim. GBank gi4886445[emb CA843370.1] - (AL050268) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264766, 264636, 264638, 264567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gi4886445[emb CA843370.1] - (AL050268) hypothetical protein [Homo sapiens]		transport	264259, 21906754, 264369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gi3334791[emb CAA119939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 29331827, 264109, 2644512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21906767, 265020, 52644150, 264691, 33657023, 33657348, 18108374, 264556, 18108385, 60432113, 22279002, 264486
1269	79821946 (2537, 2538)	Novel Protein sim. GBank gi3334791[emb CAA119939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gi2851634[sp Q50591 Y001_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	263010, 264601
1271	78840489 (2541, 2542)	Novel Protein sim. GBank gi2851634[sp Q50591 Y001_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01		ATPase associated	35696052, 264908
1272	79462878 (2543, 2544)	Novel Protein sim. GBank gi1655665[emb CA603731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gi1655665[emb CA603731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)	Novel Protein sim. GBank gi123728[sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)		UNCLASSIFIED	264905, 264908, 264909, 264769
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gi123728[sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	oph	264602
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gi123728[sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)		UNCLASSIFIED	264369
1277	20438155 (2553, 2554)	Novel Protein sim. GBank gi1175473[sp P44555 YAA1_HAEIN - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	264556
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gi1175473[sp P44555 YAA1_HAEIN - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	264603
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gi11929513 (U64319) - ATP synthase subunit beta [Moorella thermoacetica]		synthase	264605
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gi4938504[emb CA843862.1] - (AL078465) putative protein [Arabidopsis thaliana]		struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank g1136501 (J38546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - immunoglobulin domain	UNCLASSIFIED	26331825, 26331828, 264766, 63373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank g3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank g1326172 (emb)CA807031 - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank g13929022 (AF57696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank g1175415pP33126HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - Hsp90 protein		264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank g12078004 (emb)CA808451 - (Z925207) gcrA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)		UNCLASSIFIED		265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264638, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank g15353510 (p)AD42161.1 (AF08891) - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	collagen	35696052, 264107, 264508, 264509, 264805, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265008, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264764, 264286, 264685, 264766, 264687, 264769, 264769, 264686, 265020, 265021, 264534, 264682, 18108370, 264628, 18108374, 35696423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264486, 18108391, 264637
1289	11813847 (2577, 2578)	Novel Protein sim. GBank g116995 (p)P46023GPCR LYMTST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	264563
1290	19528027 (2576, 2580)	Novel Protein sim. GBank g1207267 (emb)CA808395 - (Z95120) rHE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1291	80470268 (2581, 2582)	Novel Protein sim. GBank g11635755 (U060338) - zinc finger protein Prg-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	264082, 264269, 26331822, 26331824, 264508, 264906, 264909, 264512, 265008, 265009, 264591, 265019, 264689, 264286, 264686, 264768, 264689, 18108374, 264632, 59182323, 264639, 63373044, 22279002, 264482, 264689
1292	94722316 (2583, 2584)	Novel Protein sim. GBank g12129173 (p) (J64453) - oxalacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii	UNCLASSIFIED	blotting	265006, 55812038, 264389, 264556, 264602, 264605, 264760, 18108357, 264689, 33657023, 264559
1293	80067536 (2585, 2586)	Novel Protein sim. GBank g12129173 (p) (J64453) - oxalacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii			264689
1294	82125908 (2587, 2588)	Novel Protein sim. GBank g1544177 (emb)CA848603.1 - (AL096811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	dehydrogenase		

1286	11687904 (2591, 2592)	Novel Protein sim. GBank			UNCLASSIFIED	264591, 264639
1287	79839300 (2593, 2594)	gl498219 (lgb)AD36666.1(AE0180) - directed DNA polymerase I [Thermotoga maritima]	5'-3' exonuclease		polymerase	264693
1288	94239506 (2595, 2596)	Novel Protein sim. GBank gl1943776 (UG97191) - F53F-10.1 gene product [Caenorhabditis elegans]			stuct	18108348, 265017
1289	80255378 (2597, 2598)	Novel Protein sim. GBank gl3454181 (AC005498) - R31665.2 [Homo sapiens]				264488, 264906, 264909, 22279002, 264566
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gl4062973(dg)BA336204.11 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	KRA8 box		transcriptase	264605
1301	17939614 (2601, 2602)	Novel Protein sim. GBank gl324273(emb)CAB070171 - (252669) hypothetical protein Fv0236c [Mycobacterium tuberculosis]			UNCLASSIFIED	264906
1302	95416198 (2603, 2604)	Novel Protein sim. GBank gl1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]				85658542, 265020
1303	9684121 (2605, 2606)	Novel Protein sim. GBank gl95819(gl)S16298 - ferric enterobactin transport protein fepC - Escherichia coli			UNCLASSIFIED	264908
1304	79377196 (2607, 2608)	Novel Protein sim. GBank gl545922(emb)CAB48693.11 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			UNCLASSIFIED	264508
1305	19905899 (2609, 2610)	Novel Protein sim. GBank gl324273(emb)CAB070171 - (252669) hypothetical protein Fv0236c [Mycobacterium tuberculosis]			UNCLASSIFIED	264566
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gl324273(emb)CAB070171 - (252669) hypothetical protein Fv0236c [Mycobacterium tuberculosis]			UNCLASSIFIED	264636
1307	82201029 (2613, 2614)	Novel Protein sim. GBank gl1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]			UNCLASSIFIED	264907, 264592, 264764
1308	21428814 (2615, 2616)	Novel Protein sim. GBank gl95819(gl)S16298 - ferric enterobactin transport protein fepC - Escherichia coli	Envelope glycoprotein GP120		reductase	264555
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gl545922(emb)CAB48693.11 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			transport	264906, 18108354
1310	20466319 (2619, 2620)	Novel Protein sim. GBank gl545922(emb)CAB48693.11 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			UNCLASSIFIED	264605
1311	87613142 (2621, 2622)	Novel Protein sim. GBank gl445518(lgb)AAD210841 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]				35690286, 29331827, 264908, 265008, 264784, 264786, 264686, 21906767, 21906769, 35695917, 264691, 264693, 22278995, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21906768, 265020, 265021, 33657023, 22279002, 264564
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gl445518(lgb)AAD210841 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]				22278995, 22278998, 264258, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695955, 60433113, 22279000, 264563, 18108390
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gl492933(lgb)AAD34127.1(AF151890) CGI-132 protein [Homo sapiens]	Ribosomal protein S16		ribosomalprot	264683
1314	56926053 (2627, 2628)	Novel Protein sim. GBank gl2589223 (AF026565) - ring finger protein [Mus musculus]				264691
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gl2589223 (AF026565) - ring finger protein [Mus musculus]			interleukinrecept	

1316	95361609 (2631, 2632)	Novel Protein sim. GBank gll5699407dbj BAAQ2887.1] - (ABD28958) KIAA1035 protein [Homo sapiens]	kinase	56182575, 56181686, 20281171, 29331822, 29331824, 60424999, 29331825, 35696052, 52644045, 264591, 60432229, 265018, 265019, 5581150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170615, 33657023, 63274620, 33657109, 35695763, 35695955, 18108387, 87168516, 60432113, 22779002, 264654
1317	86055167 (2633, 2634)	Novel Protein sim. GBank gll483675jgb AAD30541.1 AF13491.1 (AF134918) semaphorin subclass 4 member G [Mus musculus]	UNCLASSIFIED	264083, 264906, 264909, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gll480204jgb AAD27587.1 AF11417.1 (AF114171) hypothetical protein [Sorghum bicolor]	UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108395, 22779000
1319	94238546 (2637, 2638)			264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108368, 264628, 264629, 18108377, 264638
1320	86603587 (2639, 2640)	Novel Protein sim. GBank gll4240783jdbj BAA74870.1] - (ABD20654) KIAA0847 protein [Homo sapiens]	UNCLASSIFIED	35696266, 55812038, 265018, 21906768, 265020, 263978, 22779002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gll4886505jemb CBA43377.1] - (ALD50276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	60432049, 293331328, 264807, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gll526259jemb CBA45736.1] - (ALD80143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - dna_mn_bind	29331828, 264909, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gll5459516jdbj BAA82407.1] - (ABD29821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]	synthase	65274572, 56994075, 264758, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906768, 21906767, 35695917, 265020, 264693, 63274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gll503171TrefNP_005704.1 GCPBP - goodpasture antigen-binding protein	Contains protein domain (PF01652) - START domain	22778996, 22778998, 29331828, 264805, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264563, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gll3294507.1 (U64857) - similar to the DPTKunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	protease	35696266, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85558542, 264760, 264768, 264691, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gll139725 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi728832splP39169/ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21906754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21906767, 21906769, 29148629, 265020, 264890, 264691, 264692, 264693, 263967, 33657109, 33657182, 27486262, 33657349, 18108370, 18108374, 55810764, 36695855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567, 264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 264482, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 264482, 264567
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi4678224glg/AD2896.1/AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264584, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56526488
1331	87316764 (2661, 2662)	Novel Protein sim. GBank gi4589686/djBAA76815.1j - (AB023188) KIAA0871 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi5459516/djBAA82407.1j - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]	synthase		65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52640435, 56182435, 264510, 21906754, 87168559, 265018, 265019, 264448, 264288, 264389, 264686, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	86098476 (2665, 2666)	Novel Protein sim. GBank gi5689527/djBAA83047.1j - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]	phosphatase		264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi4240283/djBAA74921.1j - (AB020705) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 264286, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486264, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi465445[ipP33485]VNUA - PROBABLE NUCLEAR ANTIGEN		UNCLASSIFIED	264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi5689471[dbjBAA63019.1] - (AB028900) KIAA1087 protein [Homo sapiens]		UNCLASSIFIED	56182575, 56994075, 22278998, 22278999, 264092, 264259, 60432266, 26331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 58812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264369, 264688, 264689, 21906765, 21906766, 265020, 264691, 27486281, 20281068, 18108379, 58811576, 35695855, 56182323, 60432113, 22279002, 264687
1338	80366114 (2675, 2676)			UNCLASSIFIED	29331822, 265010, 264286, 264688, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	35980552, 264909, 264688, 264556, 264558
1340	68316311 (2679, 2680)				264905, 264907, 87168559, 264764
1341	68101485 (2681, 2682)				264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi5019564[embjCAB44507.1] - (AL035542) dJ99AE3.5 (p46M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - tm7 7 transmembrane receptor (rhodopsin family)		264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543[refNP_001364.1]pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - struct Leucine Rich Repeat		264910, 264686, 264534
1344	20562559 (2687, 2688)				263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi2144101[refj155210] - Iricarboxyle carrier - rat (fragment)	glycoprotein		264909, 80170394
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi381052[embjCAA19523] - (AL023843) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL M89047 comes from this gene; cDNA EST yk246a12.5 comes....	Contains protein domain (PF00089) - kinase Eukaryotic protein kinase domain		22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264586
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504373[refNP_003658.1]pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		264906, 264908, 264909, 265006, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264587, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi3399720[dbjBAA332100] - (AB010999) peptidylarginine deaminase type IV [Rattus norvegicus]	UNCLASSIFIED		264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264486

1349	91225548 (2697, 2699)	Novel Protein sim. GBank glj2144101[pr][j55210 - tincarboxylate carrier - rat (fragment)]		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 284259, 29331822, 29331824, 35696052, 284509, 284905, 284906, 284907, 284908, 284909, 284511, 285006, 284512, 284910, 60470831, 284581, 60433438, 284757, 21906754, 285017, 285018, 284605, 284780, 284782, 284288, 284786, 284689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 285020, 284534, 284691, 284692, 33657023, 284693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 284563, 284564
1350	87093136 (2698, 2700)			UNCLASSIFIED	52646842, 284259, 29331825, 384308, 284511, 284604, 284288, 21906769, 285020, 33657182, 33657349, 18108374, 35695855, 284555, 284558, 18108385, 22279002, 284486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank glj4887239[gs][AD32246.1] - (AF084564) BAW protein [Fugu rubripes]		UNCLASSIFIED	284906, 284907, 284638
1352	80076386 (2703, 2704)			UNCLASSIFIED	284653, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank glj2144101[pr][j55210 - tincarboxylate carrier - rat (fragment)]		UNCLASSIFIED	35696286, 60424269, 284905, 284509, 284906, 284907, 284908, 284909, 284511, 284512, 284910, 284758, 284598, 55811386, 285011, 284605, 55811150, 284762, 284764, 284756, 52644229, 56181562, 35695917, 285022, 33657023, 284693, 35695763, 60431528, 284629, 285978, 35696423, 35695855, 284630, 284634, 284635, 284638, 284637, 284638, 284639, 18108385, 284563, 284564, 284566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank glj489108[gs][AD27763.1AF077030] hypoetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 284906, 285008, 33657402, 21906754, 285011, 87168559, 284684, 284369, 284769, 284689, 21906765, 21906768, 52644150, 33657023, 284692, 284693, 18108374, 83373044, 87168518, 22279000
1355	86280186 (2709, 2710)	Novel Protein sim. GBank glj1465159[gs][AA09487] - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		22278996, 22278997, 284259, 68714117, 284511, 21906754, 285010, 284769, 284689, 21906765, 21906768, 21906769, 284532, 27486282, 284629, 284636, 284556, 284638, 284639, 284482, 284484

1356	65313991 (2711, 2712)	Novel Protein sim. GBank gl1113865 (U40342) - ninenin [Mus musculus]		struct	18106397, 22278995, 22278996, 22278998, 264094, 29331826, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264754, 18108354, 264689, 21906765, 265022, 18108364, 35696423, 83373044, 18108387
1357	68260288 (2713, 2714)	Novel Protein sim. GBank gl897693[emb]CAA90330] - (250028) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264259, 29331822, 29331825, 264510, 87168559, 265016, 264448, 264288, 21906765, 21906766, 21906788, 265021, 264693, 18108376
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gl556219 (36831) - transcription regulator [Mus musculus]			264757
1359	8771643 (2717, 2718)			UNCLASSIFIED	264907, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108395, 264486, 264657
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gl2598282[emb]CAA73612] - (Y15417) acetate-CoA ligase [Coprinus cinereus]		synthase	60432289, 264605
1361	87563527 (2721, 2722)	Novel Protein sim. GBank gl568943[dbj]BAA83005.1] - (AB028978) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)		35696286, 22278997, 22278999, 264259, 29331826, 264506, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21906754, 87168474, 265011, 264761, 264683, 264288, 264766, 264769, 264689, 21906765, 265020, 265021, 33857023, 55811576, 35696423, 284634, 60432113, 22279002, 364482, 264486
1362	65287961 (2723, 2724)	Novel Protein sim. GBank gl568941[dbj]BAA82989.1] - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	- eph	56182575, 35181688, 60432049, 264259, 29331822, 35182181, 29331827, 35696052, 29331826, 264905, 264906, 264908, 264956, 55812038, 65659542, 55811150, 264681, 264288, 264369, 35181562, 60431528, 55810764, 35696423, 60431850, 264558
1363	65758476 (2725, 2726)	Novel Protein sim. GBank gl1130494 (U35778) - ADP-ribosylalation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	- UNCLASSIFIED	264488, 29331826, 264907, 264887, 264889, 264693
1364	68179488 (2727, 2728)				
1365	83005108 (2729, 2730)	Novel Protein sim. GBank gl459562[dbj]BAA76803.1] - (AB023178) KIAA0959 protein [Homo sapiens]		oncogene	60432289, 60433356, 60433438, 87168559, 264603, 18108351, 21906766, 35696423, 60432113
1366	87000282 (2731, 2732)	Novel Protein sim. GBank gl1084044[pil]IS54495 - hypothetical protein YPR021c - yeast [Saccharomyces cerevisiae]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	264766, 265007

1367	87721210 (2733, 2734) Novel Protein sim. GBank glij484088[emb]CAB43240.11- (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) SAND domain	UNCLASSIFIED	264488, 52646842, 52646385, 22278995, 56994075, 35686286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35686052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265008, 60170831, 33657402, 5812038, 21906754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264534, 60170615, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695955, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18106391, 18106395, 56526486, 22279000, 264583, 264587
1368	94320078 (2735, 2736) Novel Protein sim. GBank glij64561[sp]P35280[RBI1_RAT] RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) Ras family	oncogene	264255, 29331822, 29331826, 60432289, 29331827, 35686052, 264508, 264905, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 264780, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264566, 264486, 264567 265008, 60432229, 60433336, 33657084, 21906764, 21906769, 264555, 264638, 264559, 264567
1369	[86634033 (2737, 2738) Novel Protein sim. GBank glij0062702 (J00550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264558, 264639, 18108395, 65274727, 264404, 264563, 264566, 264486
1370	[65316910 (2739, 2740) Novel Protein sim. GBank glij031823[refNP_005823.1]pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657094, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695955, 264558, 22279002, 264563
1371	[96336512 (2741, 2742) Novel Protein sim. GBank glij5032203[refNP_005714.1]TPSPA - tetraspan 5	Contains protein domain (PF00339) 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657094, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695955, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gl 840709 dbj BA009334 - (D50685) trans-sialidase [Trypanosoma cruzi]		collagen	263978
1373	80499421 (2745, 2746)			UNCLASSIFIED	264789, 21906765, 21906767, 22278999, 264691, 264910, 55812038, 265010, 264681, 264684
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gl 11876 pif JC1241 - beta-interferon-induced protein - rat		interferon	264907, 264510, 265007, 264512, 265008, 80432229, 264689, 65274791, 264555, 264556, 264557, 83373044, 60432113
1375	94236942 (2749, 2750)	Novel Protein sim. GBank gl 5648176 gb AAD03500.2 - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) WD domain, G-beta repeat	-kinase	52644507, 52645156, 52646842, 52646355, 56182575, 56181686, 22278996, 56994075, 35996286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 264805, 264509, 264906, 264907, 264908, 29331830, 264909, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109954, 33657084, 52644298, 87168474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 284764, 264288, 264389, 264766, 52644229, 21906765, 21906768, 21906787, 21906788, 21906769, 55811897, 35695917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 27486261, 33657349, 27486265, 35695763, 18108376, 55810794, 35696423, 35695855, 264630, 264631, 264634, 264638, 264555, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264553, 264654, 264656, 264557, 22278997
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gl 138350 sp P28968 VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED	264788, 264769, 35695917, 22278997, 264691, 264259, 29331822, 22278999, 35696052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264909, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 55826486, 265010, 265011, 264600, 264563, 264762, 264564, 264565, 264764, 264886, 264765
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gl 1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - ATPase-associated E1-E2 ATPase	-ATPase-associated	29331824, 264591, 265016, 264666, 264768, 55811957, 264693, 22279002

1378	87595071 (2755, 2746)	Novel Protein sim. GBank gi4107015[dbj BAA36393] - (AB001772) PEM-5 [Ciona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148827, 55811957, 264691, 18108386, 33657109, 18108368, 264635, 263981, 18108385, 265020
1379	85679344 (2757, 2748)	Novel Protein sim. GBank gi3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]		nud_rept	264510, 264512, 265009, 264288, 264564
1380	87627962 (2759, 2760)	Novel Protein sim. GBank gi4837373[gb AD30662.1] - (AF06834) germ cell specific Y box binding protein [Homo sapiens]			
1381	86179656 (2761, 2762)	Novel Protein sim. GBank gi4731580[gb AD28508.1] (AF125394) L82A [Drosophila melanogaster]		UNCLASSIFIED	87166559, 265017, 264628, 22279002
1382	94847576 (2763, 2764)		Contains protein domain (PF00543) - Acyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432228, 60433356, 85658542, 265017, 265018, 264685, 264788, 21906766, 35695817, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87660598 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264750, 18108351, 264766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264584, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gi2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	35696052, 55611386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gi2384910 (AF022382) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		ht	60432289, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264566
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gi4160304[emb CAA10600] - (AJ132192) HST binding protein 3 [Mus musculus]		UNCLASSIFIED	264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gi44895164[gb AD32753.1] (AC00723) putative disease resistance protein [Arabidopsis thaliana]		gypcoprotein	65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264682, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1389	91256016 (2777, 2718)	Novel Protein sim. GBank gl 569337 db BA-82977-1 - (A020945) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264906, 6872502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 63373944, 22279000, 264563, 264564, 52645156, 52646365, 264259, 52645030, 29331825, 29331826, 264906, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264428, 264686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 27486261, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1390	94111918 (2779, 2760)	Novel Protein sim. GBank gl 702295 (A005783) - RC3083_1 [Homo sapiens]	peptidase		52646842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264389, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486282, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264638, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gl 134691089 P28650 P04_MOUSE-ADENYLOSUCINATE SYNTHETASE, MUSCLE ISOZYME (IMP--ASPARTATE LIASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gl 726286 (U22394) - mSn3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264389, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486282, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264638, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00950) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264679
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gl 2274845 db BA-215341- (O28461) N-WASP [Rattus rattus]		UNCLASSIFIED	265008, 18108381

1396	95363253 (2791, 2792)	Novel Protein sim. GBank gi 2135904 pf 54810 - pHIL-E1f1 - human		22278957, 22278960, 264250, 29331825, 60432289, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21906767, 29148827, 21906768, 21906769, 29148828, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264553, 264561, 35696286, 264907, 66712502, 264510, 35695917, 264902, 264903, 35696422, 264259, 29331822, 29331823, 29331824, 29331825, 29331827, 35696052, 35696970, 87188474, 265018, 265019, 265022, 264788, 21906767, 265020, 33857023, 27486261, 56811576, 264632, 264639, 83373044, 87188516, 22279002
1387	87631317 (2793, 2794)		UNCLASSIFIED	
1388	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB6680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		
1389	87631076 (2797, 2798)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KO PROTEIN C09F5.2 IN CHROMOSOME III		
1400	95419064 (2799, 2800)	Novel Protein sim. GBank gi 283920 pf 527639 - lensin - chicken	UNCLASSIFIED	
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008639)d510H16.1 [Homo sapiens]	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264768, 264685, 264687, 56181562, 264769, 21906768, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811578, 264634, 264555, 264637, 264557, 264638, 18108381, 264556, 18108384, 60433113, 22279000
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nei homolog [Homo sapiens]	UNCLASSIFIED	264788, 18108370, 264909, 264759, 264905, 264907, 264908, 264909, 264112, 264693, 33857109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	56574572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90635393 (2807, 2808)		UNCLASSIFIED	56574572, 22278994, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gi854005[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264906, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264567
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gi624076[bb]AAC58425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13983 [Paramecium bursaria Chlorella virus 1]	collagen		264907, 264605
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gi282788 (AF015037) - endolipopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278998, 264094, 264759, 66714117, 29331826, 29331827, 29331828, 2946498, 264107, 264908, 265006, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21908765, 21908769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 56811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gi2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21908767, 265021, 264680, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695955, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567
1409	66644385 (2817, 2818)	Novel Protein sim. GBank gi2682165[db]JAA23714] - (AB007902) HH0712 cDNA clone for KIA00442 has a 574-bp insertion at position 1474 of the sequence of KIA00442. [Homo sapiens]			264693
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gi24937950[sp]Q60994[CR]_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	Contains protein domain (PF00346) - complement C1q domain		29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 264566

1411	67818641 (2821, 2822)	Novel Protein sim. GBank g1312151sp191343YM3M CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME 1	Contains protein domain (PF00400): WD domain, C beta repeat	kinase-receptor	22276895, 22276997, 22276999, 29331822, 60432289, 29331828, 264907, 265017, 265019, 264682, 21906767, 21906768, 21906769, 265020, 264890, 264891, 33657023, 33657109, 27486264, 264628, 263972, 264634, 264558, 18106385
1412	84390919 (2823, 2824)			UNCLASSIFIED	284737
1413	95415559 (2825, 2826)	Novel Protein sim. GBank g13879171[mb](CAA94370) - (ZT0310), predicted using GeneFinder: Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL T01923 comes from this gene; cDNA EST EMBL D32335 comes from this gene; cDNA EST EMBL D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023): Ank repeat	UNCLASSIFIED homeobox	56994075, 29331822, 36690652, 29331828, 29331830, 264909, 56440405, 264510, 5644296, 8565542, 87166474, 265017, 265016, 264681, 264687, 21906768, 36695917, 265020, 5644150, 264682, 263987, 27486294, 36695763, 264639, 18106387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank g13252981 (AF068921) - Ras- binding protein SUR-8 (Mus musculus)	Contains protein domain (PF00560): Leucine Rich Repeat	UNCLASSIFIED	264632, 264683, 265022, 264636
1415	94326546 (2829, 2830)	Novel Protein sim. GBank g11871187 (U89439) - unknown protein (Arabidopsis thaliana)			55646385, 56182575, 22276994, 22276995, 56994075, 22276996, 22276997, 22276998, 22276999, 264299, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 28146488, 66712502, 29331830, 52844045, 284113, 284511, 33657402, 264757, 21906754, 55811386, 265017, 265018, 265019, 284761, 264683, 264389, 264288, 264686, 264689, 21906766, 21906767, 28146627, 21906769, 55811957, 265020, 265021, 264890, 33657023, 65274620, 56445129, 27486282, 27486264, 60431528, 264629, 36695955, 56182323, 264559, 60432113, 284404, 22276902, 264482

1416	84325977 (2831, 2832)	Novel Protein sim. GBank gi15106557[gb AA039748.1AF12305 - (AF123052) MLL sepin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - strod Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264782, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906768, 21906766, 21906767, 29146827, 21906768, 55811057, 29148629, 265020, 52644150, 18108361, 33957023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811576, 65274791, 264634, 264638, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000, 264107, 264448
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi495893[gb AA78095.1] - (AB027570) suppressor of potassium transport defect 3 (Rattus norvegicus)	ATPase-associated	264259, 264908, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1418	87594276 (2835, 2836)			264259, 60432289, 265006, 87168474, 264288
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi2072394 (U95097) - mtotic phosphoprotein 43 [Xenopus laevis]	strod	264259, 60432289, 265006, 87168474, 264288
1420	87298628 (2839, 2840)	Novel Protein sim. GBank gi15174421[ref NP_008023.1]cpPNE - copine VI (neuronal)	ATPase-associated	264259, 60432289, 265006, 87168474, 264288
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi3976090[emb CA93459.1] - (Z69635) Similarity to Yeast uridine kinase (SWURK1_YEAST); cDNA EST EMBL Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL D67355 comes from this gene; cDNA EST y209h1.5 comes from this gene...	kinase	18108398, 18108396, 18108397, 18108397, 21906768, 18108398, 21906767, 56182575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27480261, 29331828, 35696052, 33657349, 264905, 264909, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431650, 60432229, 60431755, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906774, 55811396, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264653, 264682, 264763, 264448, 264586, 264486, 18108391

1422	86178777 (2843, 2844)	Novel Protein sim. GBank gi4505938(reINP_000928, 1bpPOLR: polymerase (RNA) II (DNA directed) polypeptide A (220KD)	mapolymerase	56994075, 35696286, 87168559, 53811957, 55811576, 2644555, 2644557, 87168518
1423	86997762 (2845, 2846)		UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - struct RhoGAP domain	29331822, 29331823, 29331827, 29146438, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi100798[pilS14959 - proline- rich protein - wheat]	UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi2078441 (U66964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP-P25386) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 60424179, 35696286, 22278997, 22278998, 22278999, 264258, 60432049, 29331822, 29331823, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108378, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi1561607(gb AAD45616.1 AF06194 - (AF061943) prota- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi138350(sp P28968 VLX_HSVEB - GLYCOPROTEIN X PRECURSOR	glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264686, 65274620, 264629, 65274791, 22279002, 264566
1429	87888689 (2857, 2858)		UNCLASSIFIED	264112, 264585, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi1181619(dbs BAA115569 - (DB2384) a variant of TSC-22 [Gallus gallus]	UNCLASSIFIED	264094, 29331824, 264591, 264593, 265016, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi542038(jemb CA46680.1 - (AJ243460) proteophosphoglycan [Luishmania major]	UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gi141797 (L18965) - pyruvate dehydrogenase phosphatase [Bos taurus]	phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263989
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	UNCLASSIFIED	264258, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)		UNCLASSIFIED	264692, 264691

1435	94708213 (2866, 2870)	Novel Protein sim. GBank g13070450j[emb]GA34785.1] - (AB015330) HRIHFB2007 [Homo sapiens]	transcriptfactor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 18108351, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182233, 264559, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565 UNCLASSIFIED
1436	86635024 (2871, 2872)	Novel Protein sim. GBank g1318397[emb]CA39515] - (X55044) protein H95C [Mus musculus]	UNCLASSIFIED	22278997, 66714117, 29331828, 264907, 56182435, 265009, 18108351, 264692, 264693
1437	87631082 (2873, 2874)	Novel Protein sim. GBank g1246887[isp]0092331YQ22 CAEE1 - HYPOTHETICAL 32.0 KD PROTEIN C9F5.2 IN CHROMOSOME III	kinase	264488, 264508, 264906, 264908, 264757, 264600, 264601, 264605, 264768, 284769, 264680, 3589423, 264558, 264563, 264566
1438	8554280 (2875, 2876)	Novel Protein sim. GBank g1190590E (AD000092) - hypothetical human serine-threonine protein kinase R31240.1 [Homo sapiens]	cathepsin	264489, 18108394, 65274572, 56182375, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432288, 29331826, 29331827, 29331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265008, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695955, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264488
1439	91231884 (2877, 2878)	Novel Protein sim. GBank g13676299[emb]CA34892] - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL.D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis]....	UNCLASSIFIED	264887, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635
1440	87423643 (2879, 2880)	Novel Protein sim. GBank g12662165[db]AA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]	UNCLASSIFIED	

[illegible]

1449	87860859 (2897, 2898)					UNCLASSIFIED	66714117, 284906, 284908, 284591, 284601, 284764, 284632
1450	87458696 (2899, 2900)	Novel Protein sim. GBank gl1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]				UNCLASSIFIED	35596286, 35596052, 285009, 285009, 30170831, 33109954, 284683, 284689, 35596423, 35595855, 56526486
1451	87797970 (2801, 2902)	Novel Protein sim. GBank gl160304(emb)CA106001 - (AJ132192) H51 binding protein 3 [Mus musculus]				UNCLASSIFIED	29331826, 284683, 284693, 283978, 284630
1452	85692889 (2803, 2904)	Novel Protein sim. GBank gl2632909(dj)AA24608.11 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]				peptidase	284681, 33657023, 284629
1453	86130434 (2805, 2906)	Novel Protein sim. GBank gl728831spIP39188[ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III]				kinase	284510, 284768
1454	11204696 (2807, 2908)						284556
1455	87797886 (2809, 2910)					UNCLASSIFIED	29331822, 66714117, 29331825, 284905, 29331830, 285008, 285008, 285009, 285011, 285019, 18108351, 21906768, 33657109, 18108376, 284632, 56182323, 87188518
1456	86320218 (2811, 2912)	Novel Protein sim. GBank gl1789230spIP41004[UT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]				transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 284107, 285017, 21906765, 21906766, 21906767, 21906769, 29148629, 18108370, 22279000, 284107, 284568
1457	80076900 (2813, 2914)	Novel Protein sim. GBank gl12246532 (U93872) - ORF 73, similarity to large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]				UNCLASSIFIED	56182575, 22278999, 00432048, 284759, 29331826, 29331827, 29331828, 284102, 284107, 284110, 285009, 60432229, 285019, 285020, 263972, 263976, 284635, 22279002, 284566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gl5524667[gb]AA044333.1[AF15935] Munc13-C2 domain				transport	22278997, 284759, 29331824, 29331826, 29331827, 29331828, 285017, 285018, 284750, 284682, 284448, 284288, 284766, 285021, 284692, 33657023, 33657109, 35595855, 284566
1459	95350920 (2917, 2918)	Novel Protein sim. GBank gl5524667[gb]AA044333.1[AF15935] Munc13-4 protein [Rattus norvegicus]				UNCLASSIFIED	29331822, 284591, 55811957, 284691, 284693, 65274620
1460	95354602 (2919, 2920)					kinase	22278997, 284759, 29331824, 29331826, 29331827, 29331828, 285017, 285018, 284750, 284682, 284448, 284288, 284766, 285021, 284692, 33657023, 33657109, 35595855, 284566
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gl1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]				UNCLASSIFIED	29331822, 284591, 55811957, 284691, 284693, 65274620
1462	87732018 (2923, 2924)	Novel Protein sim. GBank gl1770469[emb]CA669121 - (X98259) M-phase phosphoprotein 8 [Homo sapiens]				gaba	22278997, 29331822, 35596052, 285009, 284758, 285017, 285018, 285019, 284760, 284389, 284687, 21906765, 21906768, 285022, 33657109, 27486261, 284555, 83373044
1463	86090605 (2925, 2926)					UNCLASSIFIED	284555, 284556
1464	86090605 (2925, 2926)					kinase	60432049, 284259, 29146498, 284906, 284907, 284512, 285017, 284763, 284766, 18108370, 18108374, 284636, 18108385, 18108398

1464	87600482 (2827, 2928)	Novel Protein sim. GBank g1387444/jemb CAB02772 - (Z81039) predicted using GeneFinder. cDNA EST EMBL T01209 comes from this gene. cDNA EST yk278a11.3 comes from this gene. cDNA EST yk278a11.5 comes from this gene. cDNA EST yk308a9.3 comes from this gene. cDNA EST yk308a9.5 com....	UNCLASSIFIED	264569, 22278958, 22278966, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21906754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21906765, 21906766, 21906767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565, 264488, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52644045, 264511, 265007, 265008, 264596, 55812038, 55811388, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264657, 18108382, 60432113
1465	87425192 (2928, 2930)	Novel Protein sim. GBank g14585598 jemb CAA78821.1 - (AB023194) KIAA0977 protein [Homo sapiens]	glucosylase	264488, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52644045, 264511, 265007, 265008, 264596, 55812038, 55811388, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264657, 18108382, 60432113
1466	87600527 (2931, 2932)	Novel Protein sim. GBank g12246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	UNCLASSIFIED	264512, 265017, 264689, 264558, 264683, 264636
1467	87614328 (2933, 2934)	Novel Protein sim. GBank g1450724 jemb NP_003137 - structure specific recognition protein 1	siRNA	22278998, 264758, 265018, 265019, 21906769, 265020, 33657109, 22279002
1468	95342862 (2935, 2936)	Novel Protein sim. GBank g1450724 jemb NP_003137 - structure specific recognition protein 1	siRNA	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1469	79236174 (2937, 2938)	Novel Protein sim. GBank g11905596 (U81788) - kinesin-73 [Drosophila melanogaster]	UNCLASSIFIED	18108394, 18108398, 35696052, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 63373044, 18108384, 18108388, 87169518, 60432113, 264404, 22279002, 264482, 264567, 264487
1470	94890482 (2939, 2940)	Novel Protein sim. GBank g15649170 jemb AAO43131.2AF15909 - (AF159002) sy4709613 protein [Homo sapiens]	UNCLASSIFIED	29331822, 29331824, 29331825, 264628, 264603, 264689, 264693, 18108374, 55811576
1471	87826842 (2941, 2942)	Novel Protein sim. GBank g13876146 jemb CAB01750 - (Z78542) similar to Mitochondrial carrier proteins. cDNA EST EMBL T01651 comes from this gene [Caenorhabditis elegans]	transport	

1472	87756616 (2843, 2844)	Novel Protein sim. GBank gi 4680707 g AAU2743.1 AF13296 - (AF132968) CQI-34 protein [Homo sapiens]	UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87791609 (2845, 2846)	Novel Protein sim. GBank gi 3688789 AF042180 - testis- specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - MHC Nucleosome assembly protein (NAP)	18108394, 22778995, 56994075, 22278999, 29331822, 29331824, 66714117, 26331825, 29331826, 35696052, 264906, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264758, 21906769, 55811957, 265021, 264691, 264693, 264629, 55811576, 264634, 264638, 56182323, 22278002, 264566, 264486
1474	85800589 (2847, 2848)	Novel Protein sim. GBank gi 2494890 sp C92178 CORO_BOVIN - CORONIN-LIKE PROTEIN P37	Contains protein domain (PF00400) - struct WD domain, G-beta repeat	264488, 35695917, 35656286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264639, 264758, 60432113, 264604, 284605, 264565, 264566, 264764, 264488, 264685, 264766, 264681, 264682, 264288, 264558
1475	86871935 (2849, 2850)		UNCLASSIFIED	
1476	87548855 (2851, 2852)	Novel Protein sim. GBank gi 4757752 ref NP_046684.1 PANGP - angiotensinogen 3	Contains protein domain (PF00041) - Fibronectin type II domain Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264908, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108392, 18108398, 60432113, 22278002, 264259, 264107, 264908, 265008, 26501, 265011, 264682, 264288, 265020, 265021, 263974
1477	87774279 (2853, 2854)	Novel Protein sim. GBank gi 2468308 sp Q60870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (T82 PROTEIN HOMOLOG) (GP105)	UNCLASSIFIED	
1478	11754412 (2855, 2856)			264686

1473	91540140 (2357, 2956)	Novel Protein sim. GBank gjl5499741(gb)AAD3978.1(AF15296) - chromatin-specific transcription elongation factor FACT 140 KDa subunit [Homo sapiens]	peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264755, 33109954, 21905754, 265017, 265019, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21905765, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 56811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2958, 2960)	Novel Protein sim. GBank gjl355045(emb)CAQ6328.1(- (AJ050573)) Alix [Mus musculus]	UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35695286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 29146499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433358, 60433438, 264596, 33109954, 33657084, 52844296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264662, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2951, 2952)	Novel Protein sim. GBank gjl4836807(gb)AD30566.1(AF14679) - (AF146793) PFT27 [Mus musculus]	MHC	265006, 265007, 265010, 18108374
1482	85320442 (2953, 2964)	Novel Protein sim. GBank gjl495372(gb)AAD25403.1(AF12282) - (AF122823) Vint inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	264908, 264910, 264758
1483	94115503 (2955, 2966)	Novel Protein sim. GBank gjl355428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF000036) - struct EF hand	264259, 29331822, 52645080, 29331825, 29331826, 336566970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2957, 2968)	Novel Protein sim. GBank gjl191177(gb)80090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]	UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2959, 2970)	Novel Protein sim. GBank gjl5560128(gb)AD42883.1(AF15511) - (AF155117) NY-REN 82 antigen [Homo sapiens]	Contains protein domain (PF00225) - struct Kinesin motor domain	264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gi4589518[gdj]BA76780.1] - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	- kinase	56182575, 22278699, 264906, 264907, 21906754, 877168474, 265017, 265019, 18106331, 264288, 265020, 264566, 21906754, 264486
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi5019273[emb]CAB44431.1] - (AJ132751) xenobiotic/medium-chain fatty acid CoA ligase form XL-III [Bos taurus]	synthase		
1488	87732028 (2975, 2976)	Novel Protein sim. GBank gi5712131[gb]A047379.1[AF12049] DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Ig Viral (Superfamily 1) RNA helicase		264686, 264769, 264689, 264692, 264693, 264509, 264909, 264907, 18108370, 264908, 264629, 264909, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264662, 264682, 21906767, 22278699, 265022, 264359, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi2497303[sp]Q62786[FRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)]	Contains protein domain (PF00047) - prostaglandin immunoglobulin domain		264693, 26531824, 26531823, 26531826, 26531827, 26531828, 264103, 26539726, 26531827, 26539726, 26539726, 265007, 265008, 265009, 833731044, 21906754, 58526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87390127 (2979, 2980)		UNCLASSIFIED		56182575, 264259, 26531827, 26531824, 66714117, 26531827, 26531828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265019, 18106331, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170815, 33657109, 55859555, 264635, 60170394, 56526486, 22278699, 264663, 265007, 264448, 18106372, 264558, 56182323
1491	833594305 (2981, 2982)	Novel Protein sim. GBank gi265671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]	UNCLASSIFIED		
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi1656005 (U71205) - rat [Mus musculus]	Contains protein domain (PF00071) - oncogene Ras family	- oncogene	22278697, 22278698, 26531822, 264907, 66712502

1493	87605265 (2985, 2986)	Novel Protein sim. GBank gl 5689515db BA43041.1]- (AB 298012) KIAA1089 protein [Homo sapiens]	UNCLASSIFIED	264488, 2646365, 65274572, 56182575, 22278994, 35666286, 56994075, 22278999, 6032049, 29331824, 29331828, 35696052, 264506, 264905, 264906, 52644045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 5812038, 265010, 265011, 265017, 265018, 265019, 5811150, 264448, 264662, 264665, 264666, 52644229, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170815, 52644150, 33657023, 18108384, 18108385, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264829, 18108374, 52644332, 56182323, 87168516, 22279002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gl 728325 P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SE WARNING ENTRY IIII	Contains protein domain (PF01332) - kinase KRAB box	264907, 265009, 264769, 18108370, 55811576, 284639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gl 4589588 db BA476316.1]- (AB 203189) KIAA0977 protein [Homo sapiens]	Contains protein domain (PF01332) - Transcription factor KRAB box	22278997, 264259, 264906, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gl 542038 emb CAB46679.1]- (AJ234350) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	87695428 (2993, 2994)	Novel Protein sim. GBank gl 387492 emb CA92591]- (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW/KRAA_MOUSE); cDNA EST EMBL D27610 comes from this gene; cDNA EST EMBL T01018 comes from this gene; cDNA EST EMBL D33256 comes from this gene....	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	90934938 (2995, 2996)	Novel Protein sim. GBank gl 728325 P39189 ALU6_HUMAN - IIII ALU SUBFAMILY SE WARNING ENTRY IIII	oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gl 2570198 (U54559) - microfilament sheath protein SHP3 [Limonosoides sigmodontis]	glucosylase	263978, 264566
1500	80496386 (2999, 3000)	Novel Protein sim. GBank gl 2078483 (U43200) - antifreeze	UNCLASSIFIED	22278999, 264769, 18108379
1501	85795237 (3001, 3002)	Glycopeptide AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	264559
1502	80206141 (3003, 3004)	Novel Protein sim. GBank gl 3900855 (AC004874) - similar to N-acetylglucosaminyltransferase, similar to Q07537 (PID.g1171989) [Homo sapiens]	transferrase	264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)		Glycosyl transferases	29331822, 265007, 264369

1504	79640051 (3/07, 3/08)			Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102572 (3/09, 3/10)	Novel Protein sim. GBank g14753737jemp(AbA1970.1) - (A132345) protein kinase [Homo sapiens]		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 3569602, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 56812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566
1506	84143219 (3/11, 3/12)	Novel Protein sim. GBank g11304201jbbj(BAA06170) - (D29786) alternatively spliced product [Rattus norvegicus]		Contains protein domain (PF00019) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278697, 22278698, 22278699, 264091, 264092, 60432049, 264259, 52645080, 29331822, 29331827, 264106, 29331830, 264908, 56182435, 264110, 264511, 264512, 56812038, 21906754, 87166559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21906765, 29148627, 21906768, 21906769, 29148629, 52644150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87166518, 60432113, 22279000, 264565
1507	83738250 (3/13, 3/14)	Novel Protein sim. GBank g10568951jbbj(BAA83040.1) - (AB029011) KIAA1088 protein [Homo sapiens]			helicase	264639
1508	11618758 (3/15, 3/16)	Novel Protein sim. GBank				264593
1509	87318451 (3/17, 3/18)	g10301915jrefjnp_005875.1pPAK1 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331826, 264591, 33109954, 264563
1510	95362843 (3/19, 3/20)	Novel Protein sim. GBank g11316189p128614ACOR - ACETON CATABOLISM REGULATORY PROTEIN			UNCLASSIFIED	264597, 29331822, 265007, 18108374, 264556
1511	88318073 (3/21, 3/22)	g172883189p139188JALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III			UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345590 (3/23, 3/24)	Novel Protein sim. GBank g14559353jbbj(AA023014.1)AC006858 - (AC006858) putative extragenic suppressor protein (Arabidopsis thaliana)		Contains protein domain (PF01053) - RIO1/ZK632.3M/J044 family		52645156, 18108386, 56994075, 60432289, 265006, 60433356, 60433438, 21906754, 87168474, 87168559, 265018, 264762, 264763, 264687, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3/25, 3/26)	Novel Protein sim. GBank g11330394 (U58761) - COIF1.6 gene product [Caenorhabditis elegans]				35696052, 264495, 264906, 264907, 264908, 264909, 264910, 264591, 264765, 264689, 264692, 264629, 264636

1514	85345397 (2027, 3028)	Novel Protein sim. GBank g1455353jg1A023014.1(A-C00658) putative extrinsic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/K632.3/MJ0444 family	UNCLASSIFIED	52644307, 52645156, 52646385, 52646842, 52647452, 22278994, 35696286, 56994075, 264259, 52645080, 29331822, 29331825, 35696562, 29331830, 52644045, 56182435, 265006, 60433356, 60433438, 55812038, 21908754, 52646317, 52644296, 87168474, 87188559, 264448, 52644229, 21906765, 21908766, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486284, 27486265, 35695763, 18108376, 35696423, 35695655, 52644332, 18108385, 18108387, 87168518, 60432113, 265020, 2646339
1515	79163539 (3028, 3030)	Novel Protein sim. GBank g138379501jmb1CAA477501 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase, cDNA EST EMBL D33386 comes from this gene; cDNA EST EMBL D33963 comes from this gene; cDNA EST EMBL D33922 comes from this gene; cDNA EST EMBL D34547 comes from this gene...	ubiquitin	UNCLASSIFIED	265008, 56182333, 22278002
1516	88073539 (3031, 3032)	Novel Protein sim. GBank g1498015 (L27479) - X123 (Homo sapiens)	UNCLASSIFIED	UNCLASSIFIED	265008, 56182333, 22278002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank g13415134 (AF062024) - Phylb1 (Pseudomonas aeruginosa)	UNCLASSIFIED	UNCLASSIFIED	264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank g17283639p193719ALUS_HUMAN - III ALU SUBFAMILY SV40-ORIGIN ENTRY IIII	lm7	UNCLASSIFIED	6671417, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 284766, 264789, 18108374, 264636, 264638, 264686
1519	94326689 (3037, 3038)	Novel Protein sim. GBank g15262681jmb1CAB45771.1 - (AL080166) hypothetical protein [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	264589, 264489, 60432049, 265009, 33657402, 264586, 21906754, 265019, 264389, 21906765, 21906768, 21906769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22279002
1520	87592855 (3039, 3040)	Novel Protein sim. GBank g12662161db1BA423712 - (AB007900) H40452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970698 (3041, 3042)	Novel Protein sim. GBank g15052351jg1A030516.1AF13542 - (AF135421) GGP-mammose triphosphorylase B [Homo sapiens]	Synthase	UNCLASSIFIED	18108394, 264259, 66714117, 265011, 264603, 265019, 18108394, 35698423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)	Novel Protein sim. GBank g13776567 (AC005388) - Strong similarity to PZ187.33 g12809504 from A. italiana BAC g1pAC002660. EST g1p1685119 comes from this gene.	UNCLASSIFIED	UNCLASSIFIED	29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)	Novel Protein sim. GBank g13776567 (AC005388) - Strong similarity to PZ187.33 g12809504 from A. italiana BAC g1pAC002660. EST g1p1685119 comes from this gene.	UNCLASSIFIED	UNCLASSIFIED	65274572, 21906768, 264693
1524	80203723 (3047, 3048)	Novel Protein sim. GBank g14739340jg1NP_004283.1jPRN1 - ras inhibitor	UNCLASSIFIED	UNCLASSIFIED	264112, 21906754, 263974
1525	87799867 (3049, 3050)	Novel Protein sim. GBank g14739340jg1NP_004283.1jPRN1 - ras inhibitor	UNCLASSIFIED	UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank S1778850 [Siphi 086-40] MYH1 - YEAST - GLUCOAMYLASE S1523 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) [1,4-ALPHA-D-GLUCAN GLUCOTRIOLASE]	glycoprotein	35686286, 56182181, 60431735, 264585, 55912038, 264605, 264683, 21906765, 55911937, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank g12792496 (AF041107) - tulip 2 [Rattus norvegicus]		56182575, 264559, 60433049, 29331822, 60432289, 264908, 66712502, 60433438, 87188599, 265017, 264288, 21906766, 21906769, 265397, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)		UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank g14408663 [gb1A020053] - (AF131826) Unknown [Homo sapiens]	UNCLASSIFIED	264488, 263994, 5812575, 22278995, 35686286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 60433396, 60433438, 265017, 285018, 264760, 264448, 264764, 264369, 264288, 264768, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264929, 35695855, 80432113, 22279002, 264563, 264564, 264486, 264567
1530	95012765 (3059, 3060)	Novel Protein sim. GBank g12828710 (AF043642) - matrin cytoplasm [Rattus norvegicus]		264488, 264489, 35686286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank g11905874 (U08078) - carboxyl terminal LIM domain protein [Homo sapiens]	kinase PDZ domain (Also known as D4R or GLGF)	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433396, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810784, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gij3874716[emb]CA491269] - (Z66494) cDNA EST EMBL D85271 comes from this gene; cDNA EST EMBL D64845 comes from this gene; cDNA EST EMBL D84449 comes from this gene; cDNA EST EMBL D67438 comes from this gene; cDNA EST EMBL D86087 comes from this gene; cDN.		UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gij1490324[emb]CA801543] - (Z78141) unknown [Mus musculus]		stuct	26331824, 20146489, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 1810331, 263367, 20281149, 18103374, 263361, 264566
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gij1236[pri]S22697 - extensin - Vovox carteri (fragment)		UNCLASSIFIED	264905, 264907, 264766, 264637
1535	90038732 (3069, 3070)				65274572, 22276997, 264289, 60432049, 29331822, 60432889, 29331827, 29146499, 265008, 265008, 60170831, 60433438, 33109954, 97166559, 265018, 18103357, 21908766, 29146629, 265021, 265022, 18103377, 58182323, 60432113, 22279000, 22279002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gij106024[pri]B323891 - finger protein 2, placental - human	Contains protein domain (PF00098) Zinc finger, C2H2 type	transcript/factor	264686, 18103357, 18103394, 21908767, 21908768, 29146629, 35696286, 265020, 265021, 52344150, 264693, 68714117, 29331825, 28331628, 264308, 264905, 20281149, 264909, 18103374, 35696423, 35696585, 265009, 264634, 264636, 264638, 18103385, 56326466, 265017, 265018, 264553, 264762, 18103391, 264446, 264389, 264766
1537	963354556 (3073, 3074)	Novel Protein sim. GBank gij3876332[emb]CA802098] - (Z79754) cDNA EST EMBL D71054 comes from this gene; cDNA EST EMBL D73600 comes from this gene; cDNA EST Y428412.5 comes from this gene; cDNA EST Y43210.5 comes from this gene; cDNA EST Y47565.5 comes from this gene; cDNA EST			65274572, 58182375, 60432049, 264289, 29331826, 265006, 265007, 60433356, 60433436, 264601, 18103391, 264448, 264389, 264288, 33657023, 65274620, 33657106, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gij463440 (481757) - [Callus domesticus skeletal muscle mRNA, partial cds.] gene product [Gallus gallus]	Contains protein domain (PF00069) Eukaryotic protein kinase domain	kinase	18103394, 18103397, 264908, 265008, 265009, 265010, 18103351, 264638, 18103382, 18103385, 18103388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gll32184.1[embCAA18575.1] - (AL023859) SPBC19C7 07c, putative tRNA splicing endonuclease ga mma subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit (275aa), fasta scores, opt:269, E[6.4e-2.	nuclease	22278994, 22278996, 35666286, 56994015, 2664259, 22278998, 22278999, 60432409, 2664259, 20331822, 22278999, 60432409, 20331822, 20331826, 20331826, 20331827, 20331828, 35666052, 35666070, 58182435, 265009, 33657402, 60433356, 60433438, 55812038, 21006754, 87168559, 265017, 265018, 265019, 18108351, 264288, 52644225, 18108359, 21006764, 21006767, 21006768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27485261, 18108370, 18108376, 35696423, 55811576, 65274570, 264558, 56192323, 60170394, 83373944, 87168518, 60432113, 22279000, 22279002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gll5052634[gbAA038647.1]AF14567 (AF145672) BCDA GH12174 [Drosophila melanogaster]	UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gll5052349[gbAA039515.1]AF13501 (AF135018) protein phosphatase 2A, 48 kDa regulatory subunit [Homo sapiens]	phosphatase	264488, 264489, 22278999, 264259, 20331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21006769, 55811587, 35695917, 265020, 264681, 33657023, 264632, 264634, 264635, 264639, 18108374, 264632, 264634, 264635, 264639, 18108385, 264683, 264564, 264585, 264586, 264486
1542	90337549 (3083, 3084)	Novel Protein sim. GBank gll505702[gbAA041778.1]AF12686 (AF126867) calpain-like protease [Mus musculus]	calthopsin	18108392, 18108394, 63274572, 20331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264635, 18108381, 18108392, 264106, 3310954, 265019, 264683, 35695917, 264680, 264692, 33657109
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gll28832[spP39189]ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	nuclease	35666286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gll4933162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	nud_recpt	264112, 264692, 264693, 55811576
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gll1065591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP-P2082) in a region of Gly-arg repeats [Caenorhabditis elegans]	UNCLASSIFIED	264905, 264686
1546	79476369 (3091, 3092)	Novel Protein sim. GBank gll2661132 (AF-035683) - p21 [Mus musculus]	UNCLASSIFIED	264259, 20331822, 66714117, 265007, 55811366, 265010, 264600, 265017, 265019, 264288, 264769, 265020, 265022, 55811576, 18108380, 264583

1548	94233065 (3095, 3096)	Novel Protein sim. GBank gll3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	UNCLASSIFIED	29331824, 60431528, 264509, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gll5695519[dbj BAA43043.1] - (AB025014) KIAA1091 protein [Homo sapiens]	eph	80424175, 22278995, 3568286, 22278998, 22278999, 264092, 264094, 29331822, 56182161, 29331824, 35696032, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811362, 87169559, 265017, 265018, 5581019, 55811150, 264682, 264288, 264389, 56181562, 264765, 21906765, 21906768, 21906769, 55811937, 265020, 264691, 33657108, 60431528, 35696423, 35695855, 35695856, 60432113, 22279002, 264563, 264565
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gll544483[sp P33500 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)]	Contains protein domain (PF00001) 7 transmembrane receptor (rhodopsin family)	63274372, 60432789, 265008, 264910, 265011, 265017, 265019, 264766, 56182323
1551	86077111 (3101, 3102)	Novel Protein sim. GBank gll758566[ref NP_004798.1 phS6S - heparan-sulfate 6-sulfotransferase	UNCLASSIFIED	22278990, 29331822, 264508, 264509, 264905, 264907, 264908, 265007, 264512, 264910, 21906754, 265016, 265019, 264681, 264765, 264766, 264688, 264768, 21906769, 264692, 35695763, 264635, 264385, 264395, 264396, 264397, 264638, 264655, 264563
1552	87617114 (3103, 3104)	Novel Protein sim. GBank gll4589570[dbj BAA76807.1] - (AB023180) KIAA0963 protein [Homo sapiens]	UNCLASSIFIED	264238, 29331828, 60772502, 264764, 264235, 264958, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gll4589570[dbj BAA76807.1] - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) Gamma-thionin family	56182371, 35698286, 26476499, 264509, 264907, 264908, 264909, 56182335, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181582, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gll3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) Gonadotropin-releasing hormone	35696286, 22278997, 264289, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264389, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3108, 3110)	Novel Protein sim. GBank g12527495[ojl]BAA213921 - (AB004534) p015 [Schistosomacantharines pome]	Contains protein domain (PF00400) - WD domain, C-beta repeat	UNCLASSIFIED	264259, 29331828, 35696052, 264508 264905, 264900, 264907, 264908, 32640045, 264909, 264910, 60432229, 60433356, 59812038, 264916, 598129, 3565709, 265011, 87196559, 264601, 265018, 265019, 264763, 264764, 264768, 264769, 264768, 21906765, 35689917, 3569222, 264691, 35657023, 35696423, 35695855, 264635, 264935, 264636, 264638, 264639, 1106385, 35526485
1556	91229568 (3111, 3112)			UNCLASSIFIED	8337304, 264758, 265022, 264600 35696032, 264630, 35696443, 265018, 264632, 264632, 25331822, 265029, 265011 60432289, 264905, 264906, 264907, 264908, 264909, 264910, 264758, 53811385, 264761, 264762, 264766, 264769, 264690, 263976, 264634, 264635, 264639, 264584, 253859, 22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1557	87640509 (3113, 3114)	Novel Protein sim. GBank g13328611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam, z1-C3HC4 hmm. score: 34.08); most similar to drophila goliath protein (SW: 006003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1558	94840376 (3115, 3116)	Novel Protein sim. GBank g13360105[gl]AA042871.1[AF15510] putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1559	88224865 (3117, 3118)	Novel Protein sim. GBank g1129009[gl]02750[AGL] HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1560	84590675 (3119, 3120)	Novel Protein sim. GBank g13880146[em]CAA427041 - (Z88319) Similarity to Human hRNP P protein (PIR Acc. No. S43464); cDNA EST EMBL-D34218 comes from this gene; cDNA EST EMBL-D37248 comes from this gene; cDNA EST EMBL-D71817 comes from this gene; cDNA EST EMBL-D74531 comes from...		UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1561	86609159 (3121, 3122)			UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1562	83359682 (3123, 3124)			UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1563	85508694 (3125, 3126)			UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1564	87766371 (3127, 3128)	Novel Protein sim. GBank g1168287[sp]P49593[ACD] RAT - ACYL-CoA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1565	86609159 (3121, 3122)			UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855
1566	84590675 (3119, 3120)			UNCLASSIFIED	22278984, 22278986, 22278987, 22278989, 22278989, 60432049, 264285, 25331824, 25331825, 25331828, 25331827, 264908, 264909, 60433356, 21906765, 265011, 265022, 265018, 264446, 21906765, 265011, 265022, 35657023, 35689917, 3569222, 264691, 35370204, 87196559, 1813737, 53811376, 22278984, 22278986, 22278987, 22278989, 264769, 26331822, 60432289, 35696052, 265027, 264410, 21906764, 33109654, 87108559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35656855

1565	87683381 (3129, 3130)	Novel Protein sim. G.Bank g 128726 p P05307 PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P45)	isomerase	264488, 264489, 1810358, 55811957, 264494, 264495, 264498, 264500, 264509, 1810372, 264510, 264511, 264512, 265008, 264630, 265009, 264610, 264635, 264638, 264691, 264655, 264692, 264637, 264693, 264694, 264695, 264696, 265011, 264693, 22270002, 110103351, 264762, 264655, 264667
1566	87424749 (3131, 3132)	Novel Protein sim. G.Bank g 3880445 em CAX20329 - (AL031266) VM106R.1 [Caenorhabditis elegans]	Wt	22278566, 22278569, 264259, 29331822, 26331824, 60432389, 29331827, 66713502, 264908, 285008, 18103351, 5564239, 21906765, 21906767, 21906768, 21906769, 33857109, 264555, 264639, 264482, 56182575, 21906769, 264692
1567	84695006 (3133, 3134)	Novel Protein sim. G.Bank g 4929699 p AAD34110.1 AF:15187 - (AF:15173) CGH-115 protein [Homo sapiens]	UNCLASSIFIED	
1568	87648761 (3135, 3136)	Novel Protein sim. G.Bank g 4827063 ref NP_005072.1 pZNF1 - zinc finger protein 142 Zinc finger, C2H2 type (clone pHZ-49)	transcript factor	29331827, 29331830, 264511, 265009, 264758, 21906767, 22279068, 264691, 264693, 22279000, 22279002, 65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21906765, 21906769, 55811957, 60170915, 57644150, 264692, 33857023, 33857109, 18103377, 264583, 264587
1569	90036665 (3137, 3138)	Novel Protein sim. G.Bank g 5686451 p BAA83009.1 - (AB028880) KIAA1057 protein [Homo sapiens]	ubiquitin	
1570	86943981 (3139, 3140)	Novel Protein sim. G.Bank g 1255430 (U53155) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	264695, 264683, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. G.Bank g 4507731 ref NP_001061.1 pTUBG - tubulin, gamma polypeptide	tubulin	22278566, 35666236, 22278967, 264091, 264259, 29331824, 29331825, 29331827, 35666042, 264508, 264905, 56182435, 264450, 265007, 264758, 265011, 18103351, 264448, 264388, 264369, 21906765, 21906767, 21906768, 21906769, 35895917, 285020, 285031, 33857023, 264693, 18103370, 18103377, 35666423, 35666555, 264534, 264555, 264556, 18103358, 35666042, 264905, 264906, 264908, 264910, 264758, 264766, 35665917, 264637, 265972
1572	81201664 (3143, 3144)		UNCLASSIFIED	
1573	80207066 (3145, 3146)		UNCLASSIFIED	

1574	94216142 (3147, 3148)	Novel Protein sim. GBank g 4758334 ref NP_004255.1 pFADS_delta-6 fatty acid desaturase	Contains protein domain (PF00173) Heme-binding domain in cytochrome b5 and oxidoreductases	Cytochrome	18108394, 264887, 18108397, 18108398, 22278986, 22278987, 22278989, 264249, 26331925, 26331827, 29116485, 29146489, 264100, 264807, 264808, 3204605, 264511, 265001, 265010, 265031, 264931, 264794, 265011, 265019, 18108334, 264782, 264784, 18108354, 264330, 264286, 264682, 264768, 264686, 264769, 264688, 21908785, 21908786, 21908787, 21908788, 21908789, 29148829, 264880, 264691, 264693, 20281069, 18108370, 18108374, 18108379, 35895855, 264634, 18108384, 18108385, 22278992, 264563, 264566,
1575	95340019 (3149, 3150)	Novel Protein sim. GBank g 3841810 emb CA046561 - (Z70783) similar to EF-hand calcium binding protein, cDNA (EST ENBL.C08700 comes from this gene [Caenorhabditis elegans])	Contains protein domain (PF00036) EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331925, 60432369, 29331828, 264809, 265006, 265008, 265009, 265010, 87168559, 55911150, 264448, 18108354, 264369, 264288, 18108357, 55811857, 265020, 265021, 60170915, 264691, 33657023, 33657109, 60431528, 65274791, 35895855, 18108385, 60432313, 22278992, 264369, 264568, 264092, 264594, 264095, 264369, 264608, 264095, 264099, 264097, 264099, 264510, 264511, 265006, 264110, 21908784, 265010, 265011, 87168559, 264761, 264782, 264888, 264785, 264789, 264691, 264693, 83595855, 264632, 264634, 264635, 264638, 83595859, 264639,
1576	85314019 (3151, 3152)	Novel Protein sim. GBank g 273195 (AF039711) - contains similarity to Physconitella priens glyceroldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264568, 264092, 264594, 264095, 264369, 264608, 264095, 264099, 264097, 264099, 264510, 264511, 265006, 264110, 21908784, 265010, 265011, 87168559, 264761, 264782, 264888, 264785, 264789, 264691, 264693, 83595855, 264632, 264634, 264635, 264638, 83595859, 264639,
1577	87613800 (3153, 3154)	Novel Protein sim. GBank g 2498130 sp P70315 WASP. MOUSE - WSKOTT - ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264311, 265011, 264681, 264369, 264686, 264688, 264620, 264555, 264558, 264559,
1578	87232138 (3155, 3156)	Novel Protein sim. GBank g 2978255 db BA25190 - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00086) Zinc finger, C2H2 type	UNCLASSIFIED	264258, 29331826, 265017, 264689, 264692, 60432113,
1579	88085141 (3157, 3158)	Novel Protein sim. GBank g 2978255 db BA25190 - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00086) Zinc finger, C2H2 type	UNCLASSIFIED	35895858, 264808, 264809, 60432369, 55911386, 264369, 264685, 33657023, 264555, 264558, 264557, 87168518,
1580	87255702 (3159, 3160)	Novel Protein sim. GBank g 4324682 gb AA016966 - (AF108674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) SCP-like extracellular protein	glycoprotein	22278589, 35896092, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000,
1581	95087437 (3161, 3162)	Novel Protein sim. GBank g 2088838 (AF003336) - FS9E12.4 gene product [Caenorhabditis elegans]			22278585, 29331822, 29331824, 29331826, 56182435, 264885, 35812038, 87168559, 265017, 264888, 21908784, 35811957, 35895857, 264632, 35811576, 264637, 56182423, 264639, 83373044, 60432113

1582	95356052 (3163, 3164)	Novel Protein sim. GBank glj5420387[emb][CAB46079.1] - (A4214349) proteoglycan [Leishmania major]	phosphatase	264259, 60432289, 26331827, 264509, 264505, 264506, 264507, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264539, 56526466, 22279000, 60170831, 33365702, 264662, 21900766, 36695855, 264563
1583	87622715 (3165, 3166)	Novel Protein sim. GBank glj578968[emb][CAB51351.1] - (A4503306) dA7597.2 (novel protein) [Homo sapiens]	UNCLASSIFIED	60241170, 52646842, 65274572, 56182575, 22278995, 36696286, 22278996, 22278998, 22278999, 264259, 26331822, 56182181, 60432369, 60432289, 26331827, 26331828, 36696052, 26146498, 66712502, 26331830, 52640045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 56812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 36695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811576, 36696423, 65274791, 36695855, 56182333, 83373044, 18108387, 87168518, 60432113, 22279002
1584	95337722 (3167, 3168)	Novel Protein sim. GBank glj5531615[gbp][C44462.1] - (A7078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00100): short chain dehydrogenase	36695268, 22278998, 264259, 26331822, 26331924, 26331825, 264605, 265005, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1585	87626117 (3169, 3170)	Novel Protein sim. GBank glj420132[db][BAX74846.1] - (A8020630) KIA0823 protein [Homo sapiens]	Contains protein domain (PF00023): Atk repeat	265017, 265018, 264688, 33657023, 263978, 264506, 264563
1586	86067081 (3171, 3172)	Novel Protein sim. GBank glj3786494 (AF068993) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	264259, 264761, 264762, 264909, 264910, 264594, 264629, 264631, 264653, 264483, 264567
1587	87617126 (3173, 3174)	Novel Protein sim. GBank glj2331319 (AF003355) - translation initiation factor eIF2C [Oryzopsis curvicaulis]	UNCLASSIFIED	334259, 33331028, 264905, 265006, 264758, 21906754, 264761, 264762, 264909, 21906765, 60170615, 52644150, 33657109, 36695855, 56182333, 18108385
1588	87602536 (3175, 3176)	Novel Protein sim. GBank glj07573[pir][S52806 - probable ribosomal protein L34, mitochondrion - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00468): Ribosomal protein L34	65274572, 264400, 26331822, 66714117, 26331827, 26331828, 56182435, 265008, 60170831, 264506, 264758, 264696, 265011, 264686, 21906765, 21906768, 55811957, 27485265, 264639, 18108385, 56526486, 60432113
1589	90980653 (3177, 3178)	Novel Protein sim. GBank glj2137756[pir][48746 - semaphorin C - mouse (fragment)]	UNCLASSIFIED	

1590	95319825 (3179, 3180)			UNCLASSIFIED	264489, 2278996, 264259, 26331824, 26331825, 26331826, 26331827, 265006, 6043356, 21906754, 265017, 265018, 265019, 264448, 264765, 264288, 5264428, 21906755, 21906767, 21906768, 21906769, 265021, 264892, 27446265, 35695763, 56526486, 60432113, 22279000, 22279002, 264584
1591	96877160 (3181, 3182)	Novel Protein sim. GBank		MHC	
1592	8782533 (3183, 3184)	gl4557749[re]NP_000237.1[pMHC2 - MHC class II transactivator]			264259, 264905, 26331830, 264595, 265017, 264448, 264288, 264690, 264629, 87188518
1593	94991661 (3185, 3186)			UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35696423, 22279000, 264585, 264587, 264488, 26331827, 264905, 264906, 264907, 264908, 264909, 264910, 264592, 264593, 264757, 264802, 264804, 264769, 264681, 264288, 264768, 264769, 29148929, 35695917, 264692, 264693, 264699, 264630, 264632, 264634, 264635, 264636, 264639, 264553, 264564, 264565
1595	79919425 (3189, 3190)	Novel Protein sim. GBank gl3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]		UNCLASSIFIED	26331828, 264908, 55811857
1596	79933928 (3191, 3192)			UNCLASSIFIED	29146498, 264758, 263967
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gl5257114[gb]AAD41244.1[AF09448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]]		cyto450	264092, 26331824, 264508, 264682, 264569, 264686, 264630, 264553
1598	87652939 (3195, 3196)				264259, 264634
1599	87649829 (3197, 3198)	Novel Protein sim. GBank gl4505797[re]NP_000324.1pSCAY - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)		UNCLASSIFIED	5264509, 26331824, 26331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108395
1600	80056002 (3199, 3200)			UNCLASSIFIED	26331828, 264603, 264691, 264653
1601	15023246 (3201, 3202)				264635
1602	8626987 (3203, 3204)	Novel Protein sim. GBank gl5305704[gb]AAD41780.1[AF12853 - (AF128539) cytoplasmic phosphoprotein PACSIN2 [Mus musculus] chicken]		SH3 domain	29146499, 264112, 264762, 18108351, 29148827, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gl2839292[re]gl527939 - tensin - chicken]		collagen	264490, 26331824, 264607, 264509, 264511, 265009, 264592, 265010, 265011, 264762, 264764, 264769, 264288, 264887, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108395
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gl4768831[gb]AAD29633.1[AF11682 - (AF116827) unknown] [Homo sapiens]		ATPase-associated	263977

1605	91221129 (3205, 3210)			struct	264905, 264509, 264906, 264907, 264909, 264910, 264900, 264604, 264765, 264768, 264692, 264693, 35857109, 264659, 35869855, 264693, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank g14505313[re]NP_003794.1[pmYOM - UNKNOWN g14505313[re]NP_003794.1[pmYOM - UNKNOWN g15174473[re]NP_005888.1[pmYOM - intracisternal A particle-promoted polypeptide	Contains protein domain (PF00047) Immunoglobulin domain	struct	22277896, 22277899, 264259, 334857402, 265017, 10108331, 264448, 21906767, 21908769, 25844130, 256691, 87165118, 264689
1607	10871905 (3213, 3214)	Novel Protein sim. GBank g15174473[re]NP_005888.1[pmYOM - intracisternal A particle-promoted polypeptide		transcript/factor	
1608	80428900 (3215, 3216)	Novel Protein sim. GBank g1224629[db][AA20802] - (A8002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264906, 264907, 264909, 264910, 264911, 264903, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank g14884073[emb][CAB43213.1] - (AL049534) hypothetical protein [Homo sapiens]		UNCLASSIFIED	52044307, 524945156, 53645365, 52464842, 56162375, 22276894, 56094075, 3586985, 22278997, 22278999, 26478999, 264259, 52045000, 53147605, 3581829, 36469052, 35869870, 56495035, 2644309, 264907, 52044045, 56181455, 264510, 264511, 244312, 33657402, 21906764, 53646317, 33109594, 56444286, 87168474, 358017, 265018, 265019, 18108375, 264448, 264288, 264768, 52044239, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35869917, 265020, 265021, 265022, 52044150, 33657023, 33657109, 524645129, 27486261, 27486262, 35869873, 264628, 18108370, 18108376, 358698423, 264630, 52044332, 18108387, 87168518, 22279000, 264593, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank g1283920[re]IS27939 - tensin - chicken		UNCLASSIFIED	264951, 264757, 55812038, 265018, 265020, 264951, 264692, 264693, 264631, 264634, 264635, 264636, 22279000, 264640, 35869266, 21908765, 264691, 358698423
1611	94122843 (3221, 3222)	Novel Protein sim. GBank g107284[re]J33415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) EGF-like domain	peroxidase	
1612	85746031 (3223, 3224)	Novel Protein sim. GBank g1387486[emb][CA049337] - (Z70307) Similarity to B subtilis tetracycline resistance protein (SWTOR2_BACSU); cDNA EST EMBL-C09951 comes from this gene; cDNA EST EMBL-C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	91728634 (3227, 3278)	Novel Protein sim. GBank gjl4680673epIAA027726.1jAF-13295.1 (AF-13295.1) CGH-17 protein [Homo sapiens]	Contains protein domain (PF01605) eRF1 like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264459, 20331822, 264908, 264412, 265009, 265011, 265017, 265018, 265019, 1103351, 264063, 264438, 264766, 21906767, 21906768, 21907693, 35695917, 265021, 265022, 35696423, 35695855, 2170394, 59162323, 5337304, 264358, 22278999, 35696266, 22278997, 26531822, 35696266, 26531819, 264508, 264509, 264692, 5316435, 265311, 1810374, 264765, 264767, 264768, 264769, 264991, 264768, 264769, 264768, 264769, 264991, 59162323, 264558, 264955, 264956, 59162323, 264558, 22278992
1615	86121909 (3229, 3230)	Novel Protein sim. GBank gjl5659455dbjBA43026.1j- (A8028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) Atk repeat	homeobox	22278995, 22278996, 22278997, 26531822, 35696266, 26531819, 264508, 264509, 264692, 5316435, 265311, 1810374, 264765, 264767, 264768, 264769, 264991, 59162323, 264558, 264955, 264956, 59162323, 264558, 22278992
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gjl3576265embjCA0016961- (Z78418) cDNA EST EMBL.D71020 comes from this gene; cDNA EST EMBL.D73593 comes from this gene; cDNA EST EMBL.C07649 comes from this gene; cDNA EST EMBL.C09081 comes from this gene; cDNA EST X39972.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	264487, 52644507, 52645155, 52645355, 52645442, 22278994, 22278995, 35696266, 22278996, 22278997, 22278999, 52645080, 26531822, 20331824, 20331825, 20331827, 20331928, 35696052, 35696970, 264905, 264906, 264904, 52646317, 21006754, 35657094, 52644296, 87164474, 87164559, 265017, 265018, 265019, 264681, 264448, 264684, 52644293, 21006754, 264689, 21006755, 21006756, 21006769, 35695917, 265020, 265021, 52644450, 35657093, 52645159, 35657109, 35657182, 27482651, 27486362, 35657109, 27486365, 35695763, 18103745, 35657109, 27486365, 264657, 52645159, 264558, 20331822, 264508, 35696266, 26531819, 264508, 264509, 264692, 5316435, 265311, 1810374, 264765, 264767, 264768, 264769, 264991, 59162323, 264558, 264955, 264956, 59162323, 264558, 22278992
1617	86090742 (3233, 3234)	Novel Protein sim. GBank gjl4680531epI24879YQ4.1 CAEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) DHC zinc finger domain	peptidase	22278995, 22278996, 264082, 20331824, 20331925, 35696052, 3567094, 21006765, 27486364, 63274572, 22278999, 264299, 20331822, 20331824, 20331825, 20331826, 20331927, 20331828, 35696052, 58182435, 265007, 265008, 2644910, 60170931, 60422269, 60433356, 60433439, 265019, 264442, 264984, 264689, 21906768, 265021, 60170915, 35657093, 65274620, 35657109, 1810374, 1810376, 35696423, 35695855, 59162323, 59224956
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gjl4680531epI24879YQ4.1 CAEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) DHC zinc finger domain	peptidase	22278995, 22278996, 264082, 20331824, 20331925, 35696052, 3567094, 21006765, 27486364, 63274572, 22278999, 264299, 20331822, 20331824, 20331825, 20331826, 20331927, 20331828, 35696052, 58182435, 265007, 265008, 2644910, 60170931, 60422269, 60433356, 60433439, 265019, 264442, 264984, 264689, 21906768, 265021, 60170915, 35657093, 65274620, 35657109, 1810374, 1810376, 35696423, 35695855, 59162323, 59224956
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gjl5031763jnp_005513.1pHY-1 hairy (Drosophila) homolog	Contains protein domain (PF00010) Helix-loop-helix DNA-binding domain	transcription factor	22278995, 22278996, 264082, 20331824, 20331925, 35696052, 3567094, 21006765, 27486364, 63274572, 22278999, 264299, 20331822, 20331824, 20331825, 20331826, 20331927, 20331828, 35696052, 58182435, 265007, 265008, 2644910, 60170931, 60422269, 60433356, 60433439, 265019, 264442, 264984, 264689, 21906768, 265021, 60170915, 35657093, 65274620, 35657109, 1810374, 1810376, 35696423, 35695855, 59162323, 59224956
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gjl1351047epIP45843SCRT-DROME - SCARLET PROTEIN	UNCLASSIFIED	UNCLASSIFIED	22278995, 22278996, 264082, 20331824, 20331925, 35696052, 3567094, 21006765, 27486364, 63274572, 22278999, 264299, 20331822, 20331824, 20331825, 20331826, 20331927, 20331828, 35696052, 58182435, 265007, 265008, 2644910, 60170931, 60422269, 60433356, 60433439, 265019, 264442, 264984, 264689, 21906768, 265021, 60170915, 35657093, 65274620, 35657109, 1810374, 1810376, 35696423, 35695855, 59162323, 59224956

1821	8705708 (3241, 3242)	Novel Protein sim. GBank g13822553 (AF068788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00827) - SPRY domain	UNCLASSIFIED	284910	18103592, 65274572, 18108398, 22278997, 22278999, 29146498, 29146499, 284905, 284906, 284909, 284928, 52641045, 284592, 60433356, 21906754, 284602, 285017, 284369, 21905768, 55811957, 285021, 60170615, 284635, 284557, 60170394, 83373044, 18108395, 22279000, 22279002, 284656
1823	8779106 (3245, 3246)	Novel Protein sim. GBank g1731086jg140389jUV22 - PROTEIN UV22		ribosomalprot		18108398, 284259, 284909, 58182435, 87168474, 284448, 21906788, 35695917, 284691, 87168518, 284563
1824	87338178 (3247, 3248)	Novel Protein sim. GBank g1387566jemb(CA905478) - (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL:D3865 comes from this gene; cDNA EST EMBL:D38540 comes from this gene; cDNA EST YK2408.3 comes from this gene; cDNA ES... comes from this gene; cDNA ES...		UNCLASSIFIED	284758	66714117, 29331825, 284909, 285008, 284758
1825	95354748 (3249, 3250)	Novel Protein sim. GBank g14589622jbj(BA178833.1) - (A8023206) KIAA0989 protein [Homo sapiens]		kinase		284485, 22278894, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 284092, 284259, 29331824, 29331825, 29331827, 29331828, 284102, 284106, 284508, 33657084, 285017, 285018, 18108351, 284683, 284369, 284288, 21906765, 21906766, 21906767, 21906769, 35695917, 285021, 284691, 65274620, 18108368, 263972, 18108376, 35696423, 284631, 284634, 22279000, 22279002
1828	94734369 (3251, 3252)	Novel Protein sim. GBank g18579070jg1A046844.1(AF160904) BcDNA.HL0936 [Drosophila melanogaster]				52644507, 52845156, 52846385, 52846842, 22278894, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 284906, 66712502, 284909, 285008, 285009, 60432229, 60433356, 60434338, 21906754, 52846317, 52844296, 285011, 87168559, 284604, 285018, 284448, 284369, 284288, 284766, 52844229, 284689, 21906765, 21906768, 35695917, 285021, 285022, 52844150, 33657023, 65274620, 27466261, 27486282, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 284567
1827	83388773 (3253, 3254)	Novel Protein sim. GBank g13668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	284288	284288
1828	85708459 (3255, 3256)		eph			284288, 284686, 284767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gl424075dbj EAA74866.1 - (A020850) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87778027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 2856102, 284693, 264634, 22278002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gl1915892 emb CA609995 - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264258, 33657032, 284693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 284910, 264634, 264636, 264637, 5518223, 264558, 264756, 18108385, 264653, 264263, 264766, 264768, 264687, 264769, 264691, 264692, 29145499, 264509, 264905, 264907, 284611, 284612, 264482, 264688, 264765, 284682, 284683, 264638, 264259, 264767, 264908, 264909, 264639, 264637, 284631, 265007, 284637, 22278002
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gl2556501 dbj EAA22896 - (D93850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264558
1633	87775683 (3265, 3266)				
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gl488728 gb AD3244.1 AF150755 microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) Spectrin repeat	struct	
1635	94232600 (3269, 3270)			UNCLASSIFIED	6574572, 22278998, 35696052, 52644045, 264511, 265008, 265009, 265010, 265011, 265012, 265019, 264448, 264369, 21906765, 21909765, 265021, 284930, 284932, 22278995, 294594, 264763, 265020, 264558
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gl4557511 ref NP_001339.1 pCAPK - death-associated protein kinase 3	Contains protein domain (PF00069) Eukaryotic protein kinase domain	kinase	
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gl3420051 AC004680 - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	21909765, 21909767, 22278998, 35696286, 22278999, 264550, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 284630, 265007, 33657402, 21909764, 264692, 264004, 264764, 264683, 264558, 264288
1638	87101854 (3275, 3276)			UNCLASSIFIED	264485, 18108384, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696286, 29331828, 56182435, 264112, 265008, 265009, 56182435, 264112, 264603, 264768, 284757, 264758, 55811386, 264603, 264768, 18108381, 264764, 264288, 264768, 264769, 21909767, 55811937, 264691, 33657023, 65274620, 18108370, 264764, 55811576, 264558, 264639, 83373044, 18108385, 87168518
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gl5420389 emb CA946680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			

1540	94113185 (3275, 3280)	Novel Protein sim. GBank gij2842469jemb CAA16547.1) - (AL021747) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906768, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1541	87625160 (3281, 3282)		UNCLASSIFIED	29146499, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1542	94312557 (3283, 3284)	Novel Protein sim. GBank gij1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain	22278999, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108391, 60170394, 56182323, 18108388, 87168518, 22279002, 264554
1543	94131766 (3285, 3286)			29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1544	58095125 (3287, 3288)		UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264568, 264567
1545	95013858 (3289, 3290)	Novel Protein sim. GBank gij1076802jgir S49915 - extensin like protein - maize	UNCLASSIFIED	264685, 264693
1546	95362891 (3291, 3292)		UNCLASSIFIED	22278994, 56994075, 35696286, 264229, 29331824, 29331825, 29331828, 60432289, 264508, 60433366, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1547	94276428 (3293, 3294)	Novel Protein sim. GBank gij500257jemb CA944338.1) - (Y17460) alpha-N-acetylglucosamine alpha 2,6-sialyltransferase [Puga natripis]	UNCLASSIFIED	29331822, 264908, 264908, 264369, 21906768, 60170615, 264639, 22279000
1548	87642098 (3295, 3296)		UNCLASSIFIED	265008, 264686, 55811857, 35695917, 55810764, 264566, 56182323, 264556, 18108385

1649	95347528 (3297, 3306)	Novel Protein sim. GBank gl0554065[emu]CA458337] - (XG3413) U68 [Human herpesvirus 6]	cadherin	264488, 2227895, 35695286, 22278956, 2227897, 2227898, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264805, 264907, 66712502, 264908, 52644045, 264909, 56162435, 264511, 265007, 265008, 265009, 264491, 264493, 60433438, 264596, 56812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644230, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 264682, 35691723, 33657109, 20281149, 18108370, 264692, 18108374, 18108375, 35698423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264559, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264632, 264633, 264656, 264487, 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87418539 (3299, 3300)	Novel Protein sim. GBank gl03647335[emu]CA421059] - (ALC01644) possible zinc-finger protein		264488, 52645156, 18108397, 35695286, 22278958, 22278959, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906764, 265010, 265011, 265017, 265019, 264448, 18108354, 264981, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264682, 264693, 264929, 35695855, 264558, 264637, 264653, 264658, 83373044, 56526486, 22279000, 22279002, 264554, 2227897, 26168408, 56182435, 21906754, 264265, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002, 264554
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gl1657837 (U73200) - p118[ap] [Mus musculus]	Contains protein domain (PF00169) PH domain	22278957, 26168408, 56182435, 21906754, 264265, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002, 264554
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gl03776054[emu]CA406273] - (A004939) Tapasin [Gallus gallus]	glycoprotein Contains protein domain (PF00047) immunoglobulin domain	18108368, 22278958, 22278959, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265005, 29331831, 60433365, 60433438, 29331832, 264910, 60432229, 21906764, 265010, 265011, 265017, 265019, 264448, 18108354, 264981, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264682, 264693, 264929, 35695855, 264558, 264637, 264653, 264658, 83373044, 56526486, 22279000, 22279002, 264554
1654	79756471 (3307, 3308)		UNCLASSIFIED	33657109, 264655

1655	86685346 (3309, 3310)	Novel Protein sim. GBank gll3355717[emb]CAAT7496]- (Y13053) seryl-tRNA synthetase [Zea mays]	synthase	52644507, 35696286, 22278988, 22278989, 29331824, 29331825, 29331828, 335658970, 264508, 52644505, 264511, 264510, 52646317, 5264298, 52644229, 33657023, 33657109, 52644332, 264557, 55182323, 55526486, 60432113
1656	759652297 (3311, 3312)	Novel Protein sim. GBank gll1890141[dbj]BAA18947]- (D83206) P24 protein [Mus musculus]	UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gll4557645[ref]NP_001524.1[ph-NRP - heterogeneous nuclear ribonucleoprotein L	dna_mn_bind	29331827, 265003, 21906766, 21906767, 265020, 265022, 33657109, 264638, 55526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gll3877072[emb]CAA87060]- (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	UNCLASSIFIED	52646365, 35696286, 22278988, 22278989, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146468, 264905, 264908, 52644505, 265005, 60433356, 264757, 60433438, 21906764, 265011, 18108351, 264448, 264369, 264388, 264765, 264768, 21906765, 21906767, 21906768, 21906769, 29148629, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279003, 264482
1659	88230107 (3317, 3318)	Novel Protein sim. GBank gll539218[ph]S38038 - hypothetical protein YKL201c - yeast [Saccharomyces cerevisiae]	UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278986, 265020, 22278989, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264635, 264585
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gll2497012[sp]Q10010[YSVA_CAEEL - HYPOTHETICAL 26.8 KD PROTEIN T18C3.4 IN CHROMOSOME III	UNCLASSIFIED	264488, 35696286, 264259, 35696032, 264508, 264509, 264903, 264908, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264902, 264596, 265010, 264603, 264602, 265017, 265018, 264605, 264760, 264764, 264988, 264765, 264686, 264768, 264769, 264689, 21906766, 35695917, 264690, 35696423, 264693, 33657109, 264629, 35696423, 35695955, 264624, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264553, 264483, 264564, 264565, 264566, 264486, 264487

1661	94234071 (3321, 3322)	Novel Protein sim. G.Bank glt4759100[re]NP_004759.1pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) RNA recognition motif (e.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 2227898, 264356, 29331824, 29331825, 29331827, 29331828, 264509, 65712902, 29331830, 264908, 5564045, 265007, 264511, 6043356, 6043438, 55812038, 21906754, 265019, 264448, 264765, 264768, 264769, 21906768, 21906769, 265020, 3957023, 33957109, 65274591, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. G.Bank glt1730502[sp]P52875[PF27] PROTEIN PF127			18108192, 29331822, 29331828, 20281100, 264106, 265008, 265007, 265008, 18108348, 21906765, 18108365, 18108366, 18108374, 83372944, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. G.Bank glt4884136[emb]CAB43275.11 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) WW domain	kinase	52845155, 56152575, 22278994, 22278995, 35966288, 22278996, 5694075, 22278997, 22278998, 22278999, 264259, 29331822, 29331828, 29331827, 29331828, 33956970, 29331900, 264908, 56182435, 264511, 60433568, 33957402, 33108954, 87168474, 87168559, 265017, 265018, 264505, 18108351, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 264621, 33957023, 264683, 293957, 33957109, 264630, 53644332, 83373044, 87168518, 60432113, 22273000
1664	94234076 (3327, 3328)	Novel Protein sim. G.Bank glt3043692[db]BA4355101 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263964, 35966286, 29331824, 35966092, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264581, 264582, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21906764, 21906765, 21906767, 35965957, 265021, 264354, 60170815, 264690, 264691, 264692, 33957109, 33957182, 264628, 18108370, 264628, 35968423, 35968685, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264568

1665	91226542 (3328, 3330)	Novel Protein sim. GBank gji1083506[gji10835065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 26331836, 26331838, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264502, 264503, 264505, 264758, 264506, 264680, 264760, 264762, 264764, 264766, 264768, 264639, 264630, 264634, 264636, 8337304, 264564, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gji3913431[isp042643/DDX8, SCHPO - PUTATIVE PRE- MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - ST RNA binding domain	helicase	56904075, 22278989, 264259, 26331824, 26331826, 26331827, 2645498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21906767, 21906769, 264691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91226555 (3333, 3334)	Novel Protein sim. GBank gji5689535[gbjBA83051.1] - (AB028022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	264259, 26331822, 26331826, 264905, 264906, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264766, 264686, 21906765, 21906767, 21906769, 265020, 265021, 60170915, 264680, 264682, 264693, 18108388, 18108370, 265972, 55510764, 264550, 8337304, 60432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gji207694[gpjA453683.1] - (AF021197) short region of weak similarity to protein kinase C; contains similarity to Plem domain PF00130 (DAG, PE- bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	264758, 264511, 264909, 264509, 264907, 264908, 264511, 264909, 264511, 264907, 264689, 33657109, 35696423, 35696555, 264632
1669	91227446 (3337, 3338)	Novel Protein sim. GBank gji387537[lembjCA485414.1] - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit, cDNA EST EMBL:D64658 comes from this gene, cDNA EST EMBL:D66829 comes fr ...		UNCLASSIFIED	26331825, 33109954, 264906, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 26331824, 26331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gji462451[ispjP24244KKK1 YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 22278987, 26331825, 264909, 21906764, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906766, 21906767, 21906769, 21906769, 264681, 264555, 264556, 22279000, 264556, 264906, 264909, 264632, 18108381
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gji1814270 [U74596] - double- stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	

1673	86095137 (3345, 3346)	Novel Protein sim. GBank gl2078894(gbAA83983.1) - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG PE bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130). Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264569, 18108394, 59894075, 22278996, 264259, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264910, 60170831, 264582, 264594, 264595, 264759, 264601, 264760, 264762, 264683, 264764, 264284, 264765, 264686, 264688, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264559, 264638, 264639, 264553, 264482, 264564, 264565, 264566, 264567, 264485
1674	86256028 (3347, 3348)	Novel Protein sim. GBank gl5262467(emb)CAB45693.1) - (AL080682) hypothetical protein [Homo sapiens]		kinase	29331827, 29331824, 264906, 5284045, 60433356, 87189559, 264448, 264288, 264686, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gl3128366 (AF010496) - 50S ribosomal protein l9 [Rhodospirillum rubrum]		UNCLASSIFIED	5818168, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 68712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264654
1676	85358086 (3351, 3352)	Novel Protein sim. GBank gl4164065(gbAA0406327) - (AF111091) latrophilin 3 splice variant bbsf [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264807, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373944, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gl3327046(djb)BAA31591) - (AB014518) KIAA0616 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	86966829 (3355, 3356)	Novel Protein sim. GBank gl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289). Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED carboxylase	29331824, 264102, 264488, 18108392, 18108394, 57646842, 18108397, 18108398, 35696286, 29331874, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	65274572, 22278994, 22278999, 68714117, 29331827, 56182435, 21906764, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gl5689537(djb)BAA43052.1) - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811557, 264690, 33657023, 35696423, 83373944, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1694	94208168 (3387, 3388)	Novel Protein sim. G.Bank gil545332(reINP_006225.1)pPOLR_ polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) RNA polymerases L / 13 to 16 kDa subunit	imapolymerase	35695286, 22278998, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35696092, 29146499, 264905, 264908, 2644945, 264511, 265006, 265007, 265008, 264592, 60433356, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906765, 60170615, 254691, 264692, 264693, 18108370, 18108374, 263978, 35696423, 35695855, 254556, 18108381, 18108385, 87168518, 264482, 264486, 264634
1695	94719325 (3389, 3390)	Novel Protein sim. G.Bank gil4680679(gbAAD27729.1)AF 3295 - (AF 3295A) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87624038 (3391, 3392)	Novel Protein sim. G.Bank gil4220517(emblCAA22990) - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264258, 265010, 18108351, 264764, 21906766, 18108370, 264682
1697	85740963 (3393, 3394)	Novel Protein sim. G.Bank gil505652 (U10382) - GP3db glycoprotein [Homo sapiens]		glycoprotein	
1698	87445285 (3395, 3396)	Novel Protein sim. G.Bank gil502031(gbAAD08411.1)AF 15573 - (AF 155739) axotrophin [Mus musculus]			56984075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29146827, 21906768, 29146829, 265020, 265022, 33657023, 264558, 87168516, 22279002, 35696286, 264635
1699	87424793 (3397, 3398)	Novel Protein sim. G.Bank gil543344(prrj)S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) Zinc finger, C2H2 type	UNCLASSIFIED nucl_rept	29331824, 5264045, 265008, 265009, 263969, 263971
1700	87559167 (3399, 3400)	Novel Protein sim. G.Bank gil387743(emblCAA96552) - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL.D72822 comes from this gene; cDNA EST EMBL.D75763 comes from this gene; cDNA EST y4274e3.3 comes from this gene; cDNA EST y4274e3.5 c...		UNCLASSIFIED MHC	264092, 264110, 263977, 22278995, 22278997, 264092, 29146498, 29146499, 264107, 264508, 264807, 264110, 264112, 265008, 60170831, 21906754, 265011, 265017, 264765, 18108351, 264288, 21906765, 35695817, 265021, 60170615, 263967, 33657109, 18108370, 263972, 263874, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 56526486, 87168518, 60432113
1701	86570488 (3401, 3402)	Novel Protein sim. G.Bank gil451544 (J04267) - prolins-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264605, 265017, 264622, 264628, 264638
1702	87795092 (3403, 3404)	Novel Protein sim. G.Bank gil1263289 (U47856) - fibron-4 [Araneus diadematus]		UNCLASSIFIED	264309
1703	79568651 (3405, 3406)	Novel Protein sim. G.Bank gil4519621(dbbjBA75670.1) - (AB017614) OASIS protein [Mus musculus]			264560, 35696286, 264807, 265010, 264687, 264765, 264692, 264693, 264630, 264560, 22278998, 264259, 264509
1704	86522579 (3407, 3408)	Novel Protein sim. G.Bank gil519621(dbbjBA75670.1) - (AB017614) OASIS protein [Mus musculus]			265018, 264764, 264693, 264696, 21906768, 21906769, 265022, 264691, 264558, 22279000
1705	87795175 (3409, 3410)	Novel Protein sim. G.Bank gil312034(prrj)5011Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			
1706	87790867 (3411, 3412)				

1707	58041230 (3413, 3414)	Novel Protein sim. GBank gH432166[gi AA157971] - (AF055470) ZNF28 [Homo sapiens]	UNCLASSIFIED	18103036, 22278907, 264259, 29147520, 29331926, 22916488, 264905, 264906, 265008, 264693, 264695, 264754, 264696, 265010, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35696423, 55811576, 264558, 87168518, 60432113, 264637
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gI517459[ne NP_005547] IgMTHF - 5,10-methyleneletrahydrofolate dehydrogenase, 5,10-methyleneletrahydrofolate cyclohydrolase, 10-formylletrahydrofolate synthetase	synthase	56182675, 22278906, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331928, 29146488, 29146499, 29331830, 265009, 60170931, 33657402, 33109954, 87168559, 265019, 18108351, 2644448, 121905765, 21906767, 21906768, 29148627, 29148629, 29148784, 60170615, 52844150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264583, 264707, 55811557, 263974, 263976, 263977, 263981
1709	80222583 (3417, 3418)	Novel Protein sim. GBank gI5031735[ne NP_005760] 1pHEC - N-acetylglucosamine 6-O-sulfatransferase	UNCLASSIFIED	264556
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gI5031735[ne NP_005760] 1pHEC - N-acetylglucosamine 6-O-sulfatransferase	UNCLASSIFIED	65274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264583
1711	91013729 (3421, 3422)	Novel Protein sim. GBank gI5454168[ne NP_009453] 1pX4PA - HBV associated factor	kinase	5694904, 2644093, 264259, 29331822, 264909, 29331924, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 336367, 33657109, 263974, 35696423, 35695565, 264630, 264638, 264558, 264566, 22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gI5454168[ne NP_009453] 1pX4PA - HBV associated factor	UNCLASSIFIED	22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486
1713	84143453 (3425, 3426)	Novel Protein sim. GBank gI456049 (M69183) - malaria-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	UNCLASSIFIED	22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486
1714	87420048 (3427, 3428)	Novel Protein sim. GBank gI456049 (M69183) - malaria-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	UNCLASSIFIED	22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gI456049 (M69183) - malaria-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	UNCLASSIFIED	22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gI456049 (M69183) - malaria-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	UNCLASSIFIED	22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486
1717	87400449 (3431, 3432)	Novel Protein sim. GBank gI456049 (M69183) - malaria-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	UNCLASSIFIED	22278993, 264638, 264758, 18108351, 18108370, 2933974, 18108374, 264634, 55182323, 83373044, 60432113, 22278997, 264757, 17590765, 265020, 264692, 264695, 26526486

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gll2765411[emb]CAA74749j - (Y14391) GTP-binding protein [Homo sapiens]	UNCLASSIFIED	264560, 264259, 26331925, 26331926, 26331928, 26580652, 2645009, 2649005, 2649007, 2649008, 2649009, 264517, 2655009, 264910, 264592, 264593, 264751, 264759, 265017, 264881, 264765, 264766, 264866, 18103557, 26505917, 264680, 264692, 264693, 264628, 264629, 26506423, 264630, 264631, 264635, 264636, 18103580, 264638, 264639, 18103585, 18103591
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gll2833625[sp]Q14899Y076. HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA03936)	UNCLASSIFIED	265011, 264681, 264682, 264684, 264685, 264689, 1906765, 265021, 264691, 33657023, 264693, 18103370, 35695855, 264632, 264634, 264636, 18103368, 22279002
1719	94312529 (3437, 3438)	Novel Protein sim. GBank gll2833625[sp]Q14899Y076. HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA03936)	UNCLASSIFIED	18103595, 65274572, 35696296, 22279007, 60432048, 58182161, 66714117, 60432289, 29331928, 35696052, 29331928, 2649006, 29331930, 58182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264800, 264801, 265017, 264448, 264764, 264288, 264765, 21906766, 21906769, 55811957, 265020, 265021, 59644150, 33657023, 33657109, 33657182, 27486262, 33657248, 35695763, 18103370, 60431528, 33657448, 3569623, 55811576, 35695855, 18103374, 35696423, 55811576, 35695855, 264631, 55182233, 264559, 264564, 264565, 58182575, 22279009, 264569, 264574, 265
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gll2129478[pir]S51939 - chitinase (EC 3.2.1.4) precursor - beet	UNCLASSIFIED	58182575, 22279009, 264569, 264574, 265011, 26432289, 29331927, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264801, 264760, 264765, 264288, 264766, 264886, 18103557, 264689, 21906765, 55811957, 264693, 20281140, 264693, 20281071, 264694, 65274791, 264630, 264558, 264634, 264635, 264636, 264637, 264558, 264638, 264639, 56182233, 18103581
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gll486545[emb]CA84381.11 - (AL050280) hypothetical protein [Homo sapiens]	UNCLASSIFIED	22279094, 22279099, 26331922, 265006, 265007, 265008, 55812038, 21906754, 265007, 265011, 87185559, 18103551, 18103559, 265011, 87185559, 18103551, 18103559, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18103370, 18103374, 264556, 60170394, 83373044, 18103585, 264486
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gll569375[dbj]BA62966.1 - (AB030644) tudor repeat associator with PCTAIRE 2 - (Rattus norvegicus)	Contains protein domain (PF00567) Tudor domain	56994075, 29331924, 29331928, 265009, 18103551, 21906768, 265020, 33657023, 18103374, 83373044

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gi1426862 gb A020633 - (AF126062) Afl-like 2 binding protein BAKT1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264766, 21906167, 21906768, 56162575, 55811937, 22278997, 22278998, 265020, 264239, 264692, 33657023, 29331622, 25331624, 28331825, 60432285, 33657162, 33656970, 33657349, 29146499, 264506, 264907, 18108370, 264623, 264908, 264805, 18108374, 35811376, 264510, 265006, 264511, 265007, 264910, 264632, 264591, 60432228, 264592, 60433366, 264594, 60433438, 264595, 83373044, 55812035, 33109594, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264268, 264567, 264466, 264569, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi2340162 (AF005083) - dsRBP-Zr 2 [Xenopus laevis]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264556, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gi312662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - homeobox Akr repeat	UNCLASSIFIED	264508, 264509, 264910, 264903, 264907, 264908, 264909, 264910, 265003, 264591, 264601, 264760, 18108351, 264681, 264764, 264286, 264768, 264768, 21906768, 33659377, 264628, 33659423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264595
1726	85754255 (3451, 3452)	Novel Protein sim. GBank		UNCLASSIFIED	264595, 264685, 264689
1727	85268362 (3453, 3454)	gi489348 gb A0207861 1AF13256 - (AF132562) BCDNA LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264688, 21906768

1728	85494815 (3455, 3466)	Novel Protein sim. GBank g 4406549 gb 44020027 - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424178, 18108397, 56182575, 22278995, 56994075, 35696286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432288, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264369, 264685, 264766, 264687, 264769, 21906764, 264688, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810784, 65274791, 35695955, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264584, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank g 854065 emb CAA58337 - (X83413) UB [Human herpesvirus 6]	UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	8548474 (3459, 3460)		UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88265068 (3461, 3462)	Novel Protein sim. GBank g 631600 v S47094 - hypothetical protein - rabot	UNCLASSIFIED	52646842, 264907, 264908, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank g 424023 db BAA74894.1 - (AB020878) KIAA0871 protein [Homo sapiens]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264636, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank g 15157556 (U70674) - m-Numb [Mus musculus]	- synthase Phosphotyrosine interaction domain (PTBPIP)	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264636, 264556, 264693
1734	87795261 (3467, 3468)			

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gH435607(gH435566:1AF4679:1AF46793) PF727 [Mus musculus]	Contains protein domain (PF01169) Uncategorized protein family UPF0016	264488, 18108394, 18108398, 22276988, 60432049, 264259, 29331822, 264908, 265006, 265020, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148679, 29148784, 265021, 265022, 52644150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390, 264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1736	95362384 (3471, 3472)	Novel Protein sim. GBank gH856547(reffp_005472:1pT94P: thyroid hormone receptor-associated protein complex component [Mus musculus])	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gI2143607(gI158695: BIK protein, rat)	Contains protein domain (PF00168) C2 domain	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gI2225941(gmb[CIA469714]: [108460] Mdes protein [Mus musculus])	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1739	87282576 (3477, 3478)	Novel Protein sim. GBank gI4809(gmb[CIA44309]: [A24252] YCR60) [Saccharomyces cerevisiae]	Contains protein domain (PF00441) Acyl-CoA dehydrogenase	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1740	85929339 (3479, 3480)	Novel Protein sim. GBank gI4809(gmb[CIA44309]: [A24252] YCR60) [Saccharomyces cerevisiae]	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gH463596(gH435566:1AF4679:1AF46793) PF727 protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) FYE zinc finger	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gH435596(gH435566:1AF4679:1AF46793) PF727 [Homo sapiens]	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1743	85966475 (3485, 3486)	Novel Protein sim. GBank gH435596(gH435566:1AF4679:1AF46793) PF727 [Homo sapiens]	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gH435596(gH435566:1AF4679:1AF46793) PF727 [Homo sapiens]	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1745	20290075 (3489, 3490)	Novel Protein sim. GBank gH435596(gH435566:1AF4679:1AF46793) PF727 [Homo sapiens]	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gH435596(gH435566:1AF4679:1AF46793) PF727 [Homo sapiens]	UNCLASSIFIED	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gI158695 (U75467): Alu [Drosophila melanogaster]	Contains protein domain (PF00409) WD domain, G-beta repeat	264400, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433366, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584, 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002

1748	88003580 (3495, 3496)	Novel Protein sim. GBank glt504511jipr_001530.1ipr1532 - heat shock protein, DNA-like 2	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	264489, 56102975, 29331824, 56182435, 264112, 265007, 265019, 264764, 21906768, 265020, 264691, 5811576, 264635, 264555, 264556, 264537, 264559 284106
1749	83363091 (3497, 3498)	Novel Protein sim. GBank glt5050780glaa049948 - JAF15196 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	33657402, 264288, 52644150, 263974, 83373044
1750	94321664 (3499, 3500)	Novel Protein sim. GBank glt49063164 - hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase, associated	265010, 264369
1751	83373058 (3501, 3502)	Novel Protein sim. GBank glt2760161jibj0434184 - [AD01004] outer arm dynein light chain 2 [Homo sapiens] [crassinea]	Contains protein domain (PF00849) - RNA pseudouridylation synthase	deaminase	264510, 264593, 264682, 21906765, 18108370
1752	86456530 (3503, 3504)	Novel Protein sim. GBank glt3915482gip7436j7G29_SINY3 - HYPOTHETICAL 35.0 KD PROTEIN SLR1629	Contains protein domain (PF01553) - Acyltransferase	phosphatase	56994075, 22276996, 264908, 60170831, 264682, 264764, 264309, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 85274791, 35695855, 264637, 264564
1753	94235159 (3505, 3506)	Novel Protein sim. GBank glt262636 (AF007165) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	transport	264488, 35696286, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264756, 264800, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264655, 264668, 264667, 264666
1754	88095323 (3507, 3508)	Novel Protein sim. GBank glt314218gip398117EHA_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CANT INTERGENIC REGION	UNCLASSIFIED	UNCLASSIFIED	52646842, 22276994, 22276995, 56994075, 22276996, 22276997, 264259, 29331822, 60432289, 29331827, 33656970, 265006, 265008, 60432229, 60433356, 60434338, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 27466282, 27466284, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264462
1755	79470282 (3509, 3510)	Novel Protein sim. GBank glt1176422 (U43194) - rhophilin [Mus musculus]	Contains protein domain (PF00096) - dna_rna_bind	dna_rna_bind	22276997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906766, 65274620, 18108385, 60432113, 264586, 264487
1756	92962614 (3511, 3512)	Novel Protein sim. GBank glt432860glaa027081 - [AC006300] putative glucose-induced repressor protein [Arabidopsis thaliana]	Contains protein domain (PF00096) - dna_rna_bind	dna_rna_bind	22276997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906766, 65274620, 18108385, 60432113, 264586, 264487
1757	95357380 (3513, 3514)	Novel Protein sim. GBank glt4441615jemo0484855.1 - [A388557] zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - dna_rna_bind	dna_rna_bind	22276997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906766, 65274620, 18108385, 60432113, 264586, 264487

1758	87612971 (3515, 3519)	Novel Protein sim. GBank gij388104jmbjCAA164031 - (A1021487) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33109944, 87768474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695955, 264632, 52644332, 22278002, 264583
1759	36094372 (3517, 3519)	Novel Protein sim. GBank gij526274jmbjCAB45688.1 - (A1331320) Proteome rich synapse associated protein 2 [Rattus norvegicus]	UNCLASSIFIED	264759
1760	87329716 (3519, 3520)		UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35698423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 284486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gij127749jpbjT0569MYSC_ACACA - MYOSIN IC HEAVY CHAIN	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gij3169158 (AC004770) - BC285730_2 [Homo sapiens]	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264680, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gij4805026jpbjA4D30062.1 - (A*132856) suppressor of G2 allele of shp1 homolog [Homo sapiens]		56111686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gij1360669jpbjC0HUV1 - collagen alpha 1(V) chain precursor - human	collagen	22278998, 264259, 35696052, 29331828, 56119235, 265008, 265017, 265018, 264448, 264984, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22278002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gij486806jpbjIS35603 - finger protein neutralized - fruit fly (Drosophila melanogaster)	UNCLASSIFIED	354488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264407, 264511, 265007, 265008, 264910, 265009, 21906764, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264589, 264284, 264766, 18108359, 21906766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264682, 264628, 264629, 18108374, 263976, 264636, 85373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q08332 UGGS_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	52845156, 87168559, 80710615, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 179443 emb CAA18263.1 - [AL022238] d1042K10.4 (novel protein) [Homo sapiens]			UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)				UNCLASSIFIED	264692
1769	87398988 (3537, 3538)				UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 CTR_HUMAN - COMPLEMENT C3R COMPONENT PRECURSOR		Contains protein domain (PF00089) - Trypsin	UNCLASSIFIED - complement	264483, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264780, 264563, 264782, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914191 sp P56559 GOT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (D-GLCNAC TRANSFERASE P110 SUBUNIT)		Contains protein domain (PF00515) - TPR Domain	transferase	264736, 264600, 264389, 55811957, 265020, 83373044, 22279000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb BAD34351.1 AF12136 - (AF121360) DNZDHC/NEW1 zinc finger protein 11 (Drosophila melanogaster)		Contains protein domain (PF01529) - DHHC zinc finger domain		22278996, 28331828, 33109554, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	84116827 (3545, 3546)	Novel Protein sim. GBank gi 3978464 AF035693 - G protein-coupled receptor kinase-associated AOP ribosylation factor GTPase-activating protein [Rattus norvegicus]		Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52844045, 264511, 265006, 265007, 265008, 60170831, 60433438, 264758, 55811388, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52844150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35696855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94233573 (3547, 3548)	Novel Protein sim. GBank gi 24565959 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIA0032		Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109554, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22279002

1775	95356330 (3548, 3550)	Novel Protein sim. GBank g11469199[db][BA009487] - (D30829) The KIAA1013 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 65712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 89589542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264388, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 356502, 264691, 33657023, 264692, 33657109, 27486261, 33657249, 15108370, 15108377, 35696423, 55811576, 35695855, 265032, 264634, 264636, 264639, 56182323, 8337044, 56526466, 87168518, 60432113, 22270000, 22270002, 264482, 264486, 264610
1776	94133756 (3551, 3552)	Novel Protein sim. GBank g14580675[db][BA078857.1] - (A8023220) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank g15219939[db][P115]VDK9 - HYPOTHETICAL 115.5 KD PROTEIN C20G8.08C IN CHROMOSOME 1		nucd_rept	56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811550, 264764, 56181582, 264689, 21906755, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22270000, 22270002, 264564
1778	9451624 (3555, 3556)	Novel Protein sim. GBank g1387564[db][CA091454.1] - (Z65561) Similarity to Human rtk13 protein (PIR Acc. No. A4667). Contains the ATP/GTP-binding motif (PROSITE PS00017). cDNA EST EMBL1489412 comes from this gene. cDNA EST Y42749.3 comes from this gene. cDNA EST Y42749...		UNCLASSIFIED	29331826, 29331827, 35696032, 264512, 265007, 265009, 265017, 265019, 264762, 15108351, 264769, 21906755, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 15108370, 264556, 8337044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank g14580675[db][BA078857.1] - (A8023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29146227, 35696286, 26147650, 265006, 265007, 265008, 15108385, 65274727, 264482, 264369, 264766
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apolacton	UNCLASSIFIED	264107, 33657109, 55526466
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	86094607 (3563, 3564)	Novel Protein sim. GBank g128225[db][P4123][C1XN_RAT] - CORTENIN		UNCLASSIFIED	264259, 29331822, 264508, 264805, 264806, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264983, 264768, 264769, 264635, 264636, 264637, 264639, 264663
1783	85177905 (3565, 3566)	Novel Protein sim. GBank g12237543[db][A431436] - (A8004536) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gll1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - PH domain	struct	35696286, 264259, 35696052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264365, 264766, 264687, 264768, 264688, 21908768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264635, 264637, 264638, 264639, 18108385, 22279000, 22279002, 264585, 264586, 264486
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gll45895520b(BAA76798.1) - (AB023171) KIAA0954 protein [Homo sapiens]		UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264366, 264687, 52644229, 21908767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695885, 264555, 65274727, 22279002
1786	85296465 (3571, 3572)	Novel Protein sim. GBank gll117788(isp126770)CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gll3877175(embl)CAA00338.1 - (Z50028) cDNA EST yk32 ths 5 comes from this gene; cDNA EST EMBL.D68896 comes from this gene; cDNA EST yk39519.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264905, 264906, 264908, 264595, 264764, 264766, 264692, 60431328, 264629, 264636, 264564, 264566
1788	91228779 (3575, 3576)	Novel Protein sim. GBank gll2086669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 83373044
1789	86094529 (3577, 3578)			UNCLASSIFIED	264288, 265021, 264555, 264636
1790	82488734 (3579, 3580)				35696052, 264905, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1797	912212219 (3593, 3594)	Novel Protein sim. GBank glij1842111 (U87560) - decoy [Arbidopsis thaliana]	ribosomalprot	22278996, 22278997, 22278998, 22278999, 23311822, 264810, 60110031, 21006754, 52644229, 21006705, 21006765, 21006769, 35695917, 265022, 32644150, 264691, 357023, 263997, 35671109, 22279000, 22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 35657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632
1798	91221276 (3595, 3596)	Novel Protein sim. GBank glij263206djb(AA24608.1) - (D89340) dipeptidyl peptidase III [Rattus norvegicus]	peptidase	22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 33657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632
1799	85321713 (3597, 3598)	Novel Protein sim. GBank glij5609541djb(BA43054.1) - (AB029025) KIAA1102 protein [Homo sapiens]	eph	22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 33657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632
1800	87360116 (3599, 3600)	Novel Protein sim. GBank glij4680679gjb(AAD27729.1) (AF132954) CGI-20 protein [Homo sapiens]	UNCLASSIFIED	22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 33657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632
1801	95060723 (3601, 3602)	Novel Protein sim. GBank glij134920gjb(P21997)SSGP VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 33657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank glij4680679gjb(AAD27729.1) (AF132954) CGI-20 protein [Homo sapiens]		22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 33657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632
1803	95060725 (3605, 3606)	Novel Protein sim. GBank glij4680679gjb(AAD27729.1) (AF132954) CGI-20 protein [Homo sapiens]		22278996, 56999175, 22278997, 22278998, 23311822, 265022, 29316126, 60432289, 23311823, 35695917, 265022, 60432289, 264757, 60432308, 21006754, 264691, 67116859, 265017, 18100351, 264692, 264448, 264284, 21006765, 21006766, 21006767, 21006768, 21006769, 35695917, 265020, 265021, 33657023, 33657182, 27486561, 27486285, 33657249, 263973, 18100374, 55811576, 35695885, 18100385, 67116818, 22279000, 2644486, 264903, 21006754, 21006767, 21006769, 265020, 33657023, 284692, 264693, 264404, 22279000, 264691, 264556, 264566 52644045, 265007, 264632

1504	87770203 (3607, 3608)	Novel Protein sim. GBank gji13875914(emb CAA9538.1 - ZML03)-deduced using GeneFINDER. CDNA EST ENBL C13850 comes from this gene. CDNA EST ENBL C11575 comes from this gene. CDNA EST yk343h.5 comes from this gene. [Caenorhabditis elegans]		52646365, 22378907, 22278909, 264905, 264908, 264909, 264910, 21006754, 264786, 21906785, 21906786, 35695917, 265020, 265022, 264691, 264637, 22427900, 264564, 264566
1505	94530375 (3609, 3610)	Novel Protein sim. GBank gji453644(re NP_006461.1 PEBBP - estrogen-responsive B-box Protein)		29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644220, 35696423, 264636, 60433113
1506	94133762 (3611, 3612)	Novel Protein sim. GBank gji4589676(bj BA716857.1 - (A8023230) KIAA1013 protein [Homo sapiens])	struct	2644094, 264405, 264408, 35696423, 265007, 265008, 264555, 264582, 265011, 265018, 264389
1507	86843032 (3613, 3614)			29331824, 264808, 264910, 33657023, 2633978
1508	87642711 (3615, 3616)	Novel Protein sim. GBank gji106407(emb CA93233.1 - (AL050008) hypothetical protein [Homo sapiens])	UNCLASSIFIED	264488, 35696286, 6671417, 35696052, 66712502, 264592, 60433438, 52644256, 265010, 264683, 264309, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35698423, 35695655, 56182323, 264563, 264564, 264487
1509	93521468 (3617, 3618)	Novel Protein sim. GBank gji1916827 (U87985) - putative G protein [Mus musculus]	UNCLASSIFIED	264594, 55811150, 264686, 20148629, 29148764, 264690, 264629, 18108374, 264556, 264557, 264558
1510	88066318 (3619, 3620)	Novel Protein sim. GBank gji13529446(rp P41719V JP_YEAST - HYPOTHETICAL 18 kD PROTEIN IN BATZ-DALS INTERGENIC REGION PRECURSOR	UNCLASSIFIED	264488, 35696052, 264805, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264596, 264758, 264598, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264688, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264633, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264686, 264497
1511	86066272 (3621, 3622)	Novel Protein sim. GBank gji2141684(gp j37275 - death- associated protein kinase (EC 2.7.1.1) - human	Contains protein domain (PF00023) Ank repeat	264488, 264259, 264508, 264509, 264509, 264508, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264690, 264694, 18108354, 264766, 264686, 264769, 264534, 60170815, 33657023, 264629, 264631, 264639, 264653, 264482, 264483
1512	79245772 (3623, 3624)			29331822, 29331824, 265015, 18108351, 21906769

1820	87789455 (3639, 3640)			264905, 264907, 264594
1821	80431510 (3641, 3642)			264907, 264768, 263378
1822	91221523 (3643, 3644)	Novel Protein sim. G.Bank gll1684130[emb]CAB43272.1] - (AL050101) hypothetical protein [Homo sapiens]		22278985, 56984075, 22278986, 22278987, 22278988, 264259, 29331824, 29331825, 29331826, 35698032, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264596, 265017, 265019, 18108351, 264763, 264683, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002, 264488, 264259, 264511, 264288, 264768, 264693, 35698423, 264634, 18108385, 264486
1823	85522330 (3645, 3646)		UNCLASSIFIED	
1824	86612022 (3647, 3648)	Novel Protein sim. G.Bank gll177072ip[il]A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	264907, 264908, 264009, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264668
1825	87430125 (3649, 3650)	Novel Protein sim. G.Bank gll10303603[emb]CAA18493] - (AL022373) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	
1826	91723612 (3651, 3652)	Novel Protein sim. G.Bank gll1680685[bb]AAD27732.1[AF13295 - (AF132957) CGI-23 protein [Homo sapiens]	UNCLASSIFIED	60432049, 264910, 264487
1827	81647212 (3653, 3654)		ATPase-associated	52844407, 52845156, 52846842, 22278994, 22278996, 56984075, 264259, 60432049, 52845080, 35698032, 66712502, 52844045, 265008, 265009, 60432229, 60433356, 60433438, 52846317, 52844296, 265011, 87189559, 264448, 264288, 264369, 264688, 52844229, 264689, 21906765, 21906768, 265020, 60170815, 52844150, 33657023, 27486282, 27486284, 27486285, 35695763, 35698423, 35695855, 83373044, 87168518, 264404, 22279002, 264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gll4503571 e NP_001419.1 pEN01 - endolase 1, (alpha)	Contains protein domain (PF00113) - oncogene End-ase	264488, 52646842, 56182575, 22278956, 55596265, 22278997, 22278999, 264091, 264093, 60432049, 264335, 26331622, 29331824, 6871411, 29331625, 6043289, 29331826, 29331827, 29331628, 264105, 264169, 264907, 66712502, 52644045, 56182435, 2650068, 264611, 264917, 265007, 265009, 265009, 60770831, 60432229, 264953, 60433356, 60433438, 264756, 33108954, 21960754, 67168474, 265010, 265011, 67168559, 265017, 265019, 264761, 264762, 264446, 264764, 264663, 264286, 264685, 16106355, 264768, 16108357, 21960758, 264688, 264765, 264689, 21960760, 21960765, 35659917, 265021, 60170678, 33657023, 33657349, 263972, 55911576, 35659555, 264635, 264395, 264556, 264638, 264557, 67168516, 22279600, 22279002, 264563, 264482, 264505, 264484, 264567 264508, 264564, 264609, 264482, 29331827, 264096, 265009, 264910
1829	80197720 (3657, 3658)			
1830	84312942 (3659, 3660)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 (Kaposi's sarcoma- associated herpesvirus)	nuclease	53645156, 22278994, 22278995, 35666286, 22278995, 22278997, 22278998, 22278999, 29331622, 29331625, 35660052, 52646317, 53644288, 67168559, 265019, 21960765, 21960768, 21960767, 21960768, 21960769, 35659917, 265021, 35657023, 52645129, 35657109, 35657162, 21960761, 27486262, 35657653, 263974, 35659423, 35659555, 2644332 29331824, 35660632, 29331630, 264595, 264756, 265010, 265019, 265022, 264693, 6624791 264602
1831	94138063 (3661, 3662)		UNCLASSIFIED	
1832	84321663 (3663, 3664)	Novel Protein sim. GBank gll1330345 (U938755) - coded for by C. elegans cDNA yk461.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....		

1833	95311184 (3655, 3656)	Novel Protein sim. GBank g15174417eINP_006026_1ipCC4 - CDC42-binding protein kinase beta (DMPK like)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35896052, 29146499, 264508, 264509, 264906, 264907, 68712502, 264908, 5284045, 264909, 264512, 265008, 264591, 264593, 60433356, 21906754, 33657084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 28148629, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27488284, 33657349, 65274791, 264634, 264635, 264558, 264557, 264558, 264559, 18108385, 56526486, 87168516, 60432113, 22279000, 22279002, 264563
1834	80562790 (3657, 3658)			264239, 264907, 264689, 22279000, 22279002
1835	94135718 (3659, 3670)		UNCLASSIFIED	22278994, 29331822, 29331826, 87168474, 264603, 21906766, 263978, 35895855, 53373044
1836	87344450 (3671, 3672)	Novel Protein sim. GBank g147592861eINP_004268_1ipLCP4 - uncoupling protein 4	Contains protein domain (PF00153) - transport Mitochondrial carrier protein	29331825, 264908, 265019, 264764, 264688, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank g133344001eIQ24574IUPE DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - ubiquitin Ubiquitin carboxyl-terminal hydrolase family 2	22278995, 29146499, 265008, 265008, 265009, 265010, 264683, 21906765, 29146827, 29146829, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank g113623691p1A56154 - Abi substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain	29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank g121173101wmb1C4509116.11- (295620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264601, 21906765, 21906766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank g11275601p23249INV10 - MOUSE - PROTEIN MOV-10	UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank g145724641pA4D2834 - 1pAF12385 - (AF12385) FEZ1 [Homo sapiens]		56182575, 29331824, 29331826, 60433386, 264764, 264288, 33657023, 263987, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	9092645 (3683, 3684)	Novel Protein sim. GBank gl1326268 (U8728) - C54H2.1 gene product [<i>Caenorhabditis elegans</i>]	UNCLASSIFIED	65274572, 26331822, 26331824, 26331825, 6671417, 26331826, 26331827, 264907, 264909, 5264045, 56182435, 264510, 265005, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108364, 33657109, 18108368, 264628, 55810764, 56182323, 18108364, 264693, 264564
1843	95262692 (3685, 3686)		UNCLASSIFIED	264488, 56192435, 264769, 26331826, 26331828, 264511, 265006, 265007, 264910, 264631, 264509, 264690, 264636, 264564, 264691, 60432226, 60432049, 264259, 264620, 33657023, 264486, 264909, 264567, 264693, 264769
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gl1456897 (p009223)YQ22, CAEL - HYPOTHETICAL 32.0 KD PROTEIN C98F5.2 IN CHROMOSOME III	UNCLASSIFIED	264603, 365022, 33657023, 87168518, 22279002
1845	95066573 (3689, 3690)	Novel Protein sim. GBank gl1175494 (p00918)YAC5, SOIPO - HYPOTHETICAL 45.0 KD PROTEIN C16C8.05 IN CHROMOSOME I	transcript factor	264259, 26331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21006765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gl13891080 (mncA421728) - (A1032657) similar to EGF-like domain, cDNA EST Y299112.3 comes from this gene, cDNA EST EMBL D35398 comes from this gene, cDNA EST Y433196.5 comes from this gene, cDNA EST Y4399412.5 comes from this gene, cDNA EST Y45798.5 c...	UNCLASSIFIED	264905, 264908
1847	87821487 (3693, 3694)	Novel Protein sim. GBank gl15069323 (p0A039987) YAF15152 - (AF151522) hairy and enhancer of split related (Drosophila species)	transcript factor	22276897, 264259, 26331824, 264909, 18108351, 263974, 22279002
1848	86786360 (3695, 3696)	Novel Protein sim. GBank gl157018 (p0476m) CA632191.11 - (A245417) G6c protein (homo sapiens)	tm7	26331825, 26331826, 26331827, 265017, 264683, 264984, 264769, 264768, 21906767, 21906769, 264692, 22279002
1849	84287872 (3697, 3698)	Novel Protein sim. GBank gl1503635 (p0195) 1PFLN - fibulin 2 precursor	-ATPase-associated	55182375, 265019
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gl1458932 (p01A016813) 11 - (A602318) KIA0569 protein (homo sapiens)	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gl122033 (p01A001477) - (D10627) zinc finger protein (Mus musculus)	dna_mil_bird	26331824, 33658052, 264910, 60433438, 264683, 33658017, 265020, 52644150, 65274020, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi15174629 fNP_000590.1 pPMS - protein inhibitor of activated STAT3	UNCLASSIFIED	56112575, 35996286, 22278998, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35996052, 52644045, 265007, 264910, 60432229, 60433386, 60433436, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264697, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35996955, 56125233, 60432123, 22279002, 264583
1853	91222287 (3706, 3708)	Novel Protein sim. GBank gi185406 femj CAJ583371 - [X3415] U88 [human herpesvirus 8]	UNCLASSIFIED	264687, 264766, 5264507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 2645129, 29331827, 35959970, 33657349, 35995763, 264508, 264606, 264628, 264907, 264629, 264603, 35969423, 35995855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264534, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264487, 264288, 264389, 264766 264592
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi12072984 (U35569) - putative p150 [Homo sapiens]	nuclease	18108392, 52646385, 65274572, 56182575, 22278994, 56994075, 22278995, 35986288, 22278999, 264259, 60432048, 264908, 264510, 265007, 265008, 265009, 264395, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264766, 18108359, 21906764, 21906768, 29146627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35969423, 264631, 264636, 18108381, 264482
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi14539520 femj CAJ58994.1 - [AC03424] dK22D12.1 (novel protein similar to Drosophila Ketch [Ring Canal protein, KEL] and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucL/ rept Ketch motif	56994075, 264259, 29331828, 264511, 264910, 264759, 264693, 264637, 18108381, 83373044
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi13954978 femj CAJ00845 - [AJ008278] acetylglucosaminyltransferase-like protein [Mus musculus]	UNCLASSIFIED	22278999, 264259, 264606, 601770831, 264448, 264686, 265020, 265022, 33657109, 601770394, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi14322670 gb AAO16120 - [AF094308] dentin phosphorin [Homo sapiens]	ATPase-associated	

1856	87628311 (3715, 3716)	Novel Protein sim. GBank gi4981903 gi40038415.1 AE00178 (AE00178)	Contains protein domain (PF00312) - ribosomal prot	264757
1859	84407464 (3717, 3718)	Ribosomal protein S15 [Thermotoga maritima] Novel Protein sim. GBank gi4246371 gb BA074937.1 - (AE020721) KIA00914 protein [Homo sapiens]		22278096, 26331824, 265007 33109954, 265019 264369, 21906788, 20148784, 27486361, 52644332, 22279002
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gi44008522 (AF099731) - conexin 31.1 [Homo sapiens]		265019
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi4143537 gi44505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase	264487, 264259, 29331822, 29331824, 29331825, 265007 265009, 264591, 33109954, 265010, 265019, 264369, 264288, 264686, 264691, 264693, 27486284, 18108370, 18108374, 263077 55811576, 56192323, 264639, 22279000, 22279002, 264482
1862	87372823 (3723, 3724)	Novel Protein sim. GBank gi1254933 gi07313 KIMLC, BABIT - MYOSIN LIGHT CHAIN KINASE SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35692986, 264259, 87168474, 264369, 21906786, 264536, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi4820095 emb CAA09299.1 - (A010642) Dna protein [Desulphobactoides]	UNCLASSIFIED	264601, 264768, 2914827, 29148629, 264692, 264629, 264635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi4322263 gi43001598.5 - (AF077739) metallocarboxypeptidase CPX-1 [Homo sapiens]	Contains protein domain (PF00754) - F50 type C domain	22278589, 264259, 264907 265018, 18108370, 264634, 264635, 264655, 264656, 264638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi3459727 gi030073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIA0236		22278589, 264460, 29331822, 68714117, 68712502, 265006, 265007 265008, 265009, 264591, 60433438, 265010, 265019, 264780, 264448, 264768, 2914827, 29148629, 265020, 265023, 18108385, 60432113
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gi3262637 emb CA54748.1 - (AL001671) hypothetical protein [Homo sapiens]	kinase	18108374, 264769, 18108377, 21906785, 21906786, 36698423, 56182575, 21906769, 29148629, 36698286, 36698917, 265021, 264510, 264511, 264512, 264534, 264535, 60170931, 52644150, 264555, 264601, 264258, 264656, 264692, 264657, 33657023, 60433568, 29331822, 264559, 264595, 29331824, 18108385, 21906784, 33657182, 29331827, 36698082, 33656970, 87166518, 265017, 60431602, 22279000, 264508, 264603, 18108351, 264507, 264682, 264587, 18108372, 264765, 264486
1867	84579158 (3733, 3734)	Novel Protein sim. GBank gi3859630 (AF078098) - forkheadwinged helix-like transcription factor 7 [Homo sapiens]	UNCLASSIFIED	294094

1865	87357458 (3735, 3736)	Novel Protein sim. GBank gll3881525[emb]CA938841 - (Z70038) cDNA EST EMBL D32579 comes from this gene; cDNA EST EMBL D3254 comes from this gene; cDNA EST Y422483.5 comes from this gene; cDNA EST Y4357110.5 comes from this gene [Caenorhabditis elegans]			nuclease	264488, 22278897, 22278899, 29331825, 29331826, 265008, 265009, 33657402, 87168474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 27486264, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264566, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gll482672[refNP_004961.1]p(GFA - insulin-like growth factor binding protein, acid labile subunit)			glycoprotein	264508, 264509, 264506, 264508, 264509, 264510, 264591, 264600, 18108351, 264683, 264766, 264769, 35655855, 264634, 264558, 264539, 18108385, 264563, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gll1869859[emb]CA8067221 - (Z86089) very large tegument protein [human herpesvirus 2]			UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35695917, 60170615, 264692, 18108388, 35695763, 35696423, 65274791, 264638, 264639, 56526486
1871	60234464 (3741, 3742)	Novel Protein sim. GBank gll2460316 (AF021417) - uenues-ovary specific putative transmembrane protein [Rattus norvegicus]			UNCLASSIFIED	264509, 264505, 264595, 264768, 264635, 264636, 264563, 264486
1872	60235355 (3743, 3744)				protease	264510, 264594, 264565
1873	60213890 (3745, 3746)					
1874	95351136 (3747, 3748)					264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gll4589520[db]BA716782.1 - (AB023155) KIAA0938 protein [Homo sapiens]			UNCLASSIFIED	264488, 35655917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264536, 264537, 264538, 33657402, 264558, 18108385, 264600, 264764, 264587, 264766
1876	87112850 (3751, 3752)	Novel Protein sim. GBank gll453910[db]22320 - collagen alpha chain [Riftia pachyptila-tube worms, Peptide, 1027 aa]				35668286, 264828, 264582, 264557, 264558
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gll3983356[db]AAC83924.1 - (AF102545) nbollavin binding protein precursor [Scaphiopus couchii]			UNCLASSIFIED	264757, 264686, 264768, 263978, 264693, 264639, 265010, 264653, 264805, 264906, 264907

1876	95351056 (3755, 3756)	Novel Protein sim. GBank gll4510345(gp)AD21434.11 - (AC006621) unknown protein [Aradopsis thaliana]	Contains protein domain (PF01429) - ubiquitin AN1-like Zinc finger	264550, 264488, 3506286, 5694075, 264250, 29331822, 29331824, 29331825, 3569052, 29331828, 29148498, 264508, 264509, 264505, 264506, 264507, 264508, 264509, 264510, 264511, 264512, 265009, 264510, 33657402, 264504, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264565, 264298, 264706, 264687, 264768, 264769, 2100766, 3505917, 265021, 60170815, 33657023, 264682, 264683, 33657109, 27488265, 264628, 18108370, 264629, 18108374, 35098423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264593, 264564, 264566, 264486, 264467, 264503, 264505, 264506, 265007, 264555, 264566
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gll492664(gp)AC04082.1(AF15184) - (AF151845) CGI-87 protein [Homo sapiens]	UNCLASSIFIED	264765, 264691, 264692, 83373044
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gll1550785(gp)CA462831 - (Y13026) Immune associated protein 38 [Mus musculus]	UNCLASSIFIED	264509, 264505, 264508, 264509, 264510, 264762, 264687, 33657023, 264632
1881	80214948 (3761, 3762)	Novel Protein sim. GBank gll5144(gp)g04050 - hypothetical protein - suid herpesvirus 1 [suan Indiana-Pennsylvanica or Becke]	UNCLASSIFIED	
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gll2384956 (AF022985) - No protein in line four [Ctenomys eringalis]		264508, 21905766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gll1351218(gp)P47267TES2, MOUSE - TESTIN 2 (TES2) (CONTAINS: TESTIN 1 (TES1))	Contains protein domain (PF000412) - homeobox LIM domain containing proteins	264508, 264510, 87168559, 21906766, 264636

1884	8510885 (3767, 3768)	Novel Protein sim. GBank g149236-3/g149240-2: 1A(F15184) CGI-87 protein [Homo sapiens]	UNCLASSIFIED	264488, 18108364, 56181686, 22278988, 60432049, 264259, 29331822, 29331824, 29331825, 6671417, 29331827, 3556052, 264508, 264509, 264505, 264506, 264507, 264508, 264509, 56182435, 264510, 264511, 265007, 264512, 265008, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811366, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 55811150, 264761, 264682, 264763, 264683, 264764, 264288, 264369, 264766, 264686, 264766, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35596423, 35695555, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	8784280 (3769, 3770)	Novel Protein sim. GBank g12507153/p137370VRP1_YEAST - VERPPROLIN	UNCLASSIFIED	56182575, 264259, 264505, 264506, 265008, 264596, 264766, 265020, 264628, 60431528, 264634, 56526486, 264080, 264563, 22278988, 22278989, 60432049, 264910, 265018, 264766, 21906768, 29148629, 264690, 264693, 264628, 264555, 264486
1886	8687402 (3771, 3772)	Novel Protein sim. GBank g1285415/g1492577 11 - (AF045841) No definition line found [Caenorhabditis elegans]		29331822, 29331824, 29331825, 29331826, 29331827, 264506, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695555, 264632, 56182223, 264639, 264563
1887	94139139 (3773, 3774)	Novel Protein sim. GBank g1517421/rel/NP_058023.1/PCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - ATPase-associated C2 domain	263978
1888	8782804 (3775, 3776)	Novel Protein sim. GBank g13319931/lena/CAB108411 - (Z88946) J11-08.2 (Melanoma-Associated Antigen MAGE LKS) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	
1889	91255783 (3777, 3778)	Novel Protein sim. GBank g11083308/p1/g155559 - enhancer-1p-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	264908, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906768, 21906768, 21906769, 265021, 33657023, 33657109, 60182323, 83373044, 18108385, 22279000, 22279002
1890	87828705 (3779, 3780)	Novel Protein sim. GBank g14240195/dbj/BA474876.11 - (AB020660) KIAA0853 protein [Homo sapiens]	UNCLASSIFIED	18108398, 29147620, 264407, 265009, 264600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)		UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 2631182, 2631192, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264909, 18108379, 265007, 265008, 264410, 264632, 264691, 264639, 264596, 18108384, 265010, 265011, 264601, 264603, 264563, 264359
1892	87642825 (3783, 3784)	Novel Protein sim. GBank glij569535[dbj EAA33061.1] - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	2277895, 264509, 8719859, 18108351, 264446, 264682, 265020, 264653, 18108374, 22779000
1893	86533826 (3785, 3786)		laminin	284569, 2631182, 2631192, 26474117, 264259, 2631182, 2631192, 265008, 265009, 2631182, 264906, 265008, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264766, 264687, 264689, 21906768, 265020, 265022, 60170615, 52644150, 264680, 264681, 264692, 33857023, 264693, 33657109, 264628, 18108374, 35658555, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22779000
1894	86989120 (3787, 3788)			264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264638, 264639, 264563
1895	87631891 (3789, 3790)	Novel Protein sim. GBank glij526254[emb CAB4728.1] - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat	56182575, 264255, 60432280, 26331826, 264107, 264905, 264906, 264910, 60170831, 264758, 265010, 265014, 264448, 264288, 264768, 33657109, 264628, 55810764, 18108379, 264634, 56182323, 56528486
1896	85673555 (3791, 3792)		UNCLASSIFIED	264907, 265008, 264687, 264688, 21906768, 264629, 264631, 264634, 264555
1897	80565568 (3793, 3794)	Novel Protein sim. GBank glij28836[sp P38193]ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III	cadherin	264259
1898	87617637 (3795, 3796)	Novel Protein sim. GBank glij127560[sp P23249]MV10_MOUSE - PROTEIN MOV-10		2277898, 2277898, 2277899, 26331874, 26331825, 60432280, 26331827, 35696032, 26331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906768, 21906768, 21906768, 60170615, 55810764, 22779000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank glij290919 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	glycoprotein	264259, 264508, 264905, 60432229, 264769, 21906765, 21906769
1900	87641856 (3799, 3800)	Novel Protein sim. GBank glij412881 (AF017250) - vitellogenin precursor [Oreochromis aureus]	UNCLASSIFIED	264683

1801	95196647 (3801, 3802)	Novel Protein sim. GBank gll555959ipr38378(S51A_RAT) PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) DNA polymerase (viral) N-terminal domain	transport	264488, 2644507, 2645156, 16108396, 5264565, 2646642, 16108397, 56182575, 22278594, 22278895, 56984075, 35696286, 22278897, 22278988, 264490, 60432049, 264259, 26331822, 52645080, 26331824, 26331825, 66714117, 26331826, 60432289, 26331827, 26331828, 35696052, 33656970, 26331827, 26331828, 35696052, 33656970, 29146498, 264906, 264907, 26331830, 264908, 52644045, 264909, 264112, 265006, 264512, 265008, 264910, 265009, 56170831, 60432228, 60433356, 33657402, 60434348, 55912038, 264758, 33109854, 21909794, 33657094, 52642368, 871684, 265010, 265011, 87168459, 265017, 265018, 265019, 18108351, 264448, 264388, 264686, 52644220, 21909785, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 265021, 52644150, 18108382, 33657023, 264693, 263967, 33657109, 33657182, 27466264, 33657349, 35698473, 18108370, 18108378, 55811576, 35698473, 35698555, 60431850, 264638, 263981, 52644332, 60170394, 83372044, 16108385, 87168518, 60432113, 264664, 264107, 263976
1802	80202013 (3803, 3804)	Novel Protein sim. GBank gll4426613(gbAAID20451) - (AF098796) SLM-1 [Mus musculus]		dna_mn_bnd	264259, 26331826, 26331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21909754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 264686, 264758, 264687, 264759, 264693, 264628, 18108374, 264634, 264636, 264637, 264655
1803	87778554 (3805, 3806)	Novel Protein sim. GBank gll3747107 (AF095741) - unknown [Rattus norvegicus]		struct	264488, 264756, 264757, 264685, 29116829, 35695917, 35696286, 264259, 264692, 18108392, 33657023, 26331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696223, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264686, 264288, 264765
1804	80434213 (3807, 3808)	Novel Protein sim. GBank gll13529115ipr47147YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION	Contains protein domain (PF00293) - Bacterial muT protein		264488, 264756, 264757, 264685, 29116829, 35695917, 35696286, 264259, 264692, 18108392, 33657023, 26331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696223, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264686, 264288, 264765
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gll3043714dbjBAA35521 - (AB011167) KIA00595 protein [Homo sapiens]			264488, 264756, 264757, 264685, 29116829, 35695917, 35696286, 264259, 264692, 18108392, 33657023, 26331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696223, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264686, 264288, 264765
1906	12765822 (3811, 3812)			UNCLASSIFIED	264637

1907	65351144 (3813, 3814)	Novel Protein sim. GBank gi 4829595 gb AA03053.1 (AF:15181) - (AF:151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - hydroxase alpha/beta hydrolase fold	65274572, 22278996, 35696266, 22278998, 22278999, 264259, 60433049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21906754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906765, 21906766, 21906768, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3813, 3816)	Novel Protein sim. GBank gi 3986770 (AF:109066) - NG22 [Mus musculus]	UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60433049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29164699, 264905, 264906, 264907, 264908, 66712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52846317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264686, 264688, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148529, 35695917, 265020, 265022, 264691, 264692, 18108384, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22278900, 22278902, 264556, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 224653 db AA020813 - (AB020354) KIA0356 [Homo sapiens]	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264637, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216827 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P4226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) LIM domain containing proteins	35696266, 22278996, 22278999, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264766, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1811	81725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAU030184.1 ACD0653 - hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) DNA mismatch repair protein	nuclease	18108394, 56192575, 56182181, 26331826, 293311827, 32656920, 264906, 265448, 264591, 53812038, 87158559, 264448, 264369, 21905765, 21905768, 265022, 264691, 264693, 18108395, 55811576, 264556, 18108395, 18108388
1812	85413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 gb BAA43003.1 - (AB028874) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56192575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278998, 264259, 293311822, 29331824, 56182181, 293311823, 66714117, 35696032, 264905, 264906, 264907, 264908, 52641045, 56182433, 265007, 265008, 264810, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264688, 264765, 21905765, 21905766, 21905767, 21905768, 21905769, 55811957, 265020, 265021, 265022, 60170515, 284692, 33657003, 264683, 18108378, 55811576, 35698423, 65274791, 264637, 56182323, 83373044, 56526486, 22278993, 264683, 284666
1813	85305546 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005663.1 b2NF2 - zinc finger protein (C2H2) homologous to mouse HOK-2			56182375, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331828, 29331827, 265008, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 284685, 264686, 264769, 21905765, 21905766, 21905768, 21905769, 55811957, 265020, 265022, 264691, 55811578, 264634, 264635, 264638, 56182323, 83373044, 18108385
1814	83423982 (3827, 3828)	Novel Protein sim. GBank gi 45890415 gb BAA76824.1 - (AB023187) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) EF hand	struct	56182575, 293311824, 35666032, 264806, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657003, 264693, 264698, 264631, 264632, 264634, 264635, 264639
1815	85340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 gb BAA48299.1 - (AB028862) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 293311824, 293311826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264688, 264624, 264635, 264637, 264639, 83373044, 264665
1916	79840761 (3831, 3832)				264683, 264639

1817	87821680 (3833, 3834)	Novel Protein sim. GBank gi 5689391 db JBAA42979.1 - (AB028950) KIAA1027 protein [Homo sapiens]	struct	284789, 284889, 21906765, 21906768, 22278996, 284758, 284691, 284693, 29331824, 29331825, 29331826, 29331828, 284905, 284906, 284628, 284907, 284908, 284909, 284910, 284930, 284910, 284934, 284635, 284636, 284637, 284638, 284639, 284639, 284758, 18108385, 21906754, 285011, 284604, 284963, 18108351, 284782, 284783, 284958, 284764, 284766
1818	95302795 (3835, 3836)	Novel Protein sim. GBank gi 5281517 db AA041524.1 AF15493 - (AF15493.1) PV-1 [Rattus norvegicus]	struct	284488, 18108392, 18108357, 21906765, 21906767, 21906768, 95182575, 21906769, 22278994, 35896286, 35895917, 22278996, 22278997, 265021, 265022, 284334, 284690, 284691, 284692, 3857023, 284693, 29331824, 29331825, 3857109, 29331828, 92845129, 35896032, 29331823, 27486262, 27486264, 35895763, 284906, 284905, 284908, 284906, 284628, 284907, 18108370, 284908, 284629, 284909, 18108372, 18108374, 2833970, 35896423, 35895855, 284910, 284911, 385006, 385007, 284912, 285008, 284931, 385009, 284910, 284934, 284935, 284955, 284936, 284938, 284937, 284957, 284958, 284939, 284954, 60170394, 284955, 284959, 284956, 33373044, 284758, 32846317, 18108385, 5264298, 96529488, 97188518, 285010, 265011, 97188599, 284900, 284601, 284602, 285017, 284903, 284904, 285018, 284605, 284760, 284761, 284482, 284964, 18108351, 284762, 284682, 284965, 284446, 284764, 284966, 284486, 284967, 284369, 284286, 284766, 284487, 284985
1819	94143847 (3837, 3838)	Novel Protein sim. GBank gi 387684 emb CA001237 - (Z77867) cDNA EST EMBL:CB0125 comes from this gene; cDNA EST EMBL:CB0750 comes from this gene [Caenorhabditis elegans]	oxidase	22278997, 29331022, 285007, 60170831, 90432228, 60433438, 284448, 284682, 284286, 59811957, 3857023, 3857109, 85274791, 95182523, 22278992
1820	91229953 (3839, 3840)	Novel Protein sim. GBank gi 1809231 (AC000119) - coded for by human cDNAs H78643 (NC_0650729), H68657 (NC_0638459) and H12868 (NC_0637668) [Homo sapiens]	UNCLASSIFIED	284910, 284911, 284912, 284966
1821	79555226 (3841, 3842)	Novel Protein sim. GBank gi 4500897 db AA042457.1 AF12108 - (AF12108.1) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED	264693

1922	87641853 (3843, 3944)	Novel Protein sim. GBank gll138595(p02845)VT2, CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPVITELLIN I (LVI), PHOSVITIN (PV), LIPVITELLIN II (LVI); YGP40]		UNCLASSIFIED	264688, 264689, 264690, 1808370, 264690, 1808374, 265008, 264557, 264564, 1808351
1923	94323559 (3845, 3946)	Novel Protein sim. GBank gll118110(p0321)EBH1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 2277895, 264094, 264259, 2598052, 264509, 264905, 264906, 264907, 264908, 26512502, 264909, 264511, 264512, 265007, 264910, 265009, 264599, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 5581158, 264681, 264762, 264446, 264764, 264765, 264589, 264766, 264767, 264686, 264687, 264768, 264769, 26181562, 264689, 2190766, 264691, 3357023, 264693, 65274620, 3357109, 18105370, 264628, 264629, 33595423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264556, 53373044, 57186516, 264553, 264554, 264555, 264556, 264557, 264558, 264559, 264560, 264561, 265017, 265018, 265019, 265022, 264691, 264693, 264637, 1810365, 264565
1924	87339525 (3847, 3948)	Novel Protein sim. GBank gll387755(embl)CA98657] - (Z77511) possible zinc finger protein, cDNA EST EMBL M89115 comes from this gene; cDNA EST EMBL D71433 comes from this gene; cDNA EST EMBL D72314 comes from this gene; cDNA EST EMBL D75164 comes from this gene; cDNA EST EMBL C1	Contains protein domain (PF00097) - Zinc finger, CMC4 type (RING finger)		
1925	87626338 (3849, 3950)	Novel Protein sim. GBank gll4981903(gb)AAD38415.1(AE00178) - ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - ribosomal protein S15		2277895, 2277896, 2278697, 264259, 2651824, 6714117, 2614899, 264939, 5254404, 265009, 265009, 264758, 265011, 265017, 264665, 264448, 264286, 264692, 33597105, 18108374, 50176384
1926	86094739 (3851, 3852)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 72, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]	struct		264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264286, 264692, 264693, 265018, 264631, 264634, 264637, 264563
1927	85854857 (3853, 3854)	Novel Protein sim. GBank gll3043632(gb)BA25480] - (AB011126) KIA0054 protein (Homo sapiens)			264689, 264631
1928	87790054 (3855, 3856)	Novel Protein sim. GBank gll165675(gb)BA133771 - (DB7433) KIA0248 [Homo sapiens]	Contains protein domain (PF00143) - Extracellular link domain	inf	264489, 264259, 265017, 265021, 264682
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gll5001993(gb)AD37247.1(AF13432) chimeric AFGP/lysozyme-like serine protease precursor [Discotheca mawsoni]	UNCLASSIFIED		264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264559

1930	8786128 (3859, 3860)	Novel Protein sim. GBank gi17092309[pf2963]NBL4_MOUSE - NBL4 PROTEIN		phosphatase	3669286, 29331938, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264603, 264760, 264764, 264766, 264686, 264760, 265022, 35895423, 264639, 60432113
1931	87797279 (3851, 3852)	Novel Protein sim. GBank gi1404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264289, 265020, 264692, 264634, 264637 264694, 264691, 264635
1932	15030972 (3853, 3854)			UNCLASSIFIED	264955
1933	11513658 (3855, 3856)			struct	5612575, 56182435, 264510, 264757, 264758, 56812038, 56811366, 265016, 56811150, 21906765, 264691, 264631, 264635, 264637
1934	84426360 (3857, 3858)	Novel Protein sim. GBank gi1151748[gbA38494] - (A80220223) nonmuscle myosin heavy chain 5 [Bos taurus]		UNCLASSIFIED	264686, 265017, 264511, 264905, 18108351, 264904, 264681, 264259, 18108370, 264986, 264764, 264369, 264955
1935	8775511 (3859, 3870)				60432286, 265007, 265010, 265011, 265019, 33657109, 18108374
1936	8541438 (3871, 3872)	Novel Protein sim. GBank gi4627040[trpNC_005110.1]pTROP - thyroid hormone receptor-associated protein, 150 kDa subunit	Contains protein domain (PF00023) Ank repeat	kinase	36658542, 21906767, 35695917, 60170615, 264953, 33657109
1937	94847141 (3873, 3874)	Novel Protein sim. GBank gi943157[pilG53777] - anklyrin, erythrocyte - mouse	Contains protein domain (PF00888) Cullin family	collagen	264488, 26146198, 264905, 264359
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gi494443 [gbA022340:1]AC006955 - (AC006955) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	65274577, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21908768, 21906768, 56811157, 27486294, 35956423, 60432113, 264864
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gi500859[gbA003210] - (C14169) 50kDa lectin [Bombayx mori]		struct	264488, 33631822, 264448, 264683, 264288, 265020, 3357023, 264631
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gi194630[emeCJA73132] - (T12259) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) Leucine Rich Repeat	UNCLASSIFIED	56994075, 22278999, 264259, 26331824, 26331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264887, 21906765, 21906766, 21906767, 265020, 56844150, 27486284, 83370044, 19108387, 60432113, 22279002, 264585
1941	84147177 (3881, 3882)	Novel Protein sim. GBank gi14206386 [AF080570] - flg-1 protein [Mus musculus]		UNCLASSIFIED	264488, 18108358, 26331825, 27486261, 264909, 18108370, 18108374, 264462
1942	87641870 (3883, 3884)	Novel Protein sim. GBank gi4927204[gbA033049:1]AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	22278999, 26331822, 26331827, 35696082, 264511, 265008, 264592, 60432229, 265017, 265018, 265019, 264684, 264692, 33657109, 65274791, 264636
1943	94325298 (3885, 3886)	Novel Protein sim. GBank gi31225952[gbO157361]TPD_DICD1 - TPD PROTEIN WD domain, G-beta repeat	Contains protein domain (PF00400) WD domain, G-beta repeat	kinase	

1944	94232858 (3887, 3888)	Novel Protein sim. GBank gji1799570[dbj AA13432] - (D87671) T1P120 [Rattus norvegicus]	UNCLASSIFIED	63274572, 22278984, 22278955, 22278986, 22278988, 22278989, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432229, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906766, 21906767, 21906769, 356595917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 2646339, 83373044, 18108395, 56526486, 87168518, 60432113, 22279000, 264563
1945	87641872 (3889, 3890)	Novel Protein sim. GBank gji492720[gb AAD330049.1]AF13391 - (AF133911) ARL-6 Interacting protein-4 [Mus musculus]	UNCLASSIFIED	264488, 22278986, 264510, 264511, 18108351, 264683, 264446, 264567
1946	87443990 (3891, 3892)	Novel Protein sim. GBank gji249910[sp Q27969]AD50, BOVIN - ADRENAL MEDULLA 50 KD PROTEIN	UNCLASSIFIED	60432289, 20331837, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21906767, 52644150, 264693, 27485264, 264637, 87168518, 264563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gji39148[sp O54888]RPA2, RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)	UNCLASSIFIED	22278988, 264905, 264906, 264908, 264909, 264912, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gji5420387[emb CA16678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264909, 60170831, 264591, 264594, 335010, 265011, 264764, 264369, 264689, 264691, 264638
1949	7640128 (3897, 3898)	Novel Protein sim. GBank gji367676[emb CA93466.1] - (Z69537) predicted using GeneFinder. Similarity to E coli hypothetical protein YCAC (SW-YCAC_ECOLI) [Caenorhabditis elegans]	UNCLASSIFIED	2644369, 264768, 264688, 264689, 264359, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108395, 265018, 264693, 53811190, 18108391, 264369, 264286, 18108334
1950	78408531 (3899, 3900)	Novel Protein sim. GBank gji262675[dbj BA234242] - (AB008782) sulfate transporter [Arabidopsis thaliana]	UNCLASSIFIED	56182475, 22278987, 52644580, 29331824, 29331825, 29331827, 55612038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1951	86398253 (3901, 3902)	Novel Protein sim. GBank gji262675[dbj BA234242] - (AB008782) sulfate transporter [Arabidopsis thaliana]	UNCLASSIFIED	264591, 264593, 264594, 264595, 264555, 264556, 264597, 264598, 264599
1952	87068775 (3903, 3904)	Novel Protein sim. GBank gji429653[gb AAD34077.1]AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	UNCLASSIFIED	

1953	20470371 (3905, 3906)	Novel Protein sim. GBank g111897159p1317121C1Q:OB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00336) - Complement C1q domain	264259, 264558	264486, 263994, 18108394, 35696286, 22278998, 29331822, 6074117, 29331826, 29331827, 264508, 264509, 264505, 264906, 264907, 264908, 264909, 264510, 265006, 265007, 265008, 264910, 265009, 60170831, 6043229, 265011, 265017, 264803, 264604, 265019, 18108351, 264685, 264766, 264769, 35695917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264488, 264567
1954	91226025 (3907, 3908)	Novel Protein sim. GBank g14240271[db][BAA74914.1] - (A8020698) KIAA0891 protein (Homo sapiens)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	UNCLASSIFIED
1955	85300310 (3909, 3910)				56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331828, 29331827, 35696032, 264508, 29331830, 265008, 295009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906768, 21906767, 55811857, 265020, 265021, 52645120, 33657109, 27486284, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank g11655821[db][BAA734071] - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor (Homo sapiens)	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696032, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264593, 264564

1957	94320510 (3915, 3914)	Novel Protein sim. GBank gi4588671[db][BAA76856.1] - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52648842, 56183575, 22278997, 22278988, 22278999, 29331824, 60714117, 29331827, 29448499, 284583, 33837402, 33109554, 8716847, 285018, 284446, 284369, 284288, 284786, 2186586, 21800767, 21906788, 21905769, 365029, 265021, 284682, 65274630, 37485244, 33857346, 27486265, 35698555, 22790009, 26544545, 22278999, 264092, 264098, 264269, 60432049, 20331824, 56183575, 60714117, 284107, 284109, 284909, 264851, 60170831, 60432229, 21905754, 265010, 21906788, 35698517, 265022, 65274630, 26386767, 263976, 35698423, 264693, 264632, 284634, 264635, 18108385, 22790009, 22279002, 264533, 265019
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi4240227[db][BAA74892.1] - (AB020876) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi228193[emb][CAB10860] - (Z99056) hypothetical protein [Schistosoma haematophyllum]		ubiquitin	
1960	80308608 (3919, 3920)	Novel Protein sim. GBank gi2274851[db][BAA21519] - (D64159) 3-7 gene product [Homo sapiens]		stuct	264905, 264906, 264907, 264908, 264909, 265008, 265007, 264910, 284583, 265017, 264604, 265019, 18108351, 284764, 284369, 284766, 264769, 21906788, 18108386, 284639, 18108379, 284635, 284638, 284637, 284638, 284488
1961	16292607 (3921, 3922)				264635
1962	91008385 (3923, 3924)				
1963	90938017 (3925, 3926)	Novel Protein sim. GBank gi3721653[db][BAA33381] - (AB012833) acyl-CoA synthetase 5 [Rattus norvegicus]		UNCLASSIFIED	65274572, 264592, 264593, 265019, 284691, 65274572, 18108386, 35698555, 265018, 60432286, 29331827, 264428, 265008, 60433386, 60433388, 21906754, 265020, 265021, 33857023, 33657109, 27462955, 35698555, 264555, 264488, 264092, 264269, 264509, 264905, 264908, 264907, 264908, 284909, 284510, 264511, 265007, 265009, 284910, 284592, 264593, 284594, 264598, 284768, 284600, 264603, 284604, 284605, 284760, 284762, 264448, 284764, 284286, 284685, 284766, 264768, 284769, 21906788, 264691, 264692, 264693, 18108370, 284628, 284629, 18108374, 284630, 264631, 284634, 284636, 284637, 284638, 18108382, 8337044, 18108385, 284643, 284644, 284645, 284646, 284647, 284648, 284649
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gi526263[emb][CAB45757.1] - (AL080169) hypothetical protein [Homo sapiens]		cadherin	
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi4107017[db][BAA36294] - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) AN1-like Zinc finger	ubiquitin	264488, 264510, 284760, 284768, 284485

1966	941920528 (3931, 3932)	Novel Protein sim. GBank gi4929707(gb)AAD341.4.1(AFI5187) protein [Homo sapiens]	(AFI5187) CGI-119 Uncharacterized protein family	Contains protein domain (PF01027) - glycoprotein	22278999, 264092, 264259, 26331926, 29331828, 29146408, 264595, 265011, 264448, 18108354, 264285, 264884, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264488, 264567 2331824, 265010, 265017, 264728, 21908764, 233981, 59526466
1967	87396123 (3933, 3934)	Novel Protein sim. GBank gi2957720 (AF044576) - phospholipase C PLC170 [Caenorhabditis elegans]		Contains protein domain (PF00338) - esterase	35695285, 264905, 264590, 264908, 264907, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35698423, 35695955, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264585, 264566, 264567
1968	88095641 (3935, 3936)	Novel Protein sim. GBank gi2564953 (AF030001) - unknown [Mus musculus]		Contains protein domain (PF00008) - oncogene	22278995, 22278998, 35696052, 264806, 264908, 18108351, 264482
1969	84328529 (3937, 3938)	Novel Protein sim. GBank gi2911274 (U20329) - spidrov 1 [Nephila clavipes]		UNCLASSIFIED	264908, 18108351, 264482
1970	80596049 (3939, 3940)	Novel Protein sim. GBank gi4050087 (AF109507) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 18108351, 264482
1971	94843814 (3941, 3942)	Novel Protein sim. GBank gi134208(spl)P09593(SANT_ PLAFV - SANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264759, 60432046, 69714117, 29331828, 60432288, 29331827, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433358, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264765, 264766, 264768, 264769, 21906755, 35697023, 264692, 18108370, 264629, 35696423, 65274791, 35695955, 264632, 264635, 264655, 264636, 264637, 264638, 264639, 18108385, 60432113, 22279000, 264583, 264654, 264655, 264566, 264486
1972	87645444 (3943, 3944)	Novel Protein sim. GBank gi4519623(gb)(AA75871.1) - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]		Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain	22278999, 264259, 29331927, 56182181, 60432046, 29331927, 52640045, 264809, 265008, 264511, 265008, 52644298, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33957109, 33957182, 264555, 52644332, 264558, 60432111
1973	86395533 (3945, 3946)			UNCLASSIFIED	29331828, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1974	80396629 (3947, 3948)	Novel Protein sim. GBank gi3308543 (AF036382) - mL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	94316479 (3949, 3950)		UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265006, 264367, 5812038, 265010, 265017, 264369, 5811957, 65274791, 3569555, 56182323, 60432113, 264259, 35690552, 265018, 265020, 265021, 33657109, 56526486
1976	95358914 (3951, 3952)		UNCLASSIFIED	264908, 264596, 265021, 264566
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gl249526sp[007782]NA.SU.RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)	homeobox	
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gl103421[0071]A33471 - transcription factor NTF1 - fruit fly (<i>Drosophila melanogaster</i>) (fragment)	transcription factor	60770831, 264566
1979	87627709 (3957, 3958)	Novel Protein sim. GBank gl2244815[emb]CA810238.1] - (Z97336) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	29331826, 29146498, 264905, 264807, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60770615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gl4759290[ref]NP_004642.1[up]SP1 - Ubiquitin carboxyl-terminal hydrolase, X-linked (AF-131849) Unknown [Homo sapiens]	ubiquitin	264489
1981	87606874 (3961, 3962)	Novel Protein sim. GBank gl4406693[gb]A22080.1 - (AF-131849) Unknown [Homo sapiens]	UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264906, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gl5689323[dbj]BAAB3045.1] - (AB029010) KIAA1193 protein [Homo sapiens]		264909, 265008, 55811386, 264760, 264686, 264691, 27486264
1983	95098688 (3965, 3966)	Novel Protein sim. GBank gl3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00086) - Transcription factor Zinc finger, C2H2 type	22278995, 35696286, 264259, 29331822, 20281099, 29331824, 60432280, 29331827, 264509, 264905, 264906, 264907, 58712502, 264908, 52644045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433556, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695555, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373944, 18108385, 22279000, 22279002

1984	8576089 (3667, 3968)	Novel Protein sim. GBank gl 2856655emb CAA11714.1 - (A1021897) radD14 [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811957, 56904075, 265020, 265021, 22278999, 265022, 264239, 20331922, 39557182, 29146499, 264628, 18108370, 264908, 264639, 55811576, 35695455, 265005, 265007, 264591, 21906754, 39557044, 265010, 265017, 265019, 264298
1985	8553697 (3969, 3970)	Novel Protein sim. GBank gl 5712131gb AAO47379.1 AF12049 - (AF12049) DEM1 protein [Homo sapiens]		glycoprotein	264765, 264298, 263978, 55811576, 264637, 56182223, 18108385, 264584
1986	80200507 (3971, 3972)	Novel Protein sim. GBank gl 4858443gb AAO31319.1 AF14457 - (AF14457) Mz- interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gl 4858443gb AAO31319.1 AF14457 - (AF14457) Mz- interacting protein kinase PKM [Mesocricetus auratus]		UNCLASSIFIED	21905768, 39557019, 264692, 264693, 18108377, 264635, 60170394, 22278002, 264503, 264908, 264007, 264008, 264009, 264810, 264591, 264593, 264758, 264764, 264686, 264768, 265021, 264692, 264628, 264629, 35695455, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1988	84122108 (3975, 3976)	Novel Protein sim. GBank gl 2601701 (AF02379) - spindle pole body protein spc37 homolog OCP2 [Homo sapiens]		tubulin	60432549, 60432289, 55844045, 56182435, 264411, 265007, 39557102, 5364229, 21905765, 21905768, 21906759, 55811957, 3357023, 263997, 39557109, 18108370, 22278000, 22278002
1989	81252225 (3977, 3978)	Novel Protein sim. GBank gl 2601701 (AF02379) - spindle pole body protein spc37 homolog OCP2 [Homo sapiens]			264508, 264757, 264764, 18108381
1990	8569888 (3979, 3980)	Novel Protein sim. GBank gl 5701727 db BJA33074.1 - (A024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			
1991	85351114 (3981, 3982)	Novel Protein sim. GBank gl 420287 db BJA374922.1 - (A020706) NAA089 protein [Homo sapiens]	Contains protein domain (PF01602) - Adipin N terminal region	glycoprotein	18108384, 55102575, 22278994, 35695286, 56904075, 22278997, 22278999, 20331872, 20331924, 20331895, 60432289, 20331878, 264503, 264908, 264007, 264008, 56182435, 264510, 265007, 21906754, 33109954, 87189474, 265017, 265018, 265019, 264762, 18108351, 264763, 264693, 264369, 264288, 264685, 264765, 264687, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 60431526, 23397, 18108370, 35695855, 264555, 264557, 264635, 93373044, 18108384, 87188316, 60432173, 22278000, 22278002, 264554, 264488
1992	85317232 (3983, 3984)	Novel Protein sim. GBank gl 224532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kapota's sarcoma-associated herpesvirus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	shut	25331827, 264908, 264907, 264909, 265007, 264603, 264768, 264686, 264769, 21906768, 264628, 264635, 264636, 18108385, 35628462, 264566, 264567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gl 2655091 (A00761) - CIG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1994	[9420114 (3987, 3988)]	Novel Protein sim. GBank gi 5630077 gb AA045822.1 AC006017.1 similar to ALR; similar to AAC51735 (P1D.g2558287) [Homo sapiens]	Contains protein domain (PF00856) - Imapolymerase SET domain	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 2644905, 2645007, 264908, 265008, 60432220, 31657402, 60433359, 264757, 60433363, 264758, 33109954, 265011, 265017, 265016, 255019, 264684, 264389, 264685, 264686, 264766, 21906765, 21906767, 21906766, 21906769, 265020, 264680, 18108370, 264693, 55274620, 18108370, 264635, 264555, 264556, 264557, 56102323, 63370044, 264548, 22278999, 22278999, 264557, 22278998, 31658564, 22278997, 22278999, 264259, 29347620, 55165181, 29331824, 60432220, 29331823, 29331827, 34686032, 29146499, 264905, 264907, 56712902, 55182435, 265008, 265007, 265008, 265009, 60431735, 60433565, 33657402, 264595, 55412038, 30657084, 55811386, 86558542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264768, 264766, 264686, 264769, 264789, 55181552, 264685, 21905765, 21905766, 21905767, 29148827, 21905768, 21906769, 29148823, 29148764, 265020, 265021, 264680, 18108370, 264693, 27496282, 27468284, 27468285, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 55274791, 36659555, 264683, 264684, 264635, 264555, 264638, 60431950, 264557, 264558, 264559, 53373844, 20789451, 57185119, 264404, 60432113, 264567, 264564
1995	[95414353 (3989, 3990)]	Novel Protein sim. GBank gi 4827040 refNP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit	UNCLASSIFIED	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 2644905, 2645007, 264908, 265008, 60432220, 31657402, 60433359, 264757, 60433363, 264758, 33109954, 265011, 265017, 265016, 255019, 264684, 264389, 264685, 264686, 264766, 21906765, 21906767, 21906766, 21906769, 265020, 264680, 18108370, 264693, 55274620, 18108370, 264635, 264555, 264556, 264557, 56102323, 63370044, 264548, 22278999, 22278999, 264557, 22278998, 31658564, 22278997, 22278999, 264259, 29347620, 55165181, 29331824, 60432220, 29331823, 29331827, 34686032, 29146499, 264905, 264907, 56712902, 55182435, 265008, 265007, 265008, 265009, 60431735, 60433565, 33657402, 264595, 55412038, 30657084, 55811386, 86558542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264768, 264766, 264686, 264769, 264789, 55181552, 264685, 21905765, 21905766, 21905767, 29148827, 21905768, 21906769, 29148823, 29148764, 265020, 265021, 264680, 18108370, 264693, 27496282, 27468284, 27468285, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 55274791, 36659555, 264683, 264684, 264635, 264555, 264638, 60431950, 264557, 264558, 264559, 53373844, 20789451, 57185119, 264404, 60432113, 264567, 264564
1996	[80254186 (3991, 3992)]	Novel Protein sim. GBank gi 791146 emb CA460020.1 - (X86028) extensin-like protein [Vigna unguiculata]	UNCLASSIFIED	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 2644905, 2645007, 264908, 265008, 60432220, 31657402, 60433359, 264757, 60433363, 264758, 33109954, 265011, 265017, 265016, 255019, 264684, 264389, 264685, 264686, 264766, 21906765, 21906767, 21906766, 21906769, 265020, 264680, 18108370, 264693, 55274620, 18108370, 264635, 264555, 264556, 264557, 56102323, 63370044, 264548, 22278999, 22278999, 264557, 22278998, 31658564, 22278997, 22278999, 264259, 29347620, 55165181, 29331824, 60432220, 29331823, 29331827, 34686032, 29146499, 264905, 264907, 56712902, 55182435, 265008, 265007, 265008, 265009, 60431735, 60433565, 33657402, 264595, 55412038, 30657084, 55811386, 86558542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264768, 264766, 264686, 264769, 264789, 55181552, 264685, 21905765, 21905766, 21905767, 29148827, 21905768, 21906769, 29148823, 29148764, 265020, 265021, 264680, 18108370, 264693, 27496282, 27468284, 27468285, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 55274791, 36659555, 264683, 264684, 264635, 264555, 264638, 60431950, 264557, 264558, 264559, 53373844, 20789451, 57185119, 264404, 60432113, 264567, 264564
1997	[87028423 (3993, 3994)]	Novel Protein sim. GBank gi 2642034 (AE034547) - protein phosphatase M130 myosin binding [Ovis aries]	Contains protein domain (PF00023) - phosphatase link repeat	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 2644905, 2645007, 264908, 265008, 60432220, 31657402, 60433359, 264757, 60433363, 264758, 33109954, 265011, 265017, 265016, 255019, 264684, 264389, 264685, 264686, 264766, 21906765, 21906767, 21906766, 21906769, 265020, 264680, 18108370, 264693, 55274620, 18108370, 264635, 264555, 264556, 264557, 56102323, 63370044, 264548, 22278999, 22278999, 264557, 22278998, 31658564, 22278997, 22278999, 264259, 29347620, 55165181, 29331824, 60432220, 29331823, 29331827, 34686032, 29146499, 264905, 264907, 56712902, 55182435, 265008, 265007, 265008, 265009, 60431735, 60433565, 33657402, 264595, 55412038, 30657084, 55811386, 86558542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264768, 264766, 264686, 264769, 264789, 55181552, 264685, 21905765, 21905766, 21905767, 29148827, 21905768, 21906769, 29148823, 29148764, 265020, 265021, 264680, 18108370, 264693, 27496282, 27468284, 27468285, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 55274791, 36659555, 264683, 264684, 264635, 264555, 264638, 60431950, 264557, 264558, 264559, 53373844, 20789451, 57185119, 264404, 60432113, 264567, 264564
1998	[85262704 (3995, 3996)]	Novel Protein sim. GBank gi 4556834 gpi BAA76539.1 - [AB023212] KIA0995 protein [Homo sapiens]	UNCLASSIFIED	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 2644905, 2645007, 264908, 265008, 60432220, 31657402, 60433359, 264757, 60433363, 264758, 33109954, 265011, 265017, 265016, 255019, 264684, 264389, 264685, 264686, 264766, 21906765, 21906767, 21906766, 21906769, 265020, 264680, 18108370, 264693, 55274620, 18108370, 264635, 264555, 264556, 264557, 56102323, 63370044, 264548, 22278999, 22278999, 264557, 22278998, 31658564, 22278997, 22278999, 264259, 29347620, 55165181, 29331824, 60432220, 29331823, 29331827, 34686032, 29146499, 264905, 264907, 56712902, 55182435, 265008, 265007, 265008, 265009, 60431735, 60433565, 33657402, 264595, 55412038, 30657084, 55811386, 86558542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264768, 264766, 264686, 264769, 264789, 55181552, 264685, 21905765, 21905766, 21905767, 29148827, 21905768, 21906769, 29148823, 29148764, 265020, 265021, 264680, 18108370, 264693, 27496282, 27468284, 27468285, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 55274791, 36659555, 264683, 264684, 264635, 264555, 264638, 60431950, 264557, 264558, 264559, 53373844, 20789451, 57185119, 264404, 60432113, 264567, 264564

1989	94324903 (3597, 3598)	Novel Protein sim. GBank gl15225312ip1AAD0846-1(AF072441) calcineurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) TPR Domain	UNCLASSIFIED	29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 5581150, 18108351, 264763, 264682, 264369, 264685, 264686, 56181562, 265020, 264691, 33657023, 264693, 33657109, 27486284, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3599, 4000)	Novel Protein sim. GBank gl17232322ip1Q101551YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I	UNCLASSIFIED	UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644296, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645123, 27486281, 27486282, 27486284, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gl107560ip1B38637 - Ras inhibitor (clone JC265) - human (fragment)	UNCLASSIFIED	UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278998, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gl17294333ip1P38657/TER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P55)	Contains protein domain (PF00085) - isomerase Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gl86383ip1A27040 - neurofilament triplet M protein - chicken (fragment)	UNCLASSIFIED	UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008) [AL049596] hypothetical protein [Homo sapiens]	Novel Protein sim. GBank gll4864249jmb CA843230.1 - [Z47812] similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	Contains protein domain (PF00079) RNA recognition motif (p.k.a. RRM, RBD, or RNP domain)	dna_mn_bnd	52645155, 52646842, 52646385, 56182575, 22278994, 22278995, 5694075, 22278996, 35695286, 22278997, 22278998, 22278999, 60432048, 2642559, 52645080, 29331824, 29331826, 29331827, 35695052, 29331828, 33659970, 29331830, 264908, 264592, 60433556, 33657402, 52646317, 21906754, 33657084, 52644286, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264286, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27468261, 27468262, 33657349, 27468265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264403
2005	87400864 (4009, 4010) [Z47812] similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	Novel Protein sim. GBank gll3879501jmb CAA87795j - [Z47812] similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin	UNCLASSIFIED	56182575, 56181586, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424289, 60714117, 35696052, 264906, 66712502, 264909, 264510, 60433558, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 265019, 264682, 264448, 264288, 264768, 20148627, 21906769, 20148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810794, 55811576, 35695855, 87168518, 60432113, 264403, 264563, 264482
2008	95351177 (4011, 4012) [AL035064] queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Novel Protein sim. GBank gll4106673jmb CAA22613j - [AL035064] queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181586, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424289, 60714117, 35696052, 264906, 66712502, 264909, 264510, 60433558, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 20148627, 21906769, 20148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810794, 55811576, 35695855, 87168518, 60432113, 264403, 264563, 264482
2007	94325556 (4013, 4014) [AB007900] HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	Novel Protein sim. GBank gll266216jmb BAA23712j - [AB007900] HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	56182575, 56181586, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424289, 60714117, 35696052, 264906, 66712502, 264909, 264510, 60433558, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 20148627, 21906769, 20148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810794, 55811576, 35695855, 87168518, 60432113, 264403, 264563, 264482
2008	85084428 (4015, 4016) [Y07960] homeodomain protein [Mus musculus]	Novel Protein sim. GBank gll1550783jmb CAA68257j - [Y07960] homeodomain protein [Mus musculus]	Contains protein domain (PF00046) Homeobox domain	homeobox	56182575, 56181586, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424289, 60714117, 35696052, 264906, 66712502, 264909, 264510, 60433558, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 20148627, 21906769, 20148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810794, 55811576, 35695855, 87168518, 60432113, 264403, 264563, 264482

2009	85748240 (4077, 4078)	Novel Protein sim. GBank gll3682305(dj)BAA34512.1] - (AB018335) KIAA0792 protein [Homo sapiens]	UNCLASSIFIED	22278999, 264259, 264910, 264991, 255017, 264681, 264683, 21906768, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22779002, 264563
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gll526292(emc)CA845753.1] - (AL080164) hypothetical protein [Homo sapiens]	eph Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	26444507, 52645155, 52646355, 52646842, 1103397, 65274572, 22278994, 56994075, 35665286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433355, 21906754, 52646317, 33109954, 52644296, 87168474, 87168559, 265017, 265016, 265019, 264681, 264685, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 264691, 264692, 33657023, 263967, 52645120, 35695763, 18100376, 35696423, 65274791, 35695855, 264631, 264634, 60431650, 264637, 264638, 52644332, 60170394, 18106385, 87168518, 22279002, 264564, 264565, 264566, 264567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gll3477953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]	UNCLASSIFIED	56182576, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264906, 6672502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 264288, 264685, 264766, 264687, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 63373044, 87168518, 60432113, 22279002
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gll1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	UNCLASSIFIED Contains protein domain (PF000409) - Kinesin light chain repeat	264259, 29331822, 29331824, 29331825, 29148498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657100, 55811576, 264632, 264556, 56182323, 264639, 18106385, 18106384, 18106388, 22279000, 22279002, 264567
2013	94943842 (4025, 4026)	Novel Protein sim. GBank gll4507985(re)NP_003427.1(pzNF1) - zinc finger protein 135 (clone pZ-17)	dna_rna_bind Contains protein domain (PF00069) - Zinc finger, C2H2 type	18108398, 264908, 265007, 265010, 265018, 265019, 264688, 21906767, 265020, 264692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gll127720(spl)P20938(MYP0_HETFR - MYELIN P0) - PROTEIN PRECURSOR	UNCLASSIFIED	264485, 29331826, 264907, 264636, 264555, 264639, 264558

2015	86094932 (4029, 4030)	Novel Protein sim. GBank gij181260ipjil[S22697 - extensin-Volvox carterii (fragment)]	UNCLASSIFIED	56182575, 35909286, 264259, 35909052, 264506, 264906, 264907, 264510, 264512, 87188474, 265010, 264681, 264288, 264689, 264624, 35996423, 35655855, 264639, 264653, 264654
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gij28504ipjil[S26413 - 1 complex protein Tcp-10 - mouse]	struct	284102, 264508, 264110, 285009, 33109954, 21906768, 285021, 33657109, 27488282, 283972, 18108374, 263976, 264555, 264584, 284685, 284636
2017	79462933 (4033, 4034)	Novel Protein sim. GBank gij124735ipjilP18175[INVO_PIG - INVOLUCRIN]	UNCLASSIFIED	284683
2018	76637067 (4035, 4036)	Novel Protein sim. GBank gij2133910ipjil[S68216 - phosphatase-1 glycogen-binding (CL) chain - rat]	phosphatase	264107, 264110, 264112, 285017, 263976
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gij2078463 (U43200) - antifreeze glycopetide AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	264259, 284508, 264491, 285018, 264682, 264285, 264688, 22279002
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		56994075, 264593, 33109954, 21906754, 21906768, 33657023, 33657109, 27488201, 87168518
2021	85718818 (4041, 4042)	Novel Protein sim. GBank gij4510230ipjil[AAD2992 - 1A/F07334 - (AF073344) ubiquitin specific protease 3 Homo sapiens]		264757, 264767, 60170015, 18108385
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gij4510230ipjil[AAD2992 - 1A/F07334 - (AF073344) ubiquitin specific protease 3 Homo sapiens]	Contains protein domain (PF00442) ubiquitin Ubiquitin carboxyl-terminal hydrolases family 2	18108394, 22276899, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 60432113, 22279000, 284482, 264565
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gij4510230ipjil[AAD2992 - 1A/F07334 - (AF073344) ubiquitin specific protease 3 Homo sapiens]	Contains protein domain (PF00637) 7-fold repeat in Clathrin and VPS	60433438, 285017, 264686, 264692, 264693, 264636
2024	87396443 (4047, 4048)	Novel Protein sim. GBank gij475158ipjil[AAD29055 - 1A/C007018] unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	22276897, 264509, 264506, 264509, 55812038, 285017, 285021, 265022, 60170815, 264556
2025	87558853 (4049, 4050)	Novel Protein sim. GBank gij475158ipjil[AAD29055 - 1A/C007018] unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	56994075, 60432049, 264508, 65712502, 264112, 60170931, 87168559, 264288, 264684, 264689, 21906768, 33657109, 18108370, 284638, 18108385, 60432113, 22279000, 22279002, 264584, 264586, 264657
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gij155569ipjil[C4A60032] - (Y07752) phosphorin-S [Volvox carterii]	UNCLASSIFIED	263976, 284634, 264486
2027	80248001 (4053, 4054)			

2028	94599884 (4055, 4056)	Novel Protein sim. GBank gil1330345 (U59755) - coded for by C. elegans cDNA yk3461.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk466a.5; coded for by C. elegans cDNA yk46d.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk468.	Contains protein domain (PF00632) -ubiquitin-HECT domain (ubiquitin-transferase)	52644507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264559, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 264757, 55612038, 21906754, 52646317, 52644286, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264389, 264766, 52644228, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645128, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35696655, 264635, 264636, 52644332, 264558, 83373044, 58526486, 22279000, 22279002, 264563
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gil3559940 (AF617388) - facicopental cyclopasta protein 2 [Mus musculus]	Contains protein domain (PF00621) - UNCLASSIFIED	265009, 264595, 8566642, 264555, 264556, 264557, 264558, 264559, 83373044
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gil6530060gil64045825.1/AC004499 - (AC004499) similar to HUB1, similar to BAX2380 (PIDg2789430) [Homo sapiens]	Contains protein domain (PF00098) -transcriptfactor Zinc finger, C2H2 type	18108394, 56994075, 22278997, 22278999, 264255, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 68712502, 264628, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181582, 264686, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2031	80245281 (4061, 4062)			264591, 55811957, 18108385, 264557, 264558, 18108382, 18108384
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gil56589491tbljBAX3029.1; - (AB028000) KUA1077 protein [Homo sapiens]	Contains protein domain (PF00884) -hydrolase Sulfatase	65274572, 35696286, 29331824, 264908, 265009, 264595, 265018, 264288, 264686, 264769, 21906766, 21906767, 29148627, 264628, 35696423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gil24948286pQB4896ICAGT_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACTIII) (STY)	synthase	56181582, 264628, 264632, 264555, 264556
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gil46269494jefjnr_005147.1 pROD1 - UNKNOWN	Contains protein domain (PF00076) -dna_rna_bind RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4069, 4070)				264309, 264686, 265022, 26526465, 264657
2036	87115833 (4071, 4072)				29331827, 29331828, 264692, 264399, 2914867, 50432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gl2734081 (AF000190) - similar to oyster-ster-binding proteins [Caenohabditis elegans]		UNCLASSIFIED	6274572, 22278995, 22278986, 50994075, 35992626, 22278997, 22278998, 22278999, 264299, 29331824, 50432288, 29331826, 26431816, 35990932, 264907, 29331830, 65312502, 38184351, 265008, 265009, 60170302, 384560, 35912035, 33109894, 21906754, 87168569, 8590718, 85016, 265019, 264762, 264389, 264236, 21906765, 21906757, 21905768, 21906766, 5811957, 35995917, 265020, 265021, 265022, 35994150, 33657023, 33657108, 33657162, 35995763, 35995855, 264632, 264634, 264636, 56182323, 83373044, 50432113, 22278990, 22278992, 264393
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gl3890625(emb)(CAB07858) - (Z93785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST ENBL.T01682 comes from this gene; cDNA EST ENBL.M75823 comes from this gene; cDNA EST ENBL.D27559 comes from this ge...	Contains protein domain (PF01412): Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278993, 22278996, 50994075, 264259, 264382, 35990932, 264905, 264906, 32644045, 265007, 265008, 97168559, 265017, 18108351, 264446, 264389, 264766, 264767, 264686, 18108358, 21906765, 21906768, 52644150, 33657023, 264692, 18108362, 33657108, 27485262, 18108370, 18108374, 18108378, 35996423, 65274791, 264635, 264636, 18108383, 83373044, 18108395, 81695716, 22279000, 22279002, 264393, 35995763, 264399
2039	85514626 (4077, 4078)	Novel Protein sim. GBank gl2224535(db)(BAA20813) - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097): Zinc finger, C2HC4 type (RING finger)	UNCLASSIFIED	22278997, 264393, 264399, 264400, 264406, 264906, 264907, 264909, 264909, 264510, 265006, 264910, 264593, 264756, 265011, 265018, 264752, 264386, 264766, 264768, 264769, 11905766, 33657023, 264692, 264693, 33657108, 35996423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168516, 264466
2040	85308417 (4079, 4080)	Novel Protein sim. GBank gl2500825(p)(P700RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)		UNCLASSIFIED	264592, 22278998, 35990932, 264905, 264907, 264908, 264910, 265015, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657108, 264628, 264629, 35996423, 35995855, 264637, 264638, 264639, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gll4406589gll4AD20040j - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264286, 264766, 264686, 52844229, 264769, 21906765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27466261, 27486262, 27486265, 18108374, 35696423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gll5052554gll4AD38007 j(AF4563) - (AF45632) BCDNA GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) E1-E2 ATPase	transprot	264488, 52644507, 52646355, 56994075, 22278997, 22278999, 20281171, 264259, 29331822, 29331824, 6671417, 29331876, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264885, 264686, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 5581576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373944, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	struct		264903, 29331827, 264905, 6672502, 264592, 264689, 21906765, 21906769, 265020, 264692, 264482, 264566, 264692
2045	79635532 (4089, 4090)	Novel Protein sim. GBank gll4406589gll4AD20062j - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264693, 22279002
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gll4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278998, 29147620, 29331824, 29148498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gll459656j(BAA76850.1) - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264909
2048	84568378 (4095, 4096)	Novel Protein sim. GBank gll459656j(BAA76850.1) - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264765, 21906767, 21906768, 264629, 264634, 264637, 22279002, 264564, 264565, 264566, 264567

2050	79633835 (4099, 4100)				UNCLASSIFIED	284693
2051	87780168 (4101, 4102)				UNCLASSIFIED	284488, 284259, 284509, 284906, 284907, 284769, 18108374, 35696423, 284563, 284566, 284486
2052	88096393 (4103, 4104)	Novel Protein sim. GBank g14529889gipAA021812.1; - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) SET domain		kinase	284486, 283994, 35696952, 284008, 284005, 284509, 284906, 284907, 284908, 284909, 284113, 284511, 285009, 284910, 60170831, 284592, 284758, 285010, 285011, 2846095, 284760, 284682, 284784, 284388, 284765, 284686, 284785, 284789, 52644293, 284689, 35695917, 33657023, 33657109, 284628, 18108374, 35696423, 55811576, 35695855, 284630, 284631, 284632, 284639, 18108385, 284636, 284556, 284638, 284639, 18108385, 56526488, 60432113, 284563, 284564, 284566, 284486, 284467, 284489, 283994, 35696052, 284508, 284905, 284909, 284906, 284907, 284908, 284909, 284113, 284511, 285009, 284910, 60170831, 284592, 284758, 285010, 285011, 284605, 284760, 284682, 284764, 284389, 284785, 284688, 284765, 284769, 52644229, 284689, 35695917, 33657023, 33657109, 284628, 18108374, 35696423, 55811576, 35695855, 284630, 284631, 284632, 284634, 284634, 284636, 284656, 284636, 284639, 18108385, 56526488, 60432113, 284563, 284564, 284566, 284486, 284467, 284489, 283994
2053	87763078 (4105, 4106)	Novel Protein sim. GBank g12965449emb1(CAA75113) [Y14840] midline 1 protein [Mus musculus]			UNCLASSIFIED	22278996, 22276997, 284259, 28331822
2054	95358937 (4107, 4108)	Novel Protein sim. GBank g13876326jmb1(CAB02090) (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			284102, 284508, 35695917, 283972, 284482, 60424175, 284094, 284259, 28331825, 60424269, 284906, 60432226, 60433356, 87168559, 285019, 284760, 284288, 284686, 21909769, 33657023, 284683, 55810784, 55811576, 284653, 56182323, 60432113, 284488, 28331825, 60432269, 28331828, 60433356, 285019, 284683, 284684, 285021, 33657109, 18108374, 284637, 18108385, 87168516, 60432113, 22279000, 284564
2055	88259449 (4109, 4110)	Novel Protein sim. GBank g15353746gipAA042226.1(AF15913) SIR2-like protein [Oryza sativa subsp. indica]			UNCLASSIFIED	

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gl14826960[re]NP_005042.1 poARS - glutamine-IRNA synthetase	Contains protein domain (PF00749) - IRNA synthetases class I (E and Q)	synthase
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2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 246947 sp Q09298 Y009 CAEL - HYPOTHETICAL 141.2 KD PROTEIN EED8.9 IN CHROMOSOME II	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22778997, 22778998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29331829, 264906, 68712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265008, 264910, 264591, 33657402, 21906754, 65658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906755, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264656, 264657, 264658, 18108382, 264659, 83273044, 18108384, 56526486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - struct Ank repeat	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264585, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 db BAA76803.1 - (AB023176) KIA0065 protein [Homo sapiens]	Contains protein domain (PF00617) - oncogene RasGEF domain	22778994, 22778995, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811976, 18108384, 22779002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754519 db BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]	hydrolase	264488, 52646365, 56904073, 35696786, 22778997, 22778998, 264259, 29331826, 60432289, 29331827, 29331828, 35696042, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264781, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108388, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22779000, 22779002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENSIN - TENSIN	kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811986, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264657, 83273044, 18108388, 22779000, 22779002, 56182575, 264259, 264906, 264764, 264288, 56182323, 264567
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium falciparum]	UNCLASSIFIED Zinc finger, C2H2 type	

2067	95303802 (4133, 4134)				3566286, 2227897, 2227898, 60432049, 264259, 60432209, 60432438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35655855, 264558, 264404, 264553, 264486
2068	84344754 (4135, 4136)				264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank glij312682 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) Ank repeat	UNCLASSIFIED	60424178, 56192575, 22278995, 22278996, 56984075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656970, 264509, 264905, 56182435, 265009, 60433365, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 5618223, 83373944, 87168518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank glij5712131 (gb AA047379, JAF12049) - (AF12049) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35655817, 264605, 264628, 264808, 264638
2071	86948116 (4141, 4142)	Novel Protein sim. GBank glij3551531 (gb BAA33016) - (AB017437) avens (Gallus gallus)	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718428 (4143, 4144)		Contains protein domain (PF00184) - Neurolymphoid terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265018, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35696817, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27825664 (4145, 4146)	Novel Protein sim. GBank glij150426 (gb BAA13212) - (D66976) similar to C. elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank glij4240317 (gb BAA14837.1) - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264903, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264587

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gl1536930(gb)AD40382.1j - (AF093880) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35686286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35690052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21906769, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486282, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264486, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385, 264592
2077	11388977 (4153, 4154)	Novel Protein sim. GBank gl4202050(dj)BAA74579i - (D87908) nuclear protein np85 [Mus musculus]	UNCLASSIFIED		29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2079	88065916 (4157, 4158)	Novel Protein sim. GBank gl4240255(dj)BAA74906.1j - (AB020690) KIA0883 protein [Homo sapiens]	UNCLASSIFIED		264768, 22278997, 265027, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gl2406021(emb)CAB18219.1j - (Z99162) putative vacuolar protein [Schistosoma mansoni]	UNCLASSIFIED		56182575, 264492, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gl1552473(gb)AD44360.1j(AF166350) ST7 protein [Homo sapiens]		- eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85658542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22279000, 22279002
2082	87626529 (4163, 4164)	Novel Protein sim. GBank gl3880555(emb)CAAG4234j - (Z70271) predicted using GeneFinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gl2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Cryptosporidium parvum]		transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21906754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 63247491, 264631, 264555, 264563
2084	95199298 (4167, 4168)	Novel Protein sim. GBank gl728836(gp)P39193(ALLU6_HUMAN - III) ALU SUBFAMILY SP WARNING ENTRY IIII	UNCLASSIFIED		265018, 264763, 264693, 264691

2085	94969476 (4159, 4170)	Novel Protein sim. GBank gl165569[emb]CAA69032] - (Y07752) phenophorin-S [Voxox carlin]	UNCLASSIFIED	56182575, 60432289, 264008, 56182435, 8718474, 264763, 264360, 264686, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gl3875032[emb]CAA89036] - (Z49129) similarity to Trichostrogylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL D33349 comes from this gene; cDNA EST EMBL D37644 comes from this gene; cDNA EST EMBL D36149 come...	UNCLASSIFIED	35836286, 264259, 35869052, 264006, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35895917, 263978, 35896423, 35895955, 264632, 264634, 264637, 264638, 264639, 56182323, 18108365, 264482, 264486
2087	21436337 (4173, 4174)		UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gl3880930[emb]CAA16334.1] - (AL021481) similar to Phosphoglucanase and phosphotransferase phosphoserine cDNA EST EMBL D36168 comes from this gene; cDNA EST EMBL D70697 comes from this gene; cDNA EST v437398.5 comes from this gene; cDNA EST EMBL D0800...	UNCLASSIFIED	264488, 22778994, 35862586, 22278996, 29331827, 35869052, 33857402, 21906754, 33108954, 8718474, 265017, 265018, 265019, 264448, 264683, 264360, 264685, 264687, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33857023, 33857109, 33857182, 27486261, 27486262, 33857349, 27486265, 35869423, 35869585, 83373044, 87188518, 22279000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gl475818[et]NP_004823.1pDAP3 - Death associated protein 3	cdutrin	18108392, 264488, 5264507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35869288, 22278996, 5694075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264258, 26331822, 20281099, 26331824, 29331825, 29331826, 29331827, 29331828, 35869052, 33856970, 29146488, 29146499, 284102, 284106, 264107, 264108, 264508, 264905, 264508, 264906, 264907, 264908, 5672502, 264928, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 6017031, 264532, 264593, 60433356, 33857402, 60433438, 264595, 55812038, 264756, 21906754, 33857094, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264780, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181582, 264769, 18108359, 264685, 21906765, 21906766, 21906767, 21906768, 29148827, 35869597, 55811957, 29148829, 29148874, 35869597, 265020, 265021, 265022, 60170615, 264690

2090	86222470 (4179, 4180)			22278955, 22278958, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265022, 60170615, 33657023, 35696423, 35695955, 264652, 18108387, 22279000, 263984, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264289, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567	UNCLASSIFIED			22278997, 22278998, 66712502, 87168559, 264683, 265021, 264486
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gl 4380997 gb AAD24571.1 AF121081 cAMP inducible 2 protein [Mus musculus]						264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2092	86223605 (4183, 4184)	Novel Protein sim. GBank gl 2352427 AF004161 - peroxisomal Ca-dependent solute carrier [Oryzotilus curvicaulus]						264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gl 1363238 gpi A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse						264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gl 4929355 gbl AAD34036.1 AF151779 - CQI-40 protein [Homo sapiens]						264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gl 1363238 gpi A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse						264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gl 3834423 AF070689 - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]						264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi 5174502 ref NP_006051.1 p1.YF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264298, 265021, 60170615, 264682, 33657109, 18108370, 264336, 264483, 56984075, 264259, 264288, 265020, 264563
2098	87700340 (4195, 4196)	Novel Protein sim. GBank gi 4758202 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase,	phosphatase	
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gi 2695659 (AF028954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPR [Bos taurus]	Contains protein domain (PF00025) - ADP-ribosylation factor family	phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gi 3881189 emb CA616514 - (Z99281) similar to ADP-ribosylation factor, cDNA EST EMBL:CO8179 comes from this gene; cDNA EST EMBL:CO8337 comes from this gene; cDNA EST EMBL:CO8829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4....	ADP-ribosylation factor family	nuc_d_nucpt	56182575, 26278695, 22278996, 22278997, 22278998, 60432049, 2643129, 26331822, 29331824, 29331825, 29331827, 29331828, 29146488, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21906754, 65585842, 87168474, 265017, 265018, 265019, 264681, 18108351, 264782, 264448, 264369, 264288, 18108355, 264686, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373944, 87168518, 60432113, 22279000, 22279002, 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gi 4589468 db BAA76761.1 - (AB012808) mBOCT [Mus musculus]	UNCLASSIFIED	UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264788, 21906769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi 3874149 emb CA97423.1 - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	UNCLASSIFIED	
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi 42407159 db BAA74858.1 - (AB020642) KIA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56894075, 22278999, 264259, 29331824, 29331825, 35696052, 20331828, 66712502, 265009, 60170831, 264595, 33109954, 65585842, 87168559, 265017, 265019, 264448, 21906765, 21906768, 265022, 33657023, 27486262, 33657349, 35695763, 60431526, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264564
2104	85776161 (4207, 4208)		UNCLASSIFIED	UNCLASSIFIED	264582, 264604, 22279000

2105	94484030 (4209, 4210)	Novel Protein sim. GBank gll1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3, coded for by C. elegans cDNA yk21g6.3, coded for by C. elegans cDNA CEMSE18F, coded for by C. elegans cDNA yk126b1.3, coded for by C. elegans cDNA y65h8.3, coded for by C. elegans cDNA y65h8...	UNCLASSIFIED	264488, 56182575, 2227894, 56994075, 2227896, 2227897, 2227898, 2227899, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432226, 33957402, 60433356, 264595, 60433438, 264758, 33957084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264763, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170815, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264564, 264566, 264567, 265006, 265019, 264908, 264639
2106	83365475 (4211, 4212)	Novel Protein sim. GBank gll3651524[emb]CAA93883] - (Z70038) ZK1067.4 [Caenorhabditis elegans]	UNCLASSIFIED	264903, 264906, 264907, 264908, 264909, 264758, 265011, 264900, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695955, 264632, 264634, 264635, 264638, 264639, 83373944, 264486
2107	76822662 (4213, 4214)	Novel Protein sim. GBank gll3176689 (AC003871) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gll235927 from S. cerevisiae [Arabidopsis thaliana]	UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558, 264564
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gll3176689 (AC003871) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gll235927 from S. cerevisiae [Arabidopsis thaliana]	UNCLASSIFIED	264903, 264906, 264907, 264908, 264909, 264758, 265011, 264900, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695955, 264632, 264634, 264635, 264638, 264639, 83373944, 264486
2109	80478719 (4217, 4218)	Novel Protein sim. GBank gll481043[pir]S37671 - baiz protein - human	UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558, 264564
2110	87728076 (4219, 4220)	Novel Protein sim. GBank gll2113639[pir]I56542 - calmodulin-binding protein - rat	UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2111	87818419 (4221, 4222)	Novel Protein sim. GBank gll4436629[pir]A20459] - (AF100960) protocadherin [Rattus norvegicus]	UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87835783 (4223, 4224)	Novel Protein sim. GBank gll4436629[pir]A20459] - (AF100960) protocadherin [Rattus norvegicus]	UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2113	76941386 (4225, 4226)	Novel Protein sim. GBank gll3327184[db]BAA31660] - (AB014565) KIAA0685 protein [Homo sapiens]	UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2114	87886342 (4227, 4228)	Novel Protein sim. GBank gll3327184[db]BAA31660] - (AB014565) KIAA0685 protein [Homo sapiens]	UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gll4757890[ref]NP_004328.1 pIC8OR - chromosome 8 open reading frame 1	UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486

2116	85255387 (4231, 4232)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35696268, 22278909, 56182181, 29331824, 29331823, 29331827, 35698052, 264907, 56182435, 255008, 264591, 55812038, 55811365, 87168559, 264288, 264369, 21905769, 29148229, 33657023, 35695763, 55811578, 35696423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gll2330021 (AF019250) - kinesin-related protein; KRP, Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109354, 265017, 265018, 264288, 264689, 265020, 264692, 55525486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gll079307iprj[B56573] - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264905, 264907, 264908, 264510, 264511, 255009, 264910, 255010, 264402, 264288, 264768, 264693, 263987, 263972, 264638, 264559
2119	86998317 (4237, 4238)	Novel Protein sim. GBank gll4321407iprj[AD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87786395 (4239, 4240)	Novel Protein sim. GBank gll485527iprj[NP_005480.1]pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - eph Src homology domain 2		264091, 264259, 26331826, 29331828, 265017, 264604, 264268, 264693, 265020, 264591, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gll757728iprj[NP_004886.1]pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	264601, 264768, 263978
2122	81230831 (4243, 4244)	Novel Protein sim. GBank gll4829551iprj[AA034036.1]AF15179 - (AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278907, 29331822, 29331824, 29331825, 29331828, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83370044, 18108383, 18108384, 55526466, 264565, 264583, 18108388, 264757, 265011, 18108351, 18108385, 264534, 18108385
2123	86787998 (4245, 4246)	Novel Protein sim. GBank gll2245451iprj[BAA30764] - (AB022303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - struct		264259, 264509, 264907, 264511, 85658542, 264763, 21908765, 35658917, 264636, 264486
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gll5689455iprj[BAA3011.1] - (AB022892) KIAA1059 protein [Homo sapiens]	FYVE zinc finger Contains protein domain (PF00801) - transport		33331822, 264606, 264907, 264591, 264639, 264653
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gll238831iprj[P39189]ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III	UNCLASSIFIED		264259, 264509, 264907, 264511, 85658542, 264763, 21908765, 35658917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gll453924iprj[CA838853.1] - (AL048495) conserved hypothetical protein [Schistosoma mansoni]	UNCLASSIFIED		264488, 264489, 29331827, 35698052, 265009, 264609, 264908, 264909, 264410, 265009, 264691, 264692, 264693, 3365702, 264694, 264695, 264696, 264758, 264697, 264698, 265018, 264699, 264905, 264760, 264681, 264763, 264683, 264764, 264684, 264688, 264685, 264689, 60170515, 33657023, 33657109, 55810764, 264635, 264638, 264637, 264638, 264639, 83370044, 264654, 264556

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gli468435(gli)/AAD31315.1(AF-143236) apoptosis related protein APR-2 [Homo sapiens]		35696286, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264653, 264564, 264567, 56182575, 35696286, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264369, 264687, 264768, 55811957, 264692, 18108388, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)			UNCLASSIFIED
2129	85102089 (4257, 4258)			UNCLASSIFIED
2130	85417144 (4259, 4260)	Novel Protein sim. GBank. gli2649235 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]		55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22796000
2131	85723065 (4261, 4262)	Novel Protein sim. GBank. gli1086886 (U41276) - Similar to potassium channel protein, [Caenorhabditis elegans]		UNCLASSIFIED
2132	95361096 (4263, 4264)	Novel Protein sim. GBank. gli569373(jd)[BAA22973.1] - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies) E1-E2 ATPase	35696052, 264909, 264768, 35695917 264489, 22778995, 264539, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21906769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4285, 4266)	Novel Protein sim. GBank gl 4220489 (AC060686) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	60424179, 52646365, 5264682, 56994075, 3596286, 22278997, 22278998, 60432049, 56182161, 60714117, 60424269, 28331826, 29331828, 35960652, 284605, 284606, 264907, 60712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 5812038, 33109954, 21907754, 55811386, 265010, 284603, 265017, 265018, 265019, 55811150, 18100351, 264682, 264369, 264288, 52844239, 56181562, 21907765, 21907766, 21907767, 21907768, 21907769, 55811957, 35959917, 265020, 265021, 60170815, 33657023, 33657109, 60431528, 18108374, 35959423, 63274791, 35695855, 284634, 60431850, 18100380, 56182323, 83373044, 18108385, 18109387, 60432113, 22279002, 264583, 264586
2134	95412657 (4267, 4268)	Novel Protein sim. GBank gl 3875351 [emj CA809415] - (Z56047) DY3.6 [Caenorhabditis elegans]		56181686, 35960286, 21907754, 55811386, 265011, 265017, 18108351, 264765, 264768, 264688, 21907768, 35695917, 265020, 33657023, 264628, 35695855, 284632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	86078813 (4269, 4270)	Novel Protein sim. GBank gl 5689559 [emj CA43063.1] - (AB029034) KIAA1111 protein [Homo sapiens]	UNCLASSIFIED	22278999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52846317, 655011, 87168559, 284601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 284631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264594
2136	84348478 (4271, 4272)	Novel Protein sim. GBank gl 2682167 [emj CA23715] - (AB077903) KIAA0443 [Homo sapiens]	UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gl 48411 [emj CA84362.1] - (AL050590) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264589, 264909, 33109954, 264763, 21907768, 60770394, 18108385, 284563, 265259, 29331828, 35696052, 264909
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gl 514779 [emj CA40696.1] - (U87804) 30 kDa protein [Candida crescentus]	ATPase-associated	265006, 265017, 265018, 18108351, 264288, 21907768, 33657023, 33657109, 264628, 18108374, 35695855, 284634, 284555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gl 385082 [emj CA47135] - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]		264905, 264910, 264591, 55812038, 55811386, 35695854, 284760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18109364, 55811576, 83373044, 18108385, 46526486, 284482

2140	87645655 (4278, 4280)	Novel Protein sim. GBank gll441723(gipAA20418) - (AC007019) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264589, 265006, 264768, 265018, 264446, 264280, 2190766, 35811857, 295021, 3365702, 244695631, 35694423, 264636, 264558, 264557, 264359, 264366
2141	79623986 (4281, 4282)		UNCLASSIFIED	265020, 264689
2142	80041222 (4283, 4284)		UNCLASSIFIED	263978
2143	84140051 (4285, 4286)	Novel Protein sim. GBank gll2135766(gip)S53362 - muchin SAC (clone JER47) - human (fragment)	UNCLASSIFIED	22276897, 29331827, 264907, 265020, 60432411
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gll2078483 (LU3200) - antifreeze glycoprotein AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	55274572, 264259, 29331824, 29331827, 264906, 264606, 264391, 265011, 27166559, 264600, 265019, 264286, 264768, 21906765, 21906767, 35811576, 35694423, 55274791, 22279002
2145	20564305 (4289, 4290)		UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gll1255871 (U63341) - short region of weak similarity to bovine membrane receptor p63 (PIR-S28503) [Caenorhabditis elegans]	UNCLASSIFIED	264909, 60433356, 264686
2147	80432811 (4293, 4294)	Novel Protein sim. GBank gll3030358(embl)CAA18718.1 - (AL022603) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gll28837(isp)P39194/ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III	UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gll119883(isp)P20693/FC2E_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	glycoprotein	29331824, 29331826, 35568052, 264758, 87168474, 265018, 52644150, 35657109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank gll542038(embl)CAB46678.1 - (AJ243459) proteophosphoglycan [Lactinaria major]	UNCLASSIFIED	22276898, 29331822, 29331824, 29331826, 264764, 264769, 21906765, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gll5589407(pdb)j4A32837.1 - (AB028958) KIAA1035 protein (Homo sapiens)		264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264506, 264511, 60433356, 264758, 264598, 33108954, 90174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264286, 264689, 21906765, 21906766, 21906768, 265020, 80170815, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 80170394, 18108385, 87168516, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108386, 18108374, 18108396
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gll3452473 (AF04205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	

2153	86313371 (4305, 4306)	Novel Protein sim. GBank gl4758704[re]NP_004216.1p[MASSL - MFH-amplified sequences with leucine-rich tandem repeats.1	Contains protein domain (PF00560) Leucine Rich Repeat	gycoprotein	264488, 263394, 2646842, 22278996, 22278998, 22278999, 264259, 29331822, 35695052, 264508, 264509, 264509, 264509, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264369, 264766, 264687, 264769, 52644229, 2190766, 2190768, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264564, 264486
2154	87400034 (4307, 4308)	Novel Protein sim. GBank gl1225150p[1209265U - chorion protein B11 [Bombyx mori]	UNCLASSIFIED		56994075, 264094, 265009, 265019, 264288, 21905767, 35695917
2155	87424072 (4309, 4310)		UNCLASSIFIED		18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 58182323
2158	84295205 (4311, 4312)	Novel Protein sim. GBank gl3970866 (AC004974) - spa-1- like; similar to AF028504 (P10255183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gl1076211p[1550755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]	UNCLASSIFIED		264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gl4650844[db][BAA77027.1] - (AB026190) Ketch motif containing protein [Homo sapiens]	UNCLASSIFIED		264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gl2879625[db][BAA24828] - (AB007897) KIAA0437 [Homo sapiens]	Contains protein domain (PF00651) BTB/POZ domain	dna_rna_lund	29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)				264634
2161	87739131 (4321, 4322)	Novel Protein sim. GBank gl1504006[db][BAA13202] - (D86866) similarto human ZFY protein [Homo sapiens]	UNCLASSIFIED		265008
2162	84316528 (4323, 4324)		UNCLASSIFIED		65274572, 264508, 264509, 264509, 264907, 264908, 2644045, 264509, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264763, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 2633978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95411758 (4325, 4326)	Novel Protein sim. GBank gl3876537[emc][CA98270] - (Z73974) cDNA EST yk29115.3 comes from this gene; cDNA EST yk29115.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED		56182575, 22278996, 264093, 264683, 33657023, 65274620, 60432113
2164	80566456 (4327, 4328)		Contains protein domain (PF01006) Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gi1086794 (U41107). No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	5694075, 22278698, 22278697, 22278699, 264259, 20331822, 20331824, 25331823, 20331826, 20331827, 23531828, 2644906, 20331830, 56182435, 55812038, 21906734, 53857080, 2646891, 265019, 264766, 264448, 264369, 21906765, 21906768, 20148627, 265020, 265021, 264689, 264687, 33537023, 65274630, 55595855, 264558, 26470394, 83377040, 60432113, 22278698, 26574117, 52641556, 22278694, 22278698, 6574117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264683, 27486262, 55595763, 21906765, 55526486, 67168516, 264557
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gi2706522(emb)[CA75818] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin	29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264683, 27486262, 55595763, 21906765, 55526486, 67168516, 264557
2167	87716664 (4333, 4334)	Novel Protein sim. GBank gi2224713(emb)[AA20840] - (AB002384) KIA0386 [homo sapiens]	UNCLASSIFIED	56182575, 55596286, 20331824, 20331826, 20146498, 46182435, 265008, 265009, 264592, 264593, 33557402, 33100954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 20148627, 21906769, 52644150, 33557109, 33559443, 18108381, 18108384, 18108385, 60432113, 264567
2168	86998334 (4335, 4336)	Novel Protein sim. GBank gi4321407(emb)[A015748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	-transport region.	66741117, 29331827, 264007, 284511, 264591, 265018, 264764, 264683, 264766, 264768, 264566, 264639, 264555, 264559
2169	87866937 (4337, 4338)	Novel Protein sim. GBank gi5106521(emb)[A039741] - (AF105385) K-CI co-transporter KCC4 [Homo sapiens]	UNCLASSIFIED	65274572, 46182575, 22278697, 22278698, 264259, 20331825, 264500, 264006, 56182435, 60433438, 55812038, 264598, 55811386, 265019, 264762, 264765, 264448, 264764, 264684, 264288, 264766, 264685, 56181662, 264686, 55811957, 265030, 264535, 264691, 33537109, 60431238, 18108374, 33559623, 55811766, 65274791, 264634, 264639, 264558, 87168516, 60432113, 264566
2171	80194050 (4341, 4342)		UNCLASSIFIED	264569, 265020, 264558
2172	85452480 (4343, 4344)		UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gi4309681(emb)[A015478] - (AC006930) R33423.1 [Homo sapiens]	UNCLASSIFIED	264689
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gi2493778(emb)[Q94561] - Q935 CAEL - PUTATIVE CUTICLE COLLAGEN C9G5.5	UNCLASSIFIED	264906, 33595855, 264555, 264557

2175	84325550 (4349, 4350)	Novel Protein sim. GBank g11263287 (U47855) - fibron-3 [Araneus diadematus]	UNCLASSIFIED	264488, 3566286, 20281099, 29331826, 60432289, 35696032, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21906768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank g11288371sp1391941ALU7_HUMAN - IIII ALU SUBFAMILY SD WARNING ENTRY IIII	Contains protein domain (PF00803) - Pentapeptide repeats (8 copies)	252644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696032, 25331828, 33656970, 29331830, 264910, 33857402, 264758, 52644296, 87168559, 265018, 264689, 21908785, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33657249, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486, 18108382, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2177	84128942 (4353, 4354)	Novel Protein sim. GBank g115454072ref1NP_006416.1pSLU7 - step II splicing factor SLU7	kinase	
2178	87601557 (4355, 4356)	Novel Protein sim. GBank g1173407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - eph	264488, 22278996, 22278999, 29331824, 29331625, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)		UNCLASSIFIED	60424269, 264760, 264628, 264632

2180	95351397 (4359, 4360)	Novel Protein sim. G.Bank g 3122317sp p06048 KMH8_DICD1 - MYOSIN HEAVY CHAIN KINASE B (WHCK B)	Contains protein domain (PF00400) WD domain, G-beta repeat	kinase	52644507, 22278994, 35696266, 22278997, 22278998, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264506, 264508, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657108, 27486265, 33657349, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486, 29331827, 264369, 18108376, 264584
2181	85764930 (4361, 4362)	Novel Protein sim. G.Bank g 3024689sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264784, 264285, 21906767, 21908768, 21906769, 33657109, 18108378, 60170394, 22279000, 22279002, 264760
2182	87637731 (4363, 4364)	Novel Protein sim. G.Bank g 5420387emb CA946678.1 - (A243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	
2183	85460649 (4365, 4366)	Novel Protein sim. G.Bank g 3873406 gb AACT7482.1 - (U17129) unknown [Rhodococcus erythropolis]		Inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264638, 264557, 29331824, 264807, 6672502, 264757, 265019, 264288, 264692, 56526486
2184	87760690 (4367, 4368)	Novel Protein sim. G.Bank g 3114713 (AF061346) - Edp1 protein [Mus musculus]			
2185	87828463 (4369, 4370)	Novel Protein sim. G.Bank g 510686 gb AAQ9906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHO5 (Homo sapiens)		ATPase-associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264765, 55811957, 33657023, 55811576, 56182333, 264563
2186	87739227 (4371, 4372)	Novel Protein sim. G.Bank g 2864625emb CA116972.1 (AL021811) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264881, 264765, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264566, 264486, 18108398, 56994075, 264259, 29331824, 29331825, 6674117, 29331827, 264906, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2187	87388173 (4373, 4374)			histone	
2188	87771708 (4375, 4376)	Novel Protein sim. G.Bank g 5107816 gb AAQ0129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850; Score=13.3, E=-5e-10, N=1 [Arabidopsis thaliana]			
2189	85693573 (4377, 4378)	Novel Protein sim. G.Bank g 34232357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263967

2180	87639197 (4378, 4380)	Novel Protein sim. GBank gl132579sp128319FUNI_RAT - RIBONUCLEASE INHIBITOR		nucleasinhb	22278996, 22278999, 29331822, 29331824, 29331826, 2650008, 264910, 60170831, 55812038, 52644366, 265010, 265018, 264685, 264688, 56181562, 21906769, 35695917, 265022, 60170394, 22279000, 29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559, 264558
2181	95198928 (4381, 4382)	Novel Protein sim. GBank gl5327002[emb]CA46272.1) - (Y18503) XAP-5-like protein [Homo sapiens]			
2182	11126316 (4383, 4384)	Novel Protein sim. GBank gl458629sp1P3440J0M10 CAEL - MIG-10 PROTEIN			
2183	94140073 (4385, 4386)	Novel Protein sim. GBank gl5420389[emb]CA46600.1) - (A12343460) proteophosphoglycan [Leishmania major]			
2184	21418714 (4387, 4388)	Novel Protein sim. GBank gl2773341 (AF040854) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113, 264552
2185	88083023 (4389, 4390)	Novel Protein sim. GBank gl2832763[emb]CAA15685.1) - (AL009191) prediction[method:; prediction=method:; match=desc; match=desc; /mol=desc] [Drosophila melanogaster]		UNCLASSIFIED	22278998, 22278999, 35696032, 265006, 21906754, 265017, 35695917, 265021, 265022, 35695655
2186	85091631 (4391, 4392)	Novel Protein sim. GBank gl5262487[emb]CA45699.1) - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 6674117, 60432289, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264586, 264687, 52644229, 21906765, 21906766, 21906767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2187	95073813 (4393, 4394)	Novel Protein sim. GBank gl4925867[emb]CA403404.1)AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21906766, 21906767, 2914667, 55811957, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 83373044, 21906754, 265018, 265019, 22279002, 264482, 264448, 264555, 264288, 264369
2188	58080914 (4395, 4396)	Novel Protein sim. GBank gl35458787 (AC005622) - P30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank g 2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33957023, 264692, 263967, 20281071, 56526486
2200	87405385 (4399, 4400)	Novel Protein sim. GBank g 3043634 (db EAA25481) - (AB011122) KIAA0555 protein [Homo sapiens]	struct		29331824, 264765, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank g 3913470 (g Q5714DHBX, ANAPL - PUTATIVE STEROID DEHYDROGENASE SMZ)	Contains protein domain (PF00106) short chain dehydrogenase	dehydrogenase	29331824, 55696052, 264505, 264807, 33957023, 55811965, 265017, 265018, 265019, 264288, 1906765, 35695917, 265020, 265022, 3857023, 33657109, 27486251, 18108370, 35696423, 35694585, 264555, 264556, 33373944, 87188518, 60432113
2202	91677385 (4403, 4404)	Novel Protein sim. GBank g 5265265 (ambi CAB45767.1) - (AL080188) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264489, 264259, 29331824, 60432289, 55696052, 264505, 264906, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264389, 264288, 264766, 21906765, 21906766, 264690, 264691, 264692, 33957109, 264634, 264636, 264555, 264639, 264558, 264559, 83373944, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank g 1172845 (g P4629RB25_RABIT - RAS-RELATED PROTEIN RAB-25)	Contains protein domain (PF00071) Ras family	glycoprotein	5246365, 5694075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87188559, 265018, 265019, 264605, 264288, 1906765, 35695917, 33957023, 264692, 33957109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88088871 (4407, 4408)	Novel Protein sim. GBank g 12036 (g P2534 (GBT3, RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT, GUSTOUCIN ALPHA-3, CHAIN))	Contains protein domain (PF00503) - C-protein alpha subunit	UNCLASSIFIED	
2205	94147569 (4409, 4410)	Novel Protein sim. GBank g 4589480 (g EAA76768.1) - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- dna_rna_bind	18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 80432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108368, 55811576, 66274701, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264566, 264569
2206	20620008 (4411, 4412)	Novel Protein sim. GBank g 4557575 (e ncp_000372, lipMID1 - midline 1 protein)	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	29331822, 56182181, 29331827, 35696052, 52944045, 965008, 265019, 56181962, 55811957, 265021, 33957023, 35695763, 35695855, 60170394, 60432113, 264566, 264906, 265019, 18108351, 21906769, 264112, 265009, 264691, 18108365, 18108374, 264634, 20281166
2208	86100330 (4415, 4416)	Novel Protein sim. GBank g 3986746 (AF-105228) - tullein			
2209	87800420 (4417, 4418)	Novel Protein sim. GBank g 3986746 (AF-105228) - tullein [Bos taurus]	struct		

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi728837 sp P9194 ALU7_HUMAN - IIII ALU SUBFAMILY SO WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi728837 sp P9194 ALU7_HUMAN - IIII ALU SUBFAMILY SO WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22279002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi3776027 emb CAA092141 - (AU010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278999, 264032, 264094, 26331822, 68714117, 26331826, 26331828, 264907, 52644045, 265009, 60170831, 21906754, 87189559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264786, 264687, 52644239, 21906765, 21906766, 21906767, 21906768, 265021, 35657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264555
2213	91215309 (4425, 4426)	Novel Protein sim. GBank gi5420387 emb CAB46578.11 - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696032, 264905, 66712502, 264908, 264928, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264683, 264629, 2633974, 263976, 18108379, 55811576, 264556, 264637, 264558, 63373044, 22279002, 264482, 264483

2214	95361453 (4437, 4438)	Novel Protein sim. GBank gl1504325[elNP_000173.1]pHADH - hydroxacyl-Coenzyme A dehydrogenase3-ketacyl-Coenzyme A thioesteroyl-Coenzyme A hydrolase (trifunctional protein), alpha su	Contains protein domain (PF00725) 3-hydroxacyl-CoA dehydrogenase	264438, 52644507, 18108394, 56182575, 22278994, 22278995, 35696286, 56940075, 22278997, 22278998, 22278999, 264490, 60432048, 264259, 52645080, 26331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696032, 29331828, 20281100, 264509, 264907, 56182435, 264510, 265006, 264511, 264512, 66712502, 264908, 29331830, 52644045, 265007, 265008, 265009, 60170331, 264593, 60433556, 60433438, 33109954, 33657084, 52644298, 67168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21906785, 21906786, 21906787, 21906788, 21906789, 35695917, 265020, 265021, 265022, 264532, 60170615, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27466262, 27466264, 27485265, 35695763, 18108370, 264629, 60431528, 18108374, 18108378, 55810764, 35696423, 35695955, 264634, 264636, 52644332, 264638, 264555, 60170394, 18108381, 56182323, 83372004, 18108395, 18108397, 18108388, 56526488, 87168518, 60432113, 22275902, 264482, 264564, 264565, 264566, 264909, 265006, 264555, 264558, 87168518
2215	95419208 (4439, 4430)	Novel Protein sim. GBank gl11947160 (AF000238) - weak similarity to collagens, glycine- and proline-rich		
2216	87611046 (4431, 4432)	Novel Protein sim. GBank gl11572802 (U70654) - similar to [Caenorhabditis elegans] Novel Protein sim. GBank gl11572802 (U70654) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	UNCLASSIFIED	264693
2217	80389404 (4433, 4434)	Novel Protein sim. GBank gl5031707[elNP_003503.1]pGARP - glycoprotein A repetitions predominant	glycoprotein	264238, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gl387863[eml]CAA88953] - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST ENBL T00719 comes from this gene: cDNA EST y4465d8.3 comes from this gene: cDNA EST y4465d8 5 comes from this gene: cDNA EST y44924.3 comes from this gene: cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 264563
2219	87611046 (4437, 4438)	Novel Protein sim. GBank gl157802 (U70654) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family	264692, 264693, 264688, 264689, 264693, 18108370, 18108376

2220	953541165 (4439, 4440)	Novel Protein sim. GBank gi4507261 refNP_003145.1 psSTAT - statheir		264468, 18108394, 18108395, 35656286, 264259, 264097, 60432289, 264509, 264905, 264906, 264907, 26331630, 264909, 264909, 264510, 264511, 265007, 264512, 264910, 265039, 2649583, 264984, 6043356, 264955, 55812038, 264736, 58686542, 265010, 264901, 264603, 265019, 264605, 264760, 264932, 264446, 264764, 264369, 264766, 18108397, 264768, 264667, 18108398, 384769, 55811857, 264660, 264691, 33457025, 264692, 18108362, 18108368, 264928, 264929, 18108374, 263975, 264634, 264935, 264636, 264637, 264638, 18108363, 264633, 264566, 264466, 264567
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi3549154 (AC005623) - R27328_1 [Homo sapiens]		
2222	84423692 (4443, 4444)			UNCLASSIFIED
2223	95091649 (4445, 4446)			UNCLASSIFIED
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi376005 emb CAA47591 - (Z35719) cDNA EST EMBL_D57419 comes from this gene; cDNA EST EMBL_C13853 comes from this gene; cDNA EST EMBL_C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES.	Contains protein domain (PF01958) - Domain of unknown function	264408, 265020, 35655855 265010, 264665, 264660, 264693, 264628, 263974, 263976, 55811576, 264955, 264638, 53373044, 264463
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gi1255447 (U53339) - C05E11.1 gene product [Caenorhabditis elegans]		264239, 264509, 50182435, 265006, 265008, 265009, 264757, 2196754, 18108351, 264693, 18108374, 18108395
2226	86679853 (4451, 4452)	Novel Protein sim. GBank gi4826524 emb CAA42852.1 - (AL049848) hypothetical protein [Homo sapiens]	transport	22276894, 22276895, 22276899, 52644045, 264400, 265018, 2196726, 21960789, 264239, 2531822, 29331824, 29331825, 2931827, 264600, 264906, 265007, 264691, 264633, 264466
2227	87721135 (4453, 4454)			UNCLASSIFIED
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi606976 (U16800) - ribonucleoprotein [Xenopus laevis]		2914825, 2914804, 21466861, 18108374, 264637, 18108395
2229	86060931 (4457, 4458)	Novel Protein sim. GBank gi3549155 (AC005623) - R27328_2 [Homo sapiens]	Contains protein domain (PF00076) RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	264091, 264092, 264094, 26331822, 26331825, 60714117, 264693, 263972, 264639, 53373044, 264563

2230	95342515 (4459, 4460)	Novel Protein sim. GBank gij225154 prfj1412350A - DNA polymerase [Human adenovirus type 2]	UNCLASSIFIED	264488, 264768, 52944507, 264769 21905765, 21905765, 21905767, 21905769, 22278595, 22278595, 22278596, 22278597, 22278598, 22278599, 2645021, 264550, 52945129, 26331827, 264508, 264509, 264607, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21905754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	86060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328, 1 [Homo sapiens]	UNCLASSIFIED	18108394, 56182574, 22278595, 35696286, 22278597, 22278599, 2645259, 26331827, 35696052, 264507, 56182435, 265006, 265007, 265008, 264910, 264758, 55912038, 264603, 265018, 265019, 18108351, 264882, 264784, 264683, 264356, 264288, 264686, 264687, 264689, 21905755, 21905768, 21905767, 21905769, 29146629, 35695917, 264690, 52944150, 264691, 33657023, 264693, 18108370, 18108374, 55911576, 35695855, 264639, 18108385, 264664, 264606, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij581316 gAAD4176.1 AF13312 (AF133124) transcription factor IIC63 [Homo sapiens]	transcript factor	22278597, 264563, 264556, 86526466, 265020, 264603, 264556, 86526466
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gij4249733 gAAD13780 - (AF105377) uBp [Mus musculus]	kinase	265020, 264603, 264556, 86526466
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij106559 gijP4332 EAS, DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)	UNCLASSIFIED	22278597, 264563
2235	91012318 (4469, 4470)	Novel Protein sim. GBank gij4972734 gAAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) WD domain, G-beta repeat	264569, 264687, 264769, 755022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264555, 264559, 60433438, 60433113, 264761, 264762, 264763, 264764
2236	86003131 (4471, 4472)	Novel Protein sim. GBank gij1082675 gijP53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	264488, 264769, 21905765, 21905766, 21905767, 21905768, 21905769, 22278595, 22278596, 22278597, 22278598, 265020, 265021, 22278599, 2645259, 26331824, 29331825, 26331827, 35695763, 18108376, 35695855, 265007, 60432226, 33657402, 60433356, 60433438, 83373044, 18108385, 21905754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734 gAAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) WD domain, G-beta repeat	264488, 264769, 21905765, 21905766, 21905767, 21905768, 21905769, 22278595, 22278596, 22278597, 22278598, 265020, 265021, 22278599, 2645259, 26331824, 29331825, 26331827, 35695763, 18108376, 35695855, 265007, 60432226, 33657402, 60433356, 60433438, 83373044, 18108385, 21905754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	94098857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein	29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264559, 264488, 55274572, 56182575, 35656286, 22278997, 22278998, 264259, 29331827, 35696092, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21906765, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)			264693, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank g12494312: pIP0341IE2BG_RAT - TRANSLATION INITIATION FACTOR EIF-28 GAMMA SUBUNIT (EIF-28 GDP-GTP EXCHANGE FACTOR)	UNCLASSIFIED synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331828, 29331827, 29331828, 264409, 265007, 265009, 264598, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906785, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 27486264, 18108374, 35695855, 264634, 264637, 55182323, 83373044, 56526486, 87168518, 264564
2243	78902026 (4485, 4486)			265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank g12281143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank g1470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	52645156, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35696423, 264638, 18108387, 60432113, 22279000, 22279002, 264566

2246	94848710 (4491, 4492)	Novel Protein sim. GBank gl4996096[db][BAA78326.1] - (A0208069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35686286, 22276986, 22278997, 22278999, 264259, 35698032, 264106, 264905, 264907, 265006, 265007, 265008, 60433438, 33109854, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35694917, 265020, 265022, 27486264, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4483, 4494)	Novel Protein sim. GBank gl854065[emb][CAA58337] - (X83413) [088] [Human herpesvirus 6]		UNCLASSIFIED	52645156, 52648365, 52645080, 35696002, 33656970, 52648317, 33657084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 27486265, 18108387
2248	954175965 (4495, 4496)	Novel Protein sim. GBank gl4758502[refNP_004123.1]p1ABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	cathepsin	264488, 264259, 264907, 26331330, 264609, 265007, 265009, 264595, 21906754, 65274444, 264803, 264591, 264762, 264448, 264288, 264689, 21906768, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264838, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264488
2249	94885652 (4497, 4498)	Novel Protein sim. GBank gl4038461 (AF107722) - TcST11 (Trypanosoma cruzi)	Contains protein domain (PF00515) - TPR Domain	-eph	264768, 264628, 264636, 264637
2250	76827508 (4499, 4500)	Novel Protein sim. GBank gl3738140[emb][CAA2124.1] - (AL031652) vaji-lma synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gl3218467[emb][CAA07090.1] - (AJ006529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264684, 264288, 264690, 264628, 55811576, 264555, 264558, 264557, 264558, 264559, 264566
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gl4929325[db][AAD33953.1AF14531] vacuolar/ATP synthase subunit D [Homo sapiens]	Contains protein domain (PF01613) - ATP synthase subunit D	-synthase	264092, 264094, 264259, 26331322, 66714117, 26331828, 264102, 264103, 264104, 264105, 264109, 264112, 264451, 265007, 60433565, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264486, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gjl450247[refNP_001271.1]pCIRB - cold inducible RNA-binding protein	Contains protein domain (PF00076) RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264569, 1810394, 1810398, 56183575, 5694075, 35958286, 222789526, 264001, 42603, 264239, 24531822, 24531834, 23311835, 35951865, 264105, 264506, 264509, 264006, 264007, 2631830, 66712502, 264908, 264909, 264510, 265006, 264511, 265007, 265008, 265009, 264510, 60422270, 60433356, 60434338, 264758, 85658542, 265010, 265011, 87168559, 265012, 265013, 265014, 264448, 264764, 265017, 265018, 265019, 264488, 264764, 264288, 264369, 264765, 264686, 264768, 264769, 21906765, 21906767, 55811957, 264691, 33657023, 264692, 18103862, 55274620, 263969, 264628, 18103870, 60451528, 263972, 264629, 18103870, 18103877, 18103879, 55811576, 35696423, 35958555, 264630, 264634, 264635, 264636, 264658, 263981, 264638, 56182323, 60170394, 264638, 1810391, 1810392, 83370041, 1810395, 87168516, 60427113, 22279002, 264692, 264694, 264695, 264486, 264667, 18103931
2255	91010546 (4509, 4510)	Novel Protein sim. GBank gjl554185[emb]CAB51072.11 - (AL006868) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 55102575, 22278957, 22278989, 264255, 26331922, 26331825, 22331826, 26331827, 26331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182453, 264510, 264511, 265008, 264583, 264595, 21906754, 33109954, 87168474, 265011, 265017, 265019, 264682, 264764, 264685, 264288, 264765, 264685, 264686, 264768, 21906765, 21906766, 21906768, 21906769, 265020, 60170615, 52644150, 264690, 264692, 264693, 33657109, 33657149, 264632, 264636, 52644332, 55182233, 22279000, 22279002
2256	67020531 (4511, 4512)	Novel Protein sim. GBank gjl3327174[dbj]BA316559 - (AE014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	264765, 264686, 18105374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278999, 264681, 21906785, 21906786, 264687
2258	86000516 (4515, 4516)	Novel Protein sim. GBank gjl0235446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00060) Ligand-gated ion channel	misc_channel	264908, 264592, 264764

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gl14884140[emb]CAB43278.11 - (AL050110) hypothetical protein [Homo sapiens]	UNCLASSIFIED	18108396, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 264908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264369, 56181562, 265021, 60170615, 264690, 33657109, 60431528, 18108374, 52644332, 56182323, 18108395, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gl33080653 (AC004614) - similar to f-spondin proteins AB006086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - oxidase Thrombospondin type 1 domain	56182575, 265020, 264905, 264906, 264908, 35969423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264553
2261	86074157 (4521, 4522)	Novel Protein sim. GBank gl3334326[emb]CAA18138] - (AL021306) predicted using EGENEH [Homo sapiens]	UNCLASSIFIED	56182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35696052, 264508, 66712502, 52644045, 55182435, 265006, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21906767, 55811957, 35695917, 52644150, 33657023, 33857109, 55811576, 65274791, 56182323
2262	91639292 (4523, 4524)	Novel Protein sim. GBank gl1487759[gb]A031421.1/AF12444 - (AF124440) IMAGE tumor antigen D1 [Homo sapiens]		22278994, 22278997, 294807, 264828, 2644150, 18108381, 294893, 18108374
2283	87602495 (4525, 4526)	Novel Protein sim. GBank gl3341897 (AC003872) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 35695955, 264510, 264511, 264512, 265007, 265008, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264564, 264565, 264764, 264566, 264466, 264766
2284	87756525 (4527, 4528)	Novel Protein sim. GBank gl11657601 (U66220) - unknown [Nannocystis exsiliens]	UNCLASSIFIED	264689, 264910, 264764
2285	86918653 (4529, 4530)	Novel Protein sim. GBank gl1477027[pr]A48018 - mucin 7 precursor, salivary - human	UNCLASSIFIED	22278995, 22278997, 294807, 264828, 265006, 265007, 265008, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264566, 264487
2286	87773458 (4531, 4532)	Novel Protein sim. GBank gl3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF00096) - Zinc finger, C2H2 type Contains protein domain (PF01305) - ribosomal prot Ribosomal protein L15 amino terminal region	

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gl356022[emb]CAA20697.1; (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35690286, 264259, 29331824, 29331825, 35690052, 29331826, 264905, 264909, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264782, 264448, 264288, 264389, 264768, 52644229, 35695917, 264691, 33657023, 18108352, 35695709, 35696423, 264634, 18108351, 87168518, 264568, 18108351, 264766, 18108385, 264486
2268	85693867 (4535, 4536)	Novel Protein sim. GBank gl1728832[sp]P39189/ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	cadherin		264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2269	86177877 (4537, 4538)	Novel Protein sim. GBank gl103418[pil]S17885 - Tc037 protein - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		56182575, 60432048, 265007, 265009, 264591, 87168559, 264605, 18108351, 21906754, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113, 264763
2270	80410327 (4539, 4540)		CYP450		264909, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323, 264905, 264908
2271	91010392 (4541, 4542)		UNCLASSIFIED		52645156, 22277896, 22277899, 60432048, 264929, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21906754, 265018, 264689, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22277902
2272	84208220 (4543, 4544)	Novel Protein sim. GBank gl1476370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PIDg3387519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22277896, 22277899, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264691, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264768, 21906765, 21906766, 21906767, 21906768, 52644150, 264690, 18108384, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22277902
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gl1480112[emb]CAA67961 - (X39842) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22277896, 22277899, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264691, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264768, 21906765, 21906766, 21906767, 21906768, 52644150, 264690, 18108384, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22277902
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gl1480112[emb]CAA67961 - (X39842) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22277896, 22277899, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264691, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264768, 21906765, 21906766, 21906767, 21906768, 52644150, 264690, 18108384, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22277902
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gl13165406 (AC004755) - fos37502.2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	52645156, 22277896, 22277899, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264691, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264768, 21906765, 21906766, 21906767, 21906768, 52644150, 264690, 18108384, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22277902
2276	11287447 (4551, 4552)		UNCLASSIFIED		264555, 264556

2277	88004123 (4553, 4554)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID.g1369006) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat	22278999, 35690052, 265008, 265019, 264369, 265020, 265022, 55810754, 264404, 22279002
2278	94133079 (4555, 4556)	Novel Protein sim. GBank gi 2616702 (AC002510) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	18106394, 22278997, 29331826, 60433356, 60433438, 21906754, 265018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi 1197141sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	UNCLASSIFIED	
2280	94239723 (4559, 4560)	Novel Protein sim. GBank gi 4240289 cd BAX74928.1 - (AB020712) KIAA0905 protein [Homo sapiens]	Contains protein domain (PF00400) - transport WD domain, G-beta repeat	265008, 33109594, 265010, 265019, 265020, 264032, 264259, 29331822, 29331824, 29331826, 35690052, 264107, 264906, 264909, 52644045, 265006, 33657402, 60433356, 264758, 265011, 265019, 264681, 264683, 264684, 264688, 21906765, 21906767, 21906768, 21906769, 60170615, 264690, 52644150, 18108362, 264692, 18108368, 18108374, 293976, 264631, 18106381, 264559, 18108385, 56526466, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]	UNCLASSIFIED	264438, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18106351, 21906767, 21906769, 55811957, 33657023, 52644129, 33657109, 33657182, 27486282, 263972, 55811576, 87168518, 20281169, 60424179, 56182575, 22278994, 35690052, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35690052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264993, 60431735, 60433356, 33109594, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264268, 264688, 21906765, 21906767, 21906768, 29146827, 21906769, 55811957, 265020, 265022, 33657182, 27486281, 18108370, 264626, 18108374, 55810794, 18108379, 55811079, 35690052, 264630, 60431859, 60308191, 35690055, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264557
2283	95362388 (4565, 4566)	Novel Protein sim. GBank gi 2495729 ep Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)	UNCLASSIFIED	

2284	85414655 (4567, 4568)	Novel Protein sim. GBank gi2498797/99DB4311[PNAO_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAO) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAO)]			60432178, 52644507, 18108394, 52646842, 22278894, 35698286, 22278956, 22278997, 22278999, 2642259, 60432049, 26331822, 26331824, 26331825, 60432289, 26331826, 26331827, 35698082, 26331830, 52644045, 56182435, 33657402, 60433438, 33108954, 21905764, 85659542, 87169559, 265018, 265019, 5811150, 264682, 264369, 21905765, 21905766, 21905767, 21905768, 21905769, 58111957, 35695917, 265020, 265021, 60170815, 33657023, 33657192, 27486282, 27486284, 27486285, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 60432113, 264482, 264584, 35696052, 264903, 264307, 264308, 264309, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264703, 264685, 264766, 264686, 264768, 264693, 264623, 35695855, 264631, 264634, 35695265, 58182435, 60170831, 264591, 60432225, 264692, 264693, 264504, 264595, 55812038, 264698, 87168474, 35695917, 264692, 55811576, 264555, 264557, 264682
2285	87781464 (4569, 4570)	Novel Protein sim. GBank gi3342234 (U93509) - nuclear antigen EBNA-1 [Cerepithelium herpesvirus 1]	collagen		
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi3873414 (U00043) - similar to D. melanogaster inthorax protein [Caenorhabditis elegans]	kinase		
2287	82966696 (4573, 4574)	Novel Protein sim. GBank gi350605/pj1542731 - collagen alpha 1 chain - sea urchin [Hemicentrotus pulcherrimus] (fragment)	UNCLASSIFIED	Contains protein domain (PF01391) Collagen triple helix repeat (20 copies)	
2288	84133083 (4575, 4576)	Novel Protein sim. GBank gi7285236/p38169JALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY !!!	in7		
2289	86084133 (4577, 4578)	Novel Protein sim. GBank gi2887497 (AC004144) - R34001_1 [Homo sapiens]	kinase		
2290	86084137 (4579, 4580)	Novel Protein sim. GBank gi2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00400) - Contains protein domain (PF00400) - WD domain, G-beta repeat	
2291	84265281 (4581, 4582)	Novel Protein sim. GBank gi3255120 (AC005175) - R31449_3 [Homo sapiens]	strud		18108394, 264907, 265008, 265009, 33108954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gi4803672[emb]CAB42843.1; (AJ133789) nuclear transport receptor [Homo sapiens]	UNCLASSIFIED	56182575, 35696286, 56994075, 28331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264359, 264288, 56181552, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274820, 33657109, 27486264, 264623, 55810764, 55811576, 35695855, 56182323, 56526486, 87168518, 22779000, 264467
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - struct Leucine Rich Repeat	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331825, 264908, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264359, 264288, 264685, 264766, 265020, 265022, 264534, 35096423, 264631, 264837, 18108391, 56182323, 264639, 18108385, 264404, 264563, 264565
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gi2062860 (U88954) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - nuclease Exonuclease	22778997, 22778998, 22778999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22779000, 22779002, 264563, 264466, 22778998, 60432289, 264682, 264683, 264689, 18108374
2295	95312200 (4589, 4590)		UNCLASSIFIED	264689, 18108374
2296	80030781 (4591, 4592)		transcriptfactor	263974, 263978
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi56895501[db]EAA33034.1; (AB029005) KIAA1082 protein [Homo sapiens]		264488, 65274572, 56182575, 22778997, 22778999, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264807, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906765, 21906767, 21906768, 21906769, 55811557, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60770394, 63373944, 18108385, 56526486, 264564, 264486

2298	95312207 (4595, 4596)	Novel Protein sim. GBank g 387505 emb CA02849 - (Z81050) predicted using Genfinder, similar to collagen; cDNA EST EMBL D55564 comes from this gene; cDNA EST EMBL D59046 comes from this gene; cDNA EST yk369b12.3 comes from this gene; cDNA EST yk369b12.5 comes from this gene ...	collagen	60424170, 5618166, 22278995, 35696286, 22278996, 22278998, 22278999, 2644490, 264259, 26331822, 26331824, 66714117, 60424269, 35696952, 26331828, 66712502, 56182435, 264510, 265006, 60433438, 21906754, 33109954, 55811386, 265010, 265018, 55811150, 264765, 18108351, 264682, 264683, 264238, 264684, 264686, 264688, 56181562, 264689, 21906768, 21906767, 29148629, 55811957, 29148784, 55859917, 265020, 18108382, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83372044, 18108385, 80432113, 22279000, 264482, 264557, 264486
2299	80163720 (4597, 4598)	Novel Protein sim. GBank g 2443986 (AC002294) - Unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264369, 264488, 22278998, 22278999, 264259, 26331824, 66714117, 35696052, 264509, 264605, 264606, 264607, 264608, 264609, 265008, 264910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264765, 264768, 264769, 21906765, 21906767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22279002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank g 2143637 (p 184505 - calcium-dependent adin-binding protein - cat	struct	264608, 264758, 265017, 21906765, 83372044, 264553
2302	88084141 (4603, 4604)	Novel Protein sim. GBank g 2887497 (AC004144) - R34001.1 [Homo sapiens]	UNCLASSIFIED	52844045, 855019, 264283, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank g 4884194 (emb CA843220.1 - (AL049948) hypothetical protein [Homo sapiens])	Contains protein domain (PF00047) - Immunoglobulin domain	262059, 80432047, 264607, 264608, 264910, 60422239, 33657027, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83372044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank g 2641650 (p 10003 TRY1 - CAEL - HYPOTHETICAL 36 S KO PROTEIN T15H3.1 IN CHROMOSOME II PRECURSOR	UNCLASSIFIED	264239, 26331824, 21906767, 33657182, 33657349
2305	90935911 (4609, 4610)	Novel Protein sim. GBank g 4972866 (g AD94738.1 - (AF132150) unknown [Drosophila melanogaster])		55274572, 22278996, 264608, 265006, 21906769, 264691, 264486

2306	9533:040 (4611, 4612)	Novel Protein sim. GBank gi4929565 g AAD34043.1 AF15180 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) WD domain, G-beta repeat	264488, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 264801, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264766, 264769, 21906765, 21906766, 21906767, 21906768, 29148628, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264992, 18108370, 18108374, 18108376, 35696423, 35696855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264486	kinasereceptor	UNCLASSIFIED
2307	79415283 (4613, 4614)	Novel Protein sim. GBank gi4758732 g NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		35696286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404	synthase	UNCLASSIFIED
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi3876059 emb CAB17070 - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		18108397, 22278996, 22278997, 22278998, 22278999, 60432049, 29331822, 29331828, 60432285, 68712002, 60432229, 80433396, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 264691, 264692, 264693, 65274520, 65274791	glycoprotein	UNCLASSIFIED
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gi2137337 g 46281 - gene mCBP protein - mouse	Contains protein domain (PF00013) KH domain	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22279000, 264563, 264486	transcriptfactor	UNCLASSIFIED

2312	8754861 (4623, 4624)	Novel Protein sim. GBank gl2911264 (AC002550) - Unknown gene product [Homo sapiens]		5618257, 56994075, 35666286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 5264229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 21486261, 27486264, 35696423, 35695855, 18108365, 22279000, 22279002 263981
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gl3043826[BJAA254771] - (AB011123) KIAA0351 protein [Homo sapiens]	UNCLASSIFIED	52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 5064580, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696032, 33656970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645128, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gl5596714[emb] (CAG51401.1) - (AL035398) dJ798117.2 (CGI-5) [Homo sapiens]	UNCLASSIFIED	52644507, 52646335, 56182323, 18108365, 22278995, 22278996, 55994075, 35696286, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696032, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264531, 264556, 52644332, 83373044, 18108365, 18108367, 87168518, 60432113, 22279000, 264566, 264567
2315	80430119 (4629, 4630)	Novel Protein sim. GBank gl5531827[gb] (AA044488.1) - (AF078659) p47 [Homo sapiens]	UNCLASSIFIED	52644507, 52646335, 56182323, 18108365, 22278995, 22278996, 55994075, 35696286, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696032, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264531, 264556, 52644332, 83373044, 18108365, 18108367, 87168518, 60432113, 22279000, 264566, 264567

2317	87020571 (4633, 4634)		UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264666, 264687, 264688, 264689, 264556, 18108385
2318	79595879 (4635, 4636)		UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gi 5262613 emb CA045746.1 - (AL080155) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264488, 264569, 18108396, 5264365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 264259, 52945080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33857402, 21900754, 52644396, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 2644448, 18108354, 264288, 264389, 52644229, 21900764, 21900765, 21900766, 21900767, 21900768, 21900769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 83373044, 18108385, 56526486, 87166518, 264564, 264565, 264566
2320	91622426 (4639, 4640)	Novel Protein sim. GBank gi 728837 ep 39194 ALU7_SC WARNING ENTRY IIII	knase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265018, 21900765, 18108372, 18108387, 22279002, 264488, 264687, 18108394, 264689, 21900765, 18108397, 18108398, 21900767, 21900768, 63274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170615, 264555, 264636, 264556, 18108381, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264609, 18108354, 264486, 264567
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gi 3873837 emb CA007000 - (281029) Similarity to S. pombe hypothetical protein C1D4.09C (SW010154); cDNA EST EMBL.T00543 comes from this gene; cDNA EST EMBL.T01062 comes from this gene; cDNA EST EMBL.T01321 comes from this gene; cDNA EST EMBL.T02288 com...	UNCLASSIFIED	22278996, 264907, 264511, 264757, 18108351, 264768, 264638
2322	87003165 (4643, 4644)	Novel Protein sim. GBank gi 5678957 emb CA851685.1 - (AL109630) BACR7A4.y [Drosophila melanogaster]	dehydrogenase short chain dehydrogenase	

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 24941123 g O1005 YR1. CAEL - HYPOTHETICAL 39.9 KD PROTEIN T15H.9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00228) : eph DnaI domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33659970, 264509, 56182435, 264511, 265008, 60433356, 60433438, 55812038, 33109954, 21906754, 85658542, 87168474, 265011, 87168559, 265017, 265019, 264780, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21908765, 21906767, 21906768, 55611957, 35659917, 265021, 33657023, 18108362, 27486262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020
2324	86533507 (4647, 4648)	Novel Protein sim. GBank gi 5413865 emb CAB6377.1 - (AL086732) hypothetical protein [Homo sapiens]	ATPase-associated	285020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 2138859 p P2988 ICP4C_BLADI - CYTOCHROME P450 AC1 (CYP1VC1)	Contains protein domain (PF00067) : cyto450 Cytochrome P450	285006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 2420227 db BAA74892.1 - (AB020675) KIAA0869 protein [Homo sapiens]	UNCLASSIFIED	
2327	98081548 (4653, 4654)	Novel Protein sim. GBank gi 1245105 U46463 - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	264259, 264508, 264805, 264906, 264807, 264908, 265007, 264512, 264910, 264758, 265010, 264766, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264638, 264539, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 U46463 - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	50433438, 264595, 265017, 264766, 264692, 264629, 264635, 264636, 264638, 56182323, 60432113, 264560
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	UNCLASSIFIED	265017, 264685, 60432113, 264088
2330	87335395 (4659, 4660)	Novel Protein sim. GBank gi 5678136 gb AA046874.1 AF16093 - (AF160934) BCDNA.LD14.189 [Drosophila melanogaster]	transport	265009
2331	86980463 (4661, 4662)	Novel Protein sim. GBank gi 2194452 emb CAB08779 - (Z365387) unknown [Schizosaccharomyces pombe]	ATPase-associated	35696286, 22278998, 29331824, 60424269, 265006, 265008, 265012, 264448, 264764, 21908765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 387985 emb CAA92691.1 - (Z68318) cDNA EST CEMS262F comes from this gene; cDNA EST EMBL.C07930 comes from this gene; cDNA EST EMBL.C09463 comes from this gene; cDNA EST y441e6.3 comes from this gene; cDNA EST y441e6.5 comes from this gene; cDNA EST...	UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 498627 gb AA082261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2, contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank g 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - struct IQ calmodulin-binding motif	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank g 1922056 (CAA12805) - (Y12050) putative 3,4-dihydroxy-2-butanone kinase [Lycopodium esculentum]	kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank g 4459506 (emb CAB39181.1) - (Z85988) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]	UNCLASSIFIED	35696286, 22278999, 36182187, 29331825, 60424289, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87624045 (4675, 4676)	Novel Protein sim. GBank g 222468 (g BAA20819) - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	264906, 26182435, 265009, 60433438, 264586, 265010, 265019, 18108354, 264288, 264389, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85963319 (4677, 4678)	Novel Protein sim. GBank g 3873550 (emb CAA22121) - (AL033534) serine-rich protein [Schizosaccharomyces pombe]	UNCLASSIFIED	35696286, 264582, 264389, 264691, 264558
2340	90937716 (4679, 4680)			65274572, 22278994, 35696286, 22278997, 22278998, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264768, 284685, 21906769, 35695917, 284691, 264692, 35696423, 87168518, 22279000
2341	87775281 (4681, 4682)	Novel Protein sim. GBank g 3874563 (emb CAB02791) - (Z81042) similar to Yeast hypothetical protein YEY5 like; cDNA EST yk208h5.3 comes from this gene; cDNA EST yk208h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	264259, 264908, 264909, 264682, 22279000, 264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810794, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264553, 264564, 264565, 264566, 264567
2342	9534968 (4683, 4684)	g 492974 (g BAA034131.1) AF15189 - (AF15189) CGI-136 protein [Homo sapiens]	UNCLASSIFIED	264907, 264512, 265011, 264683
2343	87775448 (4685, 4686)	Novel Protein sim. GBank g 492974 (g BAA034131.1) AF15189 - (AF15189) CGI-136 protein [Homo sapiens]	UNCLASSIFIED	264758
2344	79953198 (4687, 4688)	Novel Protein sim. GBank g 2506307 (sp P13944) CA1C, CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00082) - von Willebrand factor type A domain	264488, 264259, 66712502, 264759, 83373044, 264566
2345	94319799 (4689, 4690)			

2346	94131820 (4691, 4692)	Novel Protein sim. GBank g1125411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP-P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP-P14822) [Caenorhabditis elegans]	Contains protein domain (PF00515) - proteaseinhb TPR Domain	35696286, 22278999, 264259, 35696052, 29331828, 33657402, 60433356, 33109954, 87166559, 264603, 265019, 18108351, 264681, 264685, 21006766, 265021, 33657109, 55811576, 35695855, 264637, 52844332, 264557, 83373044, 22279000, 22279002
2347	85330387 (4693, 4694)			22278997, 264511, 264683, 264684, 264768, 264687, 264688, 264691, 264692, 55811576, 18108334, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108365, 264567, 264486
2348	95196133 (4695, 4696)	Novel Protein sim. GBank g11290560[emb]CAAX72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lyopersion esculentum]	kinase	22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21006754, 265010, 87166559, 265018, 265019, 264781, 264681, 264288, 18108357, 21006768, 21006767, 264691, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2349	87778502 (4697, 4698)	Novel Protein sim. GBank g1488410[emb]CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]		56182575, 264909, 265006, 264558
2350	86200584 (4699, 4700)			
2351	86988042 (4701, 4702)	Novel Protein sim. GBank g1728832[sp]P39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY III	kinase	
2352	87337196 (4703, 4704)	Novel Protein sim. GBank g1731637[sp]P38780[YH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARGA INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank g11346955[sp]P48809[FB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (INRNP 4B) (HNP48.1)]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank g1731637[sp]P38780[YH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARGA INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	29331824, 264908, 265006, 265008

2355	91638766 (4709, 4710)	Novel Protein sim. GBank g[4938503jmb](CAB43861.1) - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00078) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	55984075, 22278996, 3596286, 22278996, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265005, 264758, 87168474, 265010, 265017, 264687, 21906765, 21906767, 21906769, 264691, 264692, 263867, 18108370, 87168518, 22279000
2356	96327688 (4711, 4712)	Novel Protein sim. GBank g[5138920jpb](AA040377.1) - (AF092135) PTSD14 [Homo sapiens]			52644507, 22278995, 3596286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 26432289, 35960052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21906754, 59811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170815, 33657109, 27486264, 35969763, 55810784, 18108379, 35969423, 55811578, 35965855, 60170394, 56182323, 83373044, 18108385, 56526488, 264404, 50432113, 22279000, 264482, 264553, 264556, 264486, 264557
2357	87775458 (4713, 4714)	Novel Protein sim. GBank g[4929741jpb](AA034131.1)(AF15189) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264782, 264565, 264566, 264369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank g[4218005](AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank g[1068330](U41284) - coded for by C. elegans cDNA yk206.5; coded for by C. elegans cDNA yk4491.5; coded for by C. elegans cDNA yk1267.5; coded for by C. elegans cDNA yk386.5; coded for by C. elegans cDNA yk206.5; coded for by C. elegans cDNA yk15g12....		UNCLASSIFIED	3596286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264682, 35969855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank g[388154jmb](CAA9377g) - (Z69904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 265981, 22279000
2361	94232191 (4721, 4722)	Novel Protein sim. GBank g[1746487](U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank g1171093jplP1906IMYSB-ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278999, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank g1854063jembCAA583371 - (X53413) U88 [Human Herpesvirus 6]		UNCLASSIFIED	264907, 264626, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank g18539930jbbIAA045896, IAF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2 hydroxypyruvate dehydrogenases	reductase	264488, 18108394, 264687, 18108398, 22278996, 56994075, 35696286, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87169474, 265010, 87166559, 264603, 265017, 265018, 265019, 264780, 264782, 18108351, 264448, 264784, 264683, 264684, 264288, 18108355, 264786, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108384, 33657109, 18108388, 18108370, 18108374, 35696423, 35696555, 264635, 264556, 264557, 264636, 60170394, 83373044, 18108383, 18108394, 18108385, 18108388, 56526486, 264482, 264564, 264485
2365	94140746 (4729, 4730)	Novel Protein sim. GBank g11840045 (U49082) - transporter protein [Homo sapiens]		transport	22278996, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264585, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695955, 52644332, 18108385, 18108387, 264564, 264566
2367	94140910 (4733, 4734)	Novel Protein sim. GBank g11065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696286, 21906768, 55810794, 65274791, 264497
2368	94322190 (4735, 4736)				264628

2369	94314334 (4737, 4738)	Novel Protein sim. GBank g1536901[poj]BAJ7813.1]- (A023343) a-helix coiled coil homologue [Homo sapiens]		stud	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644296, 52644229, 264689, 21908765, 21908766, 35695917, 265020, 52644150, 263987, 33657109, 27466265, 35655763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264509, 264596, 264369
2370	79804120 (4739, 4740)			UNCLASSIFIED	
2371	57280408 (4741, 4742)			UNCLASSIFIED	
2372	87624213 (4743, 4744)			UNCLASSIFIED	
2373	87418811 (4745, 4746)	Novel Protein sim. GBank g14589502[poj]BAJ78613.1]- (A023118) KDA0859 protein [Homo sapiens]		UNCLASSIFIED	29331826, 265010, 265019, 35695917, 264634, 60432113
2374	94123665 (4747, 4748)	Novel Protein sim. GBank g103513[poj]BAJ60445.1]- (A000061) 246aa long hypothetical ribonuclease PH [Acropora perna]	Contains protein domain (PF01138) - 3' exonuclease family	UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695955, 263981, 264557, 264665
2375	87731355 (4749, 4750)	Novel Protein sim. GBank g113513[poj]P4759JGRP.MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	60432049, 29331824, 264907, 52644045, 264512, 60433356, 21906754, 52644298, 87188559, 264448, 21908765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank g12645435 (AF007760) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - ATPase, associated PHD-finger		264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695955, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank g1257005[poj]A041239.1]- (AF083249) Ro binding protein homolog [Homo sapiens]	Contains protein domain (PF01380) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 6671417, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264794, 264288, 21906767, 21906768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264556, 83373044, 18108385, 18108388, 6526486, 22279000, 22279002, 264563
2378	94137032 (4755, 4756)	Novel Protein sim. GBank g1072198 (U49942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482, 265017, 264288, 21906768
2379	65444324 (4757, 4758)	Novel Protein sim. GBank g13337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat		

2380	68923082 (4755, 4760)	Novel Protein sim. GBank gij4502939jefNP_001845.1jpcCKL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gij4455609jmb/CAB36555j - (AL031846) dJ742C18.5 (novel Chromobox protein [homo sapiens])	Contains protein domain (PF00385) - "chromo" (Chromatin Organization Modifier) domain	helicase	56182575, 264091, 264093, 264239, 25331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264683, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 55811576, 264636, 264567
2382	91225882 (4763, 4764)	Novel Protein sim. GBank gij432130jib/AAD17276j - (AF118716) dmi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	25331824, 60432289, 264905, 264596, 21906754, 264789, 265022, 264693, 263967, 33657109, 264639, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gij1902592jib/BAA19005j - (D89049) lectinlike oxidized LDL receptor [Bos laurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	264488, 52644507, 5264156, 5264635, 35696286, 22278999, 52645060, 29331824, 25331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 6574620, 52645129, 33657109, 33657182, 27485261, 27486262, 27486264, 33657249, 27485265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)		UNCLASSIFIED		264488, 52644507, 5264156, 264887, 5264635, 22278999, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 25331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gij4929699jib/AAD34110j - [AF151873] CGL-115 protein [homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146486, 264112, 264511, 60170031, 60432229, 264595, 60433438, 87168474, 87166559, 264682, 21906765, 21906766, 21906767, 21906769, 239148629, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14937960 (4773, 4774)			UNCLASSIFIED	284634
2388	11424604 (4775, 4776)			UNCLASSIFIED	284595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank glt4750358j(nf_004372.1)CREB -cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) bZIP transcription factor		284488, 22278998, 22278999, 284509, 284605, 284606, 284607, 284608, 284609, 285008, 284611, 284612, 284610, 284631, 21906754, 284604, 284761, 16103351, 284784, 284288, 284766, 284768, 284769, 21906765, 21906769, 284692, 844953, 35695423, 284635, 284636, 284555, 837426, 527476, 284637
2390	94320912 (4779, 4780)	Novel Protein sim. GBank glt164239djb(AA122231)- (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00478) DNA polymerase family A	polymerase	5387607, 527476, 284637, 22278998, 22278999, 22278997, 22278999, 20331822, 25331823, 28531826, 35696052, 284905, 32844045, 285008, 284756, 284759, 33109954, 52844296, 85858542, 285011, 285017, 285018, 284605, 32844243, 21906765, 21906767, 21906768, 21906769, 35695917, 52844150, 33857023, 33857109, 33657349, 35695765, 18106370, 18106374, 18106376, 35696423, 35695555, 284555, 52844332, 58192323, 60170394, 63373044, 38526466
2391	80336194 (4781, 4782)	Novel Protein sim. GBank glt4240169djb(AA174883.1)- [A6020847] KIAA0940 protein [Homo sapiens]	Contains protein domain (PF00560) Leucine Rich Repeat	UNCLASSIFIED	283978
2392	94243016 (4783, 4784)			nuclease	35696258, 35696052, 284508, 284905, 284509, 284600, 284601, 284609, 284609, 284510, 284511, 284602, 284610, 285009, 284598, 284613, 284605, 284604, 284762, 284468, 284768, 284695, 284766, 284768, 284769, 284689, 35695917, 284636, 18108371, 283978, 35696423, 35695555, 284631, 284634, 284635, 284636, 284637, 284638, 60170394, 284639, 284645, 284466

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gi4506667/eflNP_000993.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00465) - Ribosomal protein L10	- ribosomal prot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 3566286, 22278996, 22278997, 22278999, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146495, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264909, 36182435, 264112, 264113, 264510, 265006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21906765, 21908766, 21906767, 21906768, 21906769, 55811957, 29148629, 29148794, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108354, 33657109, 18108368, 27486261, 27486262, 33657349, 35695763, 18108370, 263972, 264632, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21906765, 21906768, 21906769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657348, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264566, 264567
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gi45158838 (AC004308) - zinc finger protein from gene of uncertain exon structure, similar to C98876 (P1D:G3025333) [Homo sapiens]	Contains protein domain (PF00095) - Zinc finger, C2H2 type	- dna_mna_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108397, 264503, 264566
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi5712756 bb AA047636.1 AF16079 - (AF160798) calcium transporter Cat1 [Rattus norvegicus]		dna_mna_bind	

2396	95096700 (4791, 4792)	Novel Protein sim. GBank gi 106322 pir B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	52646365, 18106397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 66712502, 264106, 264907, 264591, 33657402, 60433438, 5812038, 33109954, 21906754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264768, 52644229, 21906768, 21906767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35696423, 35696555, 264631, 264556, 52644332, 264558, 83373044, 18106388, 87168518, 22279002, 264482
2397	87200854 (4793, 4794)			52644507, 52643156, 36182575, 264259, 29147620, 264905, 264907, 264908, 264909, 264910, 264758, 52644296, 264603, 264804, 264762, 264681, 264764, 18106357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264584
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi 3258609 (AC003178) - H53_GS1 [Homo sapiens]	UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gi 736117 (L11834) - nuclear protein [Ensis minor]	UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265022, 60170615, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gi 2352822 (gjaAB65285.1) - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank. gi 2352822 gb AB9285.1 - (AF008945) glucose-5-phosphatase [Haplochromis nubilus]	phosphatase	52644507, 52645156, 52644225, 264686, 21906764, 21906765, 52646365, 52646842, 21906766, 21906767, 21906768, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264106, 264805, 35696423, 35695955, 265006, 265007, 265008, 265009, 264637, 52644332, 55612038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 80432113, 265017, 265018, 265019, 264563, 264288
2402	91221408 (4803, 4804)	Novel Protein sim. GBank. gi 469259 gb AA027832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]		264907, 264908, 264909, 264566
2403	94135432 (4805, 4806)	Novel Protein sim. GBank. gi 492957 gb AA034048.1 AF15181 - (AF151811) CGI-53 Protein [Homo sapiens]	Contains protein domain (PF00062) - C-type lysozyme/alpha-lactalbumin family	22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank. gi 2315796 (AF016885) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21906769, 264584
2405	94311851 (4809, 4810)	Novel Protein sim. GBank. gi 464178 gb AA033811 - (D14835) polyprotein [Hepatitis C virus]	UNCLASSIFIED	35696286, 29331822, 265007, 21906754, 265017, 265018, 265019, 264783, 264369, 21906765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank. gi 273363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79485005 (4813, 4814)	Novel Protein sim. GBank. gi 423442 pir J33313 - gene Ff protein - mouse	UNCLASSIFIED	264685, 264686
2408	87391503 (4815, 4816)	Novel Protein sim. GBank. gi 423442 pir J33313 - gene Ff protein - mouse	UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank g 117680 lsp p45968 YN29_CAEEL - HYPOTHETICAL 20.8 KO PROTEIN T99A5.6 IN CHROMOSOME III	UNCLASSIFIED	22278955, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29146498, 52644045, 60433438, 33657084, 71168474, 264780, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281059, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank g 466262 g p AC48052.2 - (U64849) Contains similarity to Pfam domain: PF00646 (F- box). Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00680) - Copper/zinc superoxide dismutase (SOOC)	
2411	8754633 (4821, 4822)	Novel Protein sim. GBank g 3114713 (AF061346) - Edp1 protein [Mus musculus]	Inf	29331824, 29331827, 29331828, 264764, 264389, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank g 5410333 g p AUX3038.1 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	dna_rna_bind RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906768, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank g 562705 emb CAB45778.1 - (AL080214) hypothetical protein [Homo sapiens]	struct Intermediate filament proteins	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264784, 264786, 264686, 264788, 264689, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264486
2414	94372590 (4827, 4828)	Novel Protein sim. GBank g 1082340 g p S52863 - DNA- binding protein R. kappa B - human	ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696288, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181592, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170815, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657249, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22275002

2415	8808002 (4829, 4830)	Novel Protein sim. GBank gi423915[pilA45439 - myosin I heavy chain - rat]	Contains protein domain (PF00063) Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21906754, 265016, 264687, 264689, 21906769, 55811857, 265021, 264690, 264691, 33657023, 264693, 35696423, 56182323, 56526486
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gi3025445 (AC004328) - R32184.1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gi1084944[pilIS54456 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00133) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gi1176572[sp45895YMAA_CAEEL - HYPOTHETICAL 91.0 KO PROTEIN PAR 2.4 IN CHROMOSOME III]	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60433289, 29331828, 264905, 264907, 264511, 265009, 60433229, 21906754, 87166559, 265019, 264882, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264566
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gi284006[pilIS18732 - autoantigen, 64K - human]		struct	264569, 264762, 264446, 264691, 264631, 264834, 264555, 264556, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gi107621[pilIS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	29331824, 29331825, 29331828, 60433229, 33109954, 8658542, 87168474, 285018, 264288, 265020, 264564
2421	87805345 (4841, 4842)	Novel Protein sim. GBank gi224567[drjBAA207721 - (AB002311) KIAA0313 [Homo sapiens]]	Contains protein domain (PF00617) - RasGEF domain	UNCLASSIFIED	264509, 264768, 264638
2422	86058714 (4843, 4844)	Novel Protein sim. GBank gi4505153[reINP_002392.1pMEKK - MAP/ERK kinase 3]		transport	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	86058390 (4845, 4846)	Novel Protein sim. GBank gi4505153[reINP_002392.1pMEKK - MAP/ERK kinase 3]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331826, 60433289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 203971, 60432113
2424	84854047 (4847, 4848)	Novel Protein sim. GBank gi2388398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278697, 60432049, 264259, 29331826, 29331828, 264905, 60712502, 29331830, 60433356, 265011, 265019, 264766, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gi2077932[drjBAA19879] - (O86558) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gi2039368[gbAAB53003.1] - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976

2427	87622893 (4853, 4854)	Novel Protein sim. GBank g 4680695 gb AA02737.7 AC:13296 - (AF:132962) COI-28 protein [Homo sapiens]	Contains protein domain (PF00373) - Ribosomal protein L4L1 family	ribosomalprot	264259, 26281099, 35690052, 265008, 264594, 265011, 264760, 18108331, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21906786, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4853, 4856)	Novel Protein sim. GBank g 1537070 U63840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278999, 35690052, 21906754, 264286, 21906765, 21906768, 21906769, 35690917, 265020, 263972, 2279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank g 601931 MG4316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF07111) - Beta defensins	UNCLASSIFIED	22278999, 26331824, 264906, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264683, 264286, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)				254112, 264691
2431	87648864 (4861, 4862)	Novel Protein sim. GBank g 3860729 emb CAA14630) - (A235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein	UNCLASSIFIED	26331826, 26331827, 35690052, 29146499, 264905, 264906, 264681, 264288, 264689, 21906765, 264692, 35694423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank g 3876367 emb CAA93287) - (Z69380) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL.M95266 comes from this gene; cDNA EST y429569.5 comes from this gene [Caenorhabditis elegans]		protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank g 2242453 gb BAA30794) - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264469, 264905, 265018, 264762, 264683, 264691, 264538, 264537, 264639, 264558
2434	10520148 (4867, 4868)				264563
2435	20759044 (4869, 4870)				264555
2436	88044008 (4871, 4872)	Novel Protein sim. GBank g 1263289 U47856) - fibron-4 [Araneus diadematus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank g 3841332 AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	26331828, 265007, 265009, 265017, 264760, 264885, 264693, 264565
2438	94143473 (4875, 4876)	Novel Protein sim. GBank g 3860014 AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	26331826, 264508, 264905, 264509, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33857402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35690917, 33857023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850650 (4877, 4878)	Novel Protein sim. GBank gi4263519(giAAID15345) - (AC004044) small nuclear riboprotein Sm-D1 (Arabidopsis thaliana)	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182275, 56181686, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 66714117, 29331825, 60432285, 29331826, 29331827, 29331828, 35696052, 29146498, 264509, 264905, 264906, 52644045, 60431735, 33109954, 21906754, 33657084, 55811386, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486282, 27466264, 33657349, 27486285, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22279000, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gi3024889(isp56524)Y288 - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264639, 18108374, 264554
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gi4506013(iejfNP_002703.1)ppp1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gi1170659(isp002975)KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - hZIP transcription factor	transcription factor	264906
2444	86086345 (4887, 4888)	Novel Protein sim. GBank gi4758824(iejfNP_004280.1)pnrf3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - hZIP transcription factor	transcription factor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gi2135950(pri)S58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108361
2446	86059293 (4891, 4892)	Novel Protein sim. GBank gi4753887(emb)CAUG4509.2 - (AJ002424) p65 protein (Rattus norvegicus)	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein)	protease inhibitor	265011, 264688, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gi4486513(iejfNP_005409.1)ps1s1 - suppression of tumorigenicity 5	'four-disulfide core'	cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	8774980 (4895, 4896)			UNCLASSIFIED	22278996, 22278997, 22278999, 29331826, 35696052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank g11728837isp39194ALUT_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		cadherin	264259, 264428, 265007, 264595, 265021, 56526486
2450	86597784 (4899, 4900)	Novel Protein sim. GBank g11710027isp325290R24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	UNCLASSIFIED glycoprotein	264906
2451	91014353 (4901, 4902)				264083, 293331822, 29331824, 29331825, 26714117, 29331826, 29331828, 35696052, 264907, 66712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33857023, 264693, 33857109, 263969, 83373044, 18108385
2452	91230309 (4903, 4904)	Novel Protein sim. GBank g11504034(dj)BAA13216] - [D69980] KIAA0227 Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264593
2453	84201088 (4905, 4906)	Novel Protein sim. GBank g12800079 (AC004142) - similar to murine leucine-rich repeat protein, possible role in neural development by protein-protein interactions; 93% similarity to D4802 (P10.g1389905) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nglrecep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank g11076802(pj)S49915 - extensin like protein - maize	Contains protein domain (PF00770) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264782, 18108381, 264784, 264785, 264786, 264686, 264788, 264789, 264534, 264691, 264692, 33857023, 264693, 33857109, 264628, 263978, 35695955, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264593, 264594, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank g1943817isp35585AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278996, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108381, 264683, 264764, 18108384, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148529, 35695917, 265020, 265022, 33857023, 33857109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264586, 264587
2456	86166700 (4911, 4912)	Novel Protein sim. GBank g12586830 (AC003079) - Ankyrin like, 54% similar to 2022340A (NID-g1092123) in exons spanning 43974 to 11551 of clone [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank g/j025447 (AC004328) - R32184_3 [Homo sapiens]	UNCLASSIFIED	56181686, 264905, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526486, 264563
2458	85675304 (4915, 4916)	Novel Protein sim. GBank g/j0236492 (AF229865) - Similar to collagen Catenohabillis elegans	UNCLASSIFIED	264691, 264693, 264694, 264695
2459	87551913 (4917, 4918)	Novel Protein sim. GBank g/j0441942/g/j044043167: AC004909 - (AC004997) supported by mouse EST A538043 (MD.g2284036)	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	27486265
2460	94315288 (4919, 4920)	Novel Protein sim. GBank g/j462970/g/j04A034111: JAF15187 - (AF151874) CGH-116 protein [Homo sapiens]	kinase	65274572, 35696286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 29146498, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906769, 35695917, 265020, 264691, 33657023, 27486261, 18108374, 35695855, 87186518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank g/j428962/g/j04A020633: (AF128062) Ar-like 2 binding protein BART1 [Homo sapiens]	UNCLASSIFIED	264259, 28331828, 264910, 18108351, 19108370, 18108374
2462	86980002 (4923, 4924)	Novel Protein sim. GBank g/j0420387/emb/CAB46679.1: (AJ242459) proteoglycophycin [Leishmania major]	UNCLASSIFIED	264905, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank g/j0502516/g/j04A038588.1: JAF14561 - (AF145613) ScDNA CHD3108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank g/j041030/g/j04A13021.1: (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278998, 264259, 28331822, 29331824, 66714117, 29331825, 29331828, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264786, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22275002, 264486

2465	95357483 (4929, 4930)	Novel Protein sim. GBank gi 4506407 ref NP_02871.1 PRAF1 - v-ra1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	oncogene	18108392, 52645107, 52645156, 52646363, 22278994, 22278995, 35696286, 35696287, 22278998, 2642259, 29331822, 29331824, 25331825, 2642269, 50432269, 29331827, 35696032, 29331828, 264907, 29331830, 52640435, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21069754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264787, 21906755, 21906767, 21906768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27468261, 27468264, 35695763, 264628, 265972, 18108374, 35695555, 264636, 264637, 80170394, 56526486, 87168518, 60432113, 264553, 264564, 264566, 264487, 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi 4321619 pb AA015788.1 - (AF051088) seven transmembrane domain orphan receptor (Mus musculus)			
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi 513300 (AC005585) - F18601.1, partial CDS [Homo sapiens]		UNCLASSIFIED	56994075, 264908, 21900768, 33657023
2468	87614596 (4935, 4936)	Novel Protein sim. GBank gi 214345 j j 58106 - gene DMR-N9 protein - mouse (tagment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	25331824, 52644045, 265008, 264910, 265019, 21906755, 21906769, 265021 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gi 5420389 tm CAB46840.1 - (A.243460) proteoglycan (Leishmania major)		UNCLASSIFIED	264592, 264832, 264535, 264536, 264557, 264558, 264559, 18108385, 264442
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419882 tm CAB46424.1 - (AL0096749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 33666286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gi 4929747 pb AA034134.1 AF:151897 CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264692, 604432049, 29331825, 60433356, 265010, 265011, 18108351, 264784, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi 4539009 tm CAB39630.1 - (AL049481) putative protein [Arabidopsis thaliana]			60424179, 65274572, 22278999, 60424269, 25331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gl1216486 (U48852) - HT protein (Cricetus griseus)	Contains protein domain (PF00008) - Igf EGF-like domain	-Igf	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35696423, 83373044, 18108383, 18108385, 264584, 264585, 264587
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gl3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 60424289, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)	Novel Protein sim. GBank gl1644323 (JBA11082) - (D67066) N-WASP [Bos taurus]		UNCLASSIFIED	265017
2479	94314569 (4957, 4958)			UNCLASSIFIED	56994075, 22278999, 2106754, 264652, 21906765
2480	95295605 (4959, 4960)	Novel Protein sim. GBank gl5689469 (JBA43018.1) - (AB028989) KIAA1066 protein [Homo sapiens]		UNCLASSIFIED	264905, 264907, 264785
2481	94718481 (4961, 4962)			collagen	65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 52844045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264780, 264782, 18108351, 264764, 264288, 264766, 264686, 264789, 21906768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gl321249 (JBA128407) - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)			UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433436, 264448, 264288, 263987, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gl728831 (JBA12831) - HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gl1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264789, 264689, 35695917, 265022, 264692, 264693, 56182333

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2682167 dbj BAJ237151 - (AB007603) KIAA0443 [Homo sapiens]			265017, 264555	
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 4045595 pp35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family		22278986, 35606286, 22278987, 22278988, 22278989, 264082, 264259, 26331622, 35690032, 264106, 264905, 264907, 26331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109854, 87160559, 265018, 264681, 264288, 264687, 21906785, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 16103377, 35696423, 35695855, 60170394, 16108395, 36526486, 22279000, 22279002, 264563, 264462, 264565, 20281189, 16108391	
2488	87652451 (4975, 4976)			UNCLASSIFIED	264970, 264446, 264288, 264684, 264691, 264634	
2489	82980585 (4977, 4978)	Novel Protein sim. GBank gi 486439 emb CA G43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)		264686, 264693, 55811576, 22279002	
2490	80069609 (4979, 4980)	Novel Protein sim. GBank gi 2588624 AC003083 - Rap2 interacting protein-like, similar to U73941 (PID:g 916018) [Homo sapiens]	UNCLASSIFIED		264907, 265008, 22279002	
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 7285329 pp349189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	im7		264259, 29331826, 265008, 264762, 16108370, 16108376, 16108379	
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 AF001549 - Unknown gene product [Homo sapiens]	transcription factor		264488, 22278688, 22278699, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906766, 264692, 60431528, 87168518, 60432113, 22279000	

2483	95422415 (4985, 4986)	Novel Protein sim. GBank g1j4240307[dbj]GAA74932.1] - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct RH domain	18108394, 264887, 65274572, 36182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264509, 264906, 264907, 29331830, 264909, 264510, 265008, 264511, 265007, 264512, 265008, 265009, 264910, 21906754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264782, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55610764, 18108379, 65274791, 284630, 264832, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264586, 264488
2484	30783118 (4987, 4988)	Novel Protein sim. GBank g1j5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264907, 264601
2485	94234351 (4988, 4990)		collagen	263994, 22278997, 35696032, 264509, 264905, 264908, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264788, 264789, 264689, 265020, 264682, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264584, 264587, 264486
2486	80018765 (4991, 4992)	Novel Protein sim. GBank g1j4806220[emb]CAB42832.1] - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]	struct	29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2487	91723554 (4993, 4994)		UNCLASSIFIED	52844507, 22278996, 22278999, 29331824, 29331828, 33657402, 21906754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
2488	87724633 (4995, 4996)	Novel Protein sim. GBank g1j1200503 (U47924) - B [Homo sapiens]	UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35696855
2489	94685125 (4997, 4998)	Novel Protein sim. GBank g1j310234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	Contains protein domain (PF000069) - kinase	264909, 55812038, 264631, 264637, 264558

2500	94649324 (4999, 5000)	Novel Protein sim. GBank gi 3881275 emb CAA217251 - (A032635) predicted using Genefinder, similar to inositol monophosphatase family; cDNA EST Y425511.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	5284507, 52645156, 22278995, 56894075, 35696286, 22278998, 264259, 52645080, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 264681, 264448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303886 (5001, 5002)	Novel Protein sim. GBank gi 4295159 gb AA030088.1 AF:15183 - (AF:15183) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00037) - BTB/POZ domain	- dna_mna_bind	65274572, 56182575, 35696286, 22278998, 56994075, 22278997, 60432048, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264581, 60432229, 33657402, 60433366, 264595, 55812038, 264758, 264596, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264389, 264288, 264786, 18108357, 21906765, 21906766, 21906767, 21906769, 29148529, 35695917, 264692, 33657023, 284629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 50432113, 22279002, 264565
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi 3041847 (AC006542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID.g125008) [Homo sapiens]	Contains protein domain (PF010237) - Oysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264907, 18108351, 264448, 264389, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264593, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi 2196874 emb CAA72638 (Y11886) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148827, 264693, 18108370, 18108374, 18108385

2504	87669706 (5007, 5008)	Novel Protein sim. GBank glij550420[embjCA48220] - (X6810.1) vs [Rattus norvegicus]		264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264606, 264908, 52644045, 265009, 60433356, 33657402, 60433436, 264595, 33109954, 87168474, 265017, 264595, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			264488, 52644507, 52645156, 52646365, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264606, 264908, 52644045, 265009, 60433356, 33657402, 60433436, 264595, 33109954, 87168474, 265017, 264595, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2506	91232326 (5011, 5012)	Novel Protein sim. GBank glij2137562[ipK49635 - mouse Dhml protein - mouse		UNCLASSIFIED nuclease
2507	95316233 (5013, 5014)	Novel Protein sim. GBank glij5174489[ipNP_008035, ipK1AA, histone desecylase 6		264488, 263994, 264592, 264595, 264389, 264688, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank glij4926433[embjCAB2889.1] - (AL031447) dJ126A5.2.1 (novel protein) (isolom 1) [Homo sapiens]		UNCLASSIFIED Contains protein domain (PF00850) - histone Histone desecylase family
2509	87813741 (5017, 5018)	Novel Protein sim. GBank glij1263289 (U47856) - fibron-4 [Araneus diadematus]		264488, 263994, 264592, 264595, 264389, 264688, 264768, 35695917, 35696423, 264563

2510	95421379 (5019, 5020)	Novel Protein sim. GBank gi 3393537 gb AAC25762.1 - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_msa_bnd	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433366, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486362, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264592
2511	87394281 (5021, 5022)	Novel Protein sim. GBank gi 4323152 gb AAO16228.1 - (AF098863) Ets-protein Sp-C [Mus musculus]			
2512	88094771 (5023, 5024)	Novel Protein sim. GBank gi 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264299, 29331825, 29331826, 29146499, 264907, 264909, 265006, 265008, 264591, 60432229, 21906754, 284763, 264683, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gi 3004657 (AF017777) - booby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52645158, 18108394, 22278994, 35896286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33857084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486262, 33657349, 18108374, 55810764, 35696423, 58182323, 264555, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gi 375727 emb CAA18783 - (AL022727) dj8019.7 (olfactory receptor-like protein (hsML-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gi 420527 emb CAA23000 - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264031, 29331834, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gl4929581[gbAAD24056, 1[AF15181 - (AF15181) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331826, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108395, 60432113, 264088, 264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gl4263748[gbAAD15420] - (AC004883) similar to KIAA0766; similar to P1D3382253 [Homo sapiens]	kinase		264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gl4526722[ie]NP_005085, 1[pe]ATP - fatty acid transport protein 4	transport		264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gl5174489[ie]NP_006035, 1[pe]KIAA - histone deacetylase 6 associated factor 1 [Homo sapiens]	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263984, 65274572, 22278995, 22278996, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265006, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811857, 264692, 264693, 27488281, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 55274727, 60432113, 264563, 264564, 264565, 264566, 264567
2522	87774032 (5043, 5044)	Novel Protein sim. GBank gl4580011[gbAAD24201, 1[U81002] - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264489, 22278997, 20281171, 21906754, 35695917, 263987, 263976, 263981, 20281169
2523	95340467 (5045, 5046)	Novel Protein sim. GBank gl1009327 (U76374) - skm-	Contains protein domain (PF01753) - MYND finger		263969
2524	95340469 (5047, 5048)	BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486281, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264587

2525	94126928 (5049, 5050)	Novel Protein sim. GBank g 2073564 (U00223) - eukaryotic initiation factor eIF-2 alpha kinase. DGNCZ [Drosophila melanogaster]		kinase	264488, 22276987, 22276989, 60432049, 60432289, 29331826, 264605, 265008, 58812038, 21900754, 265019, 264369, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657109, 60431528, 63373044, 60432113, 22279000, 22279002, 264595
2526	95289404 (5051, 5052)	Novel Protein sim. GBank g 4589625(dj)g A76836.11 - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	60424179, 264788, 264687, 264687, 264689, 65274572, 21900767, 58102573, 21900768, 21906769, 58811957, 22276994, 22276995, 35696286, 35695917, 22276996, 22276997, 265020, 22276998, 265021, 22276999, 265022, 264690, 264691, 60432049, 264299, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264905, 264907, 27486262, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264628, 264909, 18108372, 18108374, 58102435, 18108376, 58810764, 58811576, 35696423, 35895855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264838, 33657402, 58182323, 60433358, 60433438, 264595, 58812038, 264596, 264793, 83373044, 52646317, 18108385, 33657084, 18108387, 58811386, 65274727, 58526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264594, 18108391, 264448, 264586, 264288, 264486, 264587, 264786, 264510, 264512, 264630, 264591, 264592, 264299, 264594, 264595, 264603, 264605, 18108351, 264595, 264369, 18108354
2527	88094380 (5053, 5054)	Novel Protein sim. GBank g 2255437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	58812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2528	88078380 (5055, 5056)	Novel Protein sim. GBank g 2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (P1Dg1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_mn_bind	264908, 264769, 265020, 265021, 18108383
2529	86670262 (5057, 5058)	Novel Protein sim. GBank g 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW-Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				
2531	87768931 (5061, 5062)			UNCLASSIFIED	264389, 264556
2532	87419778 (5063, 5064)	Novel Protein sim. GBank g 2864625(em)CA169731 - (AL021811) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264389, 264556
2533	87000255 (5065, 5066)	Novel Protein sim. GBank g 437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264389, 264556

2534	87332322 (5067, 5068)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	UNCLASSIFIED	264259, 36696052, 264905, 265017, 21906795, 265020, 265022, 33657109, 22279000
2535	91225056 (5065, 5070)	Novel Protein sim. GBank gij448317 (hmjCAB3792) - (AL031432) dJ65N24.2.1 (PUTATIVE novel protein) (isoform 1) Homo sapiens]		65274572, 35696286, 60432289, 29331826, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906795, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gij728335 (p29103)ALUS_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III	Kinase	18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 50432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gij4557026 (elNP_003913.1)pHERC - guanine nucleotide exchange factor p532	ubiquitin	65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264780, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 356959855, 264636, 264595, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)		UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170631, 87168559, 264604, 265019, 264685, 264766, 87168518, 22279000, 264565, 264566
2539	94114816 (5077, 5078)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264756, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264467
2540	94218545 (5078, 5080)	Novel Protein sim. GBank gij1367647 (pJIS5876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)	UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264766
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gij1711658 (pF547971T10_MOUSE - SE07HR-RICH PROTEIN T10 IN DGCR REGION	UNCLASSIFIED	

2542	9528162 (5083, 5084)	Novel Protein sim: GBank gij2232320 gb AA040850.1 AF031071 sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - UNCLASSIFIED Neurohypophyseal hormones, N-terminal Domain	254485, 18108394, 52646365, 52646842, 65274457, 22278984, 35696286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35696052, 33656970, 264907, 264909, 52644045, 264510, 265006, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644296, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52644229, 264769, 21906766, 21906767, 21906769, 52644150, 33657023, 33657109, 52645129, 33657182, 27488261, 27486264, 33657349, 35695763, 18108374, 35666423, 35695655, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim: GBank gij4119827 emb CAB46374.1 - (AL096723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	65274572, 56182575, 22278999, 264259, 29331828, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 264689, 21906765, 21906767, 21906769, 80170615, 264682, 264693, 55811578, 65274791, 264636, 264556, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim: GBank gij2498110 sp Q53191 AEGP - RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - glycoprotein MAM domain.	18108337, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264686, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742545 (5089, 5090)	Novel Protein sim: GBank gij3327048 gb BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]		29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 80170615, 264692, 33657109
2546	68093361 (5091, 5092)	Novel Protein sim: GBank gij1996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - UNCLASSIFIED Zinc finger, C3HC4 type (RING finger)	29331824, 265007, 22279002

2547	94143868 (5093, 5094)	Novel Protein sim. GBank gi 492907 gb AA034064.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	Transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56994075, 22278996, 22278997, 22278999, 264259, 29331622, 28331824, 29331826, 60432289, 29331827, 3599052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 60431735, 264594, 60433438, 21900754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264389, 264684, 264686, 264687, 56181562, 264689, 264689, 21900765, 21906768, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27485261, 18108370, 18108374, 55810764, 55811576, 35996423, 35995855, 264635, 264636, 264355, 264637, 263981, 264557, 18108380, 264638, 56182323, 264356, 264359, 83373044, 18108385, 87168518, 22279002, 264564, 264566, 264489
2548	88179079 (5095, 5096)			UNCLASSIFIED	264488, 18108394, 52646385, 22278994, 3599268, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 28331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 33651023, 264682, 18108374, 52644332, 264657, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264593, 264597
2549	94156853 (5097, 5098)	Novel Protein sim. GBank gi 28637 sp 39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III	Contains protein domain (PF00412) - LIM domain containing proteins	struct	55182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 28331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108388, 60431602, 18108376, 35996423, 56182323, 18108387, 264567, 56182575, 29331822, 264105, 264512, 18108351, 35995917, 264637, 264638
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 j L52523 - nucleoprotein [p2 homolog - rat (fragment)]		UNCLASSIFIED	

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gi 4337103 g AAD180791 - (AF129756) NC26 (Homo sapiens)	Contains protein domain (PF00561) - alpha-beta hydrolase fold	UNCLASSIFIED	18100386, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35696423, 264639, 56182323, 63373044, 22279000
2552	95332820 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264506, 264907, 56182435, 265008, 264591, 33109954, 264780, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695655, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gi 1711059 g P54797 T10_MOUSE - SERVTHR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264766
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gi 728535 g P39192 ALUS_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		catenin	22278997, 29331822, 264506, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gi 4084319 g CAB43280.1 - (AL050834) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gi 4106994 (AC003039) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695655, 264556, 264567, 264595
2557	78437803 (5113, 5114)	Novel Protein sim. GBank gi 119110 g P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gi 4538999 g CAB39619.1 - (AL049481) AG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331826, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gi 5051399 g CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264256, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87168556, 265017, 265018, 265019, 264689, 21906766, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168516, 22279002
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gi 5051399 g CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Mus musculus]		UNCLASSIFIED	
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gi 526822 g A042056.1 AF04495 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gij4106984 (AC003039) - R30923_1 [Homo sapiens]	UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433366, 21900765, 55811957, 60170615, 33957023, 264693, 35695855, 87168518, 264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21900767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486282, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264586, 264486
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gij4868447/embjCAB43371_1 - (AL050270) hypothetical protein [Homo sapiens]	UNCLASSIFIED	29331822, 265007, 265010, 265019, 264789, 55811576, 56182333
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gij13529449/pj471791_jgp_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR	sulfotransferase	66714117, 264909, 263978, 264632
2565	85530908 (5128, 5130)	Novel Protein sim. GBank gij26012/pj1A53933 - myosin I myr 4 - rat	UNCLASSIFIED	18108370, 35695855, 264556, 264558, 18108383
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gij26012/pj1A53933 - myosin I myr 4 - rat	Contains protein domain (PF00083) - struct	265020, 60170615
2567	86143590 (5133, 5134)	Novel Protein sim. GBank gij466008/pj345481YNUA_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III	synthase	60424179, 18108384, 56181666, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264789, 21900766, 21906767, 18108352, 265021, 33657023, 18108362, 35695917, 33657182, 35695763, 50431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482
2568	97233099 (5135, 5136)	Novel Protein sim. GBank gij466008/pj345481YNUA_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		

2569	96313764 (5137, 5138) Novel Protein sim. GBank gi2599560 g A4894166.1 - (A4828674) basic leucine zipper protein LZ1P [Homo sapiens]	Contains protein domain (PF001170) - bZIP transcription factor	-transcriptionfactor	16108394, 56102375, 56161886, 22278995, 22278996, 56949075, 36666286, 22278997, 22278998, 22278999, 264259, 60432048, 29331822, 56102181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 36666052, 264905, 264906, 36162435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21906754, 87168599, 265017, 265018, 265019, 264682, 264446, 264288, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 36695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 36695763, 20281059, 263974, 18108374, 55810764, 36696423, 36695855, 264556, 18108381, 56102323, 18108382, 83373044, 18108385, 56268486, 37168516, 22279000, 22279002, 265586
2570	94135754 (5139, 5140) Novel Protein sim. GBank gi475854 e NP_004567.1 p PP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 32), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR35	phosphatase	22278998, 29331822, 29331824, 68714117, 29331825, 60432289, 29331827, 36696092, 264907, 264510, 265007, 265008, 264758, 3310994, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 36695855, 264634, 56102323, 264635, 60170394, 53373044, 22279002, 264442
2571	87733750 (5141, 5142) Novel Protein sim. GBank gi173278 e p P34809 Y060_CAEEL - HYPOTHETICAL 128.8 KC PROTEIN ZK1096.10 IN CHROMOSOME III		strut	264508, 264905, 264907, 264628, 18108351, 264555, 264556, 264597, 264598, 264599
2572	87627560 (5143, 5144) Novel Protein sim. GBank gi4684319 e p CAG43260.1 - (AL050084) Hypothetical protein [Homo sapiens]		UNCLASSIFIED	36696286, 29331827, 36696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29146628, 263972, 263974, 18108374, 263976, 36695855, 60170394, 264599, 18108385

2573	95313928 (5145, 5146)	Novel Protein sim. GBank g199139isp02745ICTQA_HUMAN - COMPLEMENT C10 SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181686, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21908754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21908766, 21906767, 29148627, 21906768, 21908769, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108366, 27486285, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 56182323, 60170394, 83373044, 18108394, 87168518, 60432113, 264482, 264564, 264585, 264566, 264567, 264568, 264569, 264570, 264571, 264572, 264573, 264574, 264575, 264576, 264577, 264578, 264579, 264580, 264581, 264582, 264583, 264584, 264585, 264586, 264587, 264588, 264589, 264590, 264591, 264592, 264593, 264594, 264595, 264596, 264597, 264598, 264599, 264600, 264601, 264602, 264603, 264604, 264605, 264766, 21906769, 264628, 264630, 264634, 264639, 264663, 29331822, 29331824, 264767
2574	84146814 (5147, 5148)	Novel Protein sim. GBank g13334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTBPOZ domain	UNCLASSIFIED	22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264931, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21908765, 21906766, 21906768, 55811857, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486281, 27486284, 33657349, 264636, 264555, 83373044, 18108385, 264482
2575	87734408 (5149, 5150)	Novel Protein sim. GBank g1929729jgbAAD34125 (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264910, 264901, 264883, 264889, 264900
2576	95357881 (5151, 5152)	Novel Protein sim. GBank g14600681jgbAAD27730 (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxy-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264906, 60433438, 264691, 18108351, 264288, 52644150, 264628, 35696423
2577	86996821 (5153, 5154)	Novel Protein sim. GBank g1337103jgbAAD18079j - (AF129756) NC28 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87768941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264766, 21906769, 264628, 264630, 264634, 264639, 264663, 29331822, 29331824, 264767
2579	87392879 (5157, 5158)			UNCLASSIFIED	

2580	88166788 (5159, 5160)	Novel Protein sim. GBank.gj268628 (AC003080) - Similar to KIAA0299, 60% similarity to AB002297 (PID.g2224539) [Homo sapiens]			265507, 265018, 264782
2581	87899048 (5161, 5182)	Novel Protein sim. GBank.gj4406542[gj4A020049] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00395) - collagen POZ domain (Also known as DHR or GLGF).		56954075, 29331824, 29331826, 29331828, 264905, 60433366, 60433438, 264788, 87169559, 21906769, 265022, 35695855, 263981
2582	87796789 (5163, 5164)	Novel Protein sim. GBank.gj2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]	eph		264488, 264907, 264908, 264910, 264784, 264684, 264766, 264638, 264555, 264565
2583	91220950 (5165, 5166)	Novel Protein sim. GBank.gj4378112[emb]CAA15521.1] - (AL021578) DJ453C12.2 (similar to transcription factor RBP-1) [Homo sapiens]	Contains protein domain (PF00047) - transcripflator Immunoglobulin domain		56181686, 264229, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264585
2584	80430941 (5167, 5168)		UNCLASSIFIED		264908, 264910, 264788, 264693, 18100374, 55811578, 56182323
2585	80436176 (5169, 5170)	Novel Protein sim. GBank.gj2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]	kinase		264788
2586	91226136 (5171, 5172)				22278988, 264229, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433366, 33657402, 265018, 264782, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56528486, 22279002
2587	80430943 (5173, 5174)				264908, 265019, 264788, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)		UNCLASSIFIED		264584
2589	85515607 (5177, 5178)	Novel Protein sim. GBank.gj302159[emb]CAA71415] - (Y10399) nuclear protein [Xenopus laevis]	UNCLASSIFIED		33596032, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264789, 35696423, 264636
2590	87054426 (5179, 5180)	Novel Protein sim. GBank.gj2104689 (U62793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01035) - glucoamylase Glycosyl hydrolases family 31		22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank.gj570202[gb]/AA047199.1[AF12916] - long-chain acyl-CoA synthetase 5 [Homo sapiens]	eph		264259, 29331832, 264106, 264906, 56182435, 265007, 265008, 33108954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank glj3024998sp Q6036 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN	transport	18108397, 56182275, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433366, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 56182323, 83733044, 56526486, 87168518, 264583, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank glj4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]	tm7	22278999, 29331825, 264756, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906766, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank glj4929587 gb AAD34054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]	UNCLASSIFIED	264488, 18108368, 35182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 68714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 2933975, 2933977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567
2595	75561678 (5189, 5190)	Novel Protein sim. GBank glj4309681 gb AAD154781 - (ACD06930) R33423.1 [Homo sapiens]	UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 60431528
2596	87538637 (5191, 5192)		UNCLASSIFIED	264905, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2597	94784089 (5193, 5194)		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21906766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264554, 264595
2598	86094948 (5195, 5196)	Novel Protein sim. GBank glj1001351 gb BA108381 - (D64006) hypothetical protein [Synchocystis sp.]	MHC	264756, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264669
2599	87642889 (5197, 5198)	Novel Protein sim. GBank glj3941737 (AF109719) - BA12 [Mus musculus]	kinase receptor	35696286, 264093, 264288, 21906769, 35696423, 35695855
2600	87787846 (5199, 5200)	Novel Protein sim. GBank glj48532 gb AAD153471 - (ACD00404) putative WD-repeat protein [Arabidopsis thaliana]		

2601	91243070 (5201, 5202)	Novel Protein sim. GBank g172837ispj39194JULUT_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	56182575, 22278996, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264906, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18106351, 264448, 264369, 21906769, 265020, 60170615, 2644693, 33657109, 18108370, 18108376, 56162323, 18108381, 18108385, 22279002, 264563 60433438, 21906754, 21968559, 264601, 264369, 264288, 21906767
2602	88100022 (5203, 5204)	Novel Protein sim. GBank g1406632(gpIAJ20047) - (AF131801) Unknown [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 22278996, 22278998, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696002, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486282, 18108374, 35696423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2604	94876601 (5207, 5208)	Novel Protein sim. GBank g15454030(jef)NP_006488.1jPRRP2 - RAS-related on chromosome 22	oncogene	264259, 35696002, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank g13628745(gpBA33366) - (AB013721) mltugumin 23 [Oryctolagus cuniculus]	UNCLASSIFIED	22278998, 264480, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18106351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636 22278996, 264510, 264512, 265009, 264766, 22279002, 264566
2606	87746406 (5211, 5212)			

2607	87627742 (5213, 5214)	Novel Protein sim. GBank g1482626[gb AA030202.1] - (AF135022) mediator [Homo sapiens]		29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21906765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank g1226005 (U48973) - ORF2; function unknown [Homo sapiens]	Contains protein domain (PF00850) - Histone deacetylase family	264488, 65374572, 35096286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433436, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264768, 264689, 21906765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486281, 18108370, 65274791, 264636, 264556, 56182323, 18108395, 56526486
2609	94843791 (5217, 5218)	Novel Protein sim. GBank g1302488[gb 565241Y286_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (H46116)]	histone	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263987, 33657182, 27486281, 18108374, 263976, 55811576, 264639, 87168518, 60432113, 22278999, 265017, 264684, 21906768, 22279000
2610	88177654 (5219, 5220)	Novel Protein sim. GBank g1433685[gb A017989] - (AF100473) leucine-rich domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]	transcription factor	265009, 264910, 264759, 265017, 21906767, 18108395, 18108398, 60432113
2611	87428890 (5221, 5222)	Novel Protein sim. GBank g1397676[emb CA92994] - (Z68760) predicted using GeneFinder. Similarity to Mouse FKBP-binding protein (SW-FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	264885
2612	87771198 (5223, 5224)	Novel Protein sim. GBank g1567913[gb AA046874.1]AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport	UNCLASSIFIED
2613	79481496 (5225, 5226)	Novel Protein sim. GBank g1553308[gb AA045009.1]AF16118 - (AF161181) P5ST protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase	22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52844229, 21906765, 33657109, 27486284, 18108370, 263972, 264555, 60432113
2614	87643948 (5227, 5228)	Novel Protein sim. GBank g1553308[gb AA045009.1]AF16118 - (AF161181) P5ST protein [Mus musculus]	UNCLASSIFIED	264768, 18108394, 264682, 264693, 264508, 264509, 264807, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766
2615	87331996 (5229, 5230)			

2616	81428895 (5231, 5232)	Novel Protein sim. GBlank g1307676 [Iemb]CA02994] - (260760) predicted using GeneFinder. Similarity to Mouse PK36-binding protein (SWIFR3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 6043438, 33108954, 87168474, 265011, 265017, 265019, 264288, 264766, 21906765, 21906767, 265020, 265021, 18108376, 18108377, 18108380, 87168518, 264482, 264587
2617	86976888 (5233, 5234)	Novel Protein sim. GBlank g17263318 [P318]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264389, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBlank g1313282 (AF49103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278986, 264490, 264259, 29331822, 264102, 264509, 264906, 264907, 86712502, 29331830, 265006, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264389, 264288, 264766, 264788, 264889, 21906765, 21906766, 21906787, 35895917, 265020, 265022, 33637023, 264892, 33657109, 264628, 18108374, 35895845, 18108381, 83373044, 18108385, 18108388, 9526486, 264593
2619	87694000 (5237, 5238)	Novel Protein sim. GBlank g12431772 (U66411) - putative type II alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21906754, 264389, 60432113, 264586
2620	95314841 (5239, 5240)	Novel Protein sim. GBlank g14322567 [g14322567] - (AF030436) dactshund variant 1 [Mus musculus]	Contains protein domain (PF0628) - PHD-finger	UNCLASSIFIED	52644507, 52645158, 52646842, 85274572, 22278995, 59994075, 35896286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35896052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264389, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35895917, 52644150, 264692, 33657109, 35895763, 35896423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 85274727, 87168518, 50432113, 22279002, 264594, 264638
2621	80253495 (5241, 5242)	Novel Protein sim. GBlank g1455734 [Ile]NP_001174.1 [pATPS - ATPase. H+ transporting, lysosomal subunit 1; vacuolar proton pump, H-ATPase subunit]			264488, 264908, 264907, 264908, 264512, 265007, 264758, 35895917, 264634, 264636, 264583, 264482
2623	91639306 (5245, 5246)	Novel Protein sim. GBlank g1308035 [Iemb]CA02994] - (262285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35896052, 265007, 265010, 264288, 29148529

2624	91639308 (5247, 5248)	Novel Protein sim. GBank.gli380355[emb]CAB052991 - (252285) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	56181686, 264299, 23278996, 23278997, 23278998, 23278999, 2331822, 29331824, 56182161, 29331825, 60433289, 29331828, 35696052, 29146499, 68712502, 52644045, 265007, 265008, 60433356, 33109954, 21906754, 265010, 265011, 265019, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695955, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86432068 (5249, 5250)	Novel Protein sim. GBank.gli2887429[dq]BAZ48571 - (AB007867) KIAA0427 [Homo sapiens]	UNCLASSIFIED	264091, 264511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank.gli47416 (L20302) - actin filament protein [Gallus gallus]	struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank.gli68462[pri]A27307 - proline-rich phosphoprotein [gene PRH1, Do allele] - human	UNCLASSIFIED	22278996, 265007, 265009, 264448, 21906767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank.gli312355[emb]CAA186091 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0268 LIKE) [Homo sapiens]	UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264389, 264288, 18108357, 21906765, 21906766, 265022, 65274791, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank.gli492595[pb]A034058.1AF15182 - (AF151821) CGI-83 protein [Homo sapiens]	synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79183364 (5259, 5260)	Novel Protein sim. GBank.gli321605[pri]JQ1181 - Gag protein - Viana virus (strain EV1)	UNCLASSIFIED	264638, 18108395
2631	94845909 (5261, 5262)	Novel Protein sim. GBank.gli321605[pri]JQ1181 - Gag protein - Viana virus (strain EV1)	Contains protein domain (PF00036) - dms_rna_bind Zinc finger, CCHC class	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 56940765, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331828, 264905, 264509, 264907, 264908, 264511, 264512, 264507, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264780, 264782, 264448, 264288, 264389, 264766, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52644150, 33657023, 52645128, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486, 264685
2632	36730414 (5263, 5264)			

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gii1139548[idjBAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264906, 265006, 265007, 265009, 55612038, 33657084, 55611386, 265010, 265011, 87168559, 265016, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811576, 264639, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264555
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gii541161[emb]CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gii4580663[gb]A02721.1[AF13294] CGI-12 protein [Homo sapiens]		22278997, 264259, 29331824, 56714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811576, 35695955, 87168518, 22279000
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gii387914[emb]CA807646] - (Z93386) Similarly to Yeast hypothetical 52.9 KD protein (SW-PA3516); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	264589, 29331822, 29331826, 265008, 60170831, 264681, 264765, 264685, 29148627, 21906766, 29148784, 265022, 60170515, 264635, 18108385, 56526488, 22279002, 264567
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gii4758208[ref]NP_004081.1[tpDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)]	Contains protein domain (PF00782) - phosphatase Dual specificity phosphatase, catalytic domain	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 86714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644286, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 65274620, 27486294, 18108370, 264628, 264629, 18108374, 35696423, 35696855, 264632, 264634, 264635, 264637, 264638, 5264332, 264639, 264558, 83373044, 60432113, 264554, 264555, 264586, 264486, 264587

2638	94320733 (5275, 5276)	Novel Protein sim. GBank gl4929689gbl/AAD34105 (AF15186) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424170, 5264507, 5264684, 1810838, 5618275, 2277895, 2277896, 35696286, 2277897, 2277899, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 264905, 5264405, 56182435, 60433356, 33657402, 55812038, 55811386, 265019, 264286, 264769, 52644229, 56181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810764, 35696423, 55811576, 35695955, 60431650, 56182323, 60432113, 2644404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank gl12190007dbj/EAA20355) - (AB004109) phosphatidylserine synthase II [Cricetus griseus]		synthase	264486, 29331825, 35696052, 264508, 264509, 264909, 264512, 33657402, 60433438, 264758, 8659542, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264593, 264564, 264565, 264566, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gl135516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) -Helicases conserved C-terminal domain	helicase	29331822, 29331828, 264906, 33109954, 265017, 265019, 21906769, 35695783, 264636, 264837, 18108387
2641	11669834 (5281, 5282)	Novel Protein sim. GBank gl12564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)			UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526486, 22779002
2643	87643981 (5285, 5286)	Novel Protein sim. GBank gl4480304lemb/CAB39795.1) - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAF box helicase	helicase	22778997, 264255, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264665, 264686, 29148927, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264559, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gl3789797gbl/AAG57502.1) - (AF059569) actin binding protein MAYEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	-nucd_recpt	264107, 264687
2645	11727228 (5289, 5290)	Novel Protein sim. GBank		UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	gl17067222sp/P49749JEVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264908, 264687, 264632, 83373044

2647	91212978 (5293, 5294)		UNCLASSIFIED	56182575, 22278996, 35696285, 22278998, 264259, 29331822, 56182181, 303311281, 60424269, 60432289, 35696052, 58712302, 264908, 265007, 55812038, 33109954, 21906744, 33657094, 265019, 264446, 264288, 56181562, 21906755, 21906766, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431828, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)			29146488, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113, 56182575, 22278998, 22278999, 29331824, 29331828, 60432289, 60712902, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264686, 264888, 21906765, 21906768, 60170515, 264693, 263967, 18108370, 263976, 60170394, 60432113, 22279002, 264653, 264685
2649	94128783 (5297, 5298)	Novel Protein sim. GBank glj3041852 (AC004539) - unknown function; similar to Y09105 (PID31666171) [Homo sapiens]	UNCLASSIFIED	29331824, 29331828, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2650	87297533 (5299, 5300)	Novel Protein sim. GBank glj5360271[dj]BAA481903.1] - (AB028335) HPET-3 [Haloquithia roretzi]		
2651	86088745 (5301, 5302)	Novel Protein sim. GBank glj420223[dj]BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]		
2652	10343126 (5303, 5304)	Novel Protein sim. GBank glj449395[emb]CAB11123.2] - (289551) predicted using hexExon; MAL3P5.28 (PFC0845c), Hypothetical protein, lin. 167 aa. Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe), C.elegans protein YK287.5 (TR....	UNCLASSIFIED	26508, 18108370, 18108387, 264566
2653	87798735 (5305, 5306)		UNCLASSIFIED	
2654	95103240 (5307, 5308)			
2655	91228018 (5309, 5310)	Novel Protein sim. GBank glj387527[emb]CAB02861.1] - (281051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST y4443h5.3 comes from this gene; cDNA EST y4443h5.5 comes from this gene [Caenorhabditis elegans]	transcript factor	60424179, 65274372, 56182075, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727, 56182575, 56181686, 264092, 264259, 56182181, 60432280, 264807, 33657402, 55812038, 21906754, 87198559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264356, 264639, 83373044, 55526486, 264404, 60432113
2656	84562601 (5311, 5312)	Novel Protein sim. GBank glj3043718[dj]BAA25223.1] - (AB011159) KIAA0897 protein [Homo sapiens]		264693

2657	52551728 (5313, 5314)	Novel Protein sim. GBank glj568509[glj]BAA83038.1) - (AB029009) KIAA1085 protein [Homo sapiens]		dna_na_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank glj368089 (AC005757) - R32611_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleasamb	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21906768, 35696917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87600745 (5317, 5318)	Novel Protein sim. GBank glj5420387[emb]CAB46679.1) - (A243459) proteophosphatase [Leishmania major]	Contains protein domain (PF01429) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264789, 21906769, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank glj728837[sp]P39194[Jul]_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00030) - EF hand	kinase	264488, 65274572, 35696286, 22278988, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264906, 56182435, 265008, 265009, 6043356, 264594, 265010, 265018, 5811130, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279002, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank glj758048[ef]NP_004739 [I]pCPR8 - cell cycle progression 8 protein		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264909, 264583, 33109954, 265010, 265017, 265018, 265018, 264780, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27486262, 60431528, 18108374, 35695855, 18108388, 264482, 264555, 264556, 264558, 264486
2662	80228739 (5323, 5324)	Novel Protein sim. GBank glj38747[emb]CAB91263) - (Z68494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264906, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2663	87780623 (5325, 5326)	Novel Protein sim. GBank glj389670 [U58977] - Notch homolog Scalloped wings [Lucilia cuprina]	Contains protein domain (PF00009) - EGF-like domain	oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2664	85518329 (5327, 5328)	Novel Protein sim. GBank glj389670 [U58977] - Notch homolog Scalloped wings [Lucilia cuprina]		UNCLASSIFIED	35696286, 22278989, 29331822, 35696052, 264906, 264907, 264510, 264511, 264512, 264583, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264485
2665	87770682 (5329, 5330)	Novel Protein sim. GBank glj468440[emb]CAB43311.1) - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2666	87826472 (5331, 5332)	Novel Protein sim. GBank glj5106956[glj]AAD3906.1)AF11361) - (AF11361) FH1F2 domain-containing protein FHO3 [Homo sapiens]	Contains protein domain (PF01130) - 3' exononuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567
2667	87422720 (5333, 5334)	Novel Protein sim. GBank glj505070[sp]Q17533[RNP]CAEEL - RIBONUCLEASE PH-LIKE PROTEIN 50564.1		nuclease	

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454168 ref NP_006327.1 pZYG1-ZYG homolog	UNCLASSIFIED	56181686, 35695286, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35695052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906766, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264682, 33657109, 35695763, 60431528, 18108374, 35696423, 56811576, 264634, 60431850, 83373044, 18108385, 87168518, 22279000, 264553, 264554
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 ref UC4809 - prolins rich protein - rat	UNCLASSIFIED	264439, 264689, 21906767, 65274572, 56182575, 21906768, 29314827, 21906769, 29148629, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170615, 52644150, 60432048, 264259, 264691, 33657023, 60432289, 33657109, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29146488, 29146499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265008, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2870	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1725253 ref C10852 YD8B_SCHPO - HYPOTHETICAL 84.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	18108370, 263974
2871	91214936 (5341, 5342)	Novel Protein sim. GBank gi 475827 ref JA029444.1 aF064255 - very long-chain acyl-CoA synthetase homolog 2, V LCS-H2 (Homo sapiens)	transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27466261, 27466262, 27486265, 18108376, 18108385
2872	87399123 (5343, 5344)	Novel Protein sim. GBank gi 496346 ref JA034677.1 AC09834 - (AC098341) Contains two PF01344 Kelch motif domains. (Arabidopsis thaliana)	UNCLASSIFIED Kelch motif	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank g 15457337 mb JCAB41505.2 - (A23876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331826, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33857109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank g 4758524 e NP_004280.1 NRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00710) - bZIP transcription factor	transcription factor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85656542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79528393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	94329600 (5353, 5354)	Novel Protein sim. GBank g 1079042 mj S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme	- synthase	18108394, 65274572, 35182575, 22278994, 22278995, 35696075, 22278996, 35696286, 22278997, 22278999, 264490, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 23146499, 29331830, 284908, 52644045, 265006, 265007, 265008, 265009, 60432229, 60433356, 80434338, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 284448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33857023, 263987, 33857109, 27486264, 27486265, 33857349, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695655, 83373044, 18108387, 22279000, 22279002, 264584

2678	95001684 (5355, 5356)	Novel Protein sim. GBank gji68760[pilj]A04045 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52646842, 35698286, 22278999, 264259, 29331825, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 17168559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264783, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108394, 18108374, 35696423, 33657349, 264628, 18108374, 35696423, 35695955, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gji170923[lp07514]NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase		264488, 22278999, 35695286, 264259, 29331826, 29331827, 29331828, 284909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85655542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35698423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264567
2680	87600356 (5359, 5360)	Novel Protein sim. GBank gji458950[dqj]BAA76824.11 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - struct EF hand		264259, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264788, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gji728837[spj39194]ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase		264489, 22278999, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264784, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264488
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gji423468[pqj]JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35695286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431828, 55810764, 55811576, 35696423, 65274791, 56526486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gji511351[spjA040286.11] - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - interleukinrecept		264909, 264765, 264635, 264636

2687	91638472 (5393, 5394)	Novel Protein sim. GBank gij5689473[dbj BAA83020.1] - (A8028981) KIAA1068 protein [Homo sapiens]	UNCLASSIFIED	3566286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264781, 18108351, 264448, 264286, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2688	94325891 (5395, 5396)	Novel Protein sim. GBank gij441316 (U22818) - mutant sterol regulatory element binding protein-2 [Oricotulus griseus]	transcript factor LIM domain containing proteins	22278995, 35665286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264908, 5284045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52844150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)	Novel Protein sim. GBank	UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2700	94138638 (5399, 5400)	Novel Protein sim. GBank gij5174395[ref NP_005006, 1pB120 - Brain protein 120 gene product [Caenorhabditis elegans]	UNCLASSIFIED	18108394, 52845158, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gij1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]	UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2702	57295366 (5403, 5404)	Novel Protein sim. GBank gij1605967 (AF030027) - 24 [Equine herpesvirus 4]	UNCLASSIFIED	60432289, 265007, 21906765, 21906768, 265021, 264693
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gij1685939[dbj BAA82983.1] - (A8028954) KIAA1031 protein [Homo sapiens] (end similar)	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type	

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gij4335654[igp/AB63294] - (AF008554) Implantation-associated protein [Rattus norvegicus]		264488, 22278995, 22278998, 29331828, 29146499, 264905, 264906, 264907, 52844045, 264511, 33657402, 264600, 256402, 265017, 264605, 264781, 18108351, 264764, 264687, 264769, 265021, 264691, 264692, 18108362, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5408, 5410)			264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264789, 264638, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gij255952[emb/CAA16821.1] - (AL021728) /prediction={method:,match={desc: [Drosophila melanogaster]}	UNCLASSIFIED	264488, 52646842, 65271572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33656670, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 60433438, 55812038, 21906754, 52644296, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264688, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33657033, 264692, 264693, 65274820, 27486284, 263972, 18108374, 18108377, 264635, 264636, 264556, 80170394, 83373044, 65271727, 87168518, 22279000, 22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2707	88089639 (5413, 5414)	Novel Protein sim. GBank gij3417294 (AC004381) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565
2708	91071351 (5415, 5416)	Novel Protein sim. GBank gij545790[bsi/147178 - DARPP-32-dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]		25331822, 18108370, 18108374, 63373944
2709	94853888 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F1127_1 [Homo sapiens]	UNCLASSIFIED	25331824, 264759, 264693, 18108382, 18108388
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gij446831 [emb/CA837692] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gi3122400sp O35682 MG_MOUSE - MYELOID UPREGULATED PROTEIN	UNCLASSIFIED	264488, 264687, 52645156, 264769, 21906764, 21906765, 21906767, 21906768, 21906769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 00424269, 29331826, 33657182, 29331827, 27465652, 33657349, 264506, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264555, 264764, 264566, 264286, 264766
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi508131 gi AAD9343.1 AF07680 - (AF076807) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain - transferase	264488, 35696285, 22278998, 264259, 29331824, 00432289, 35696052, 264506, 264908, 66712502, 52644045, 265006, 60432229, 33657402, 60433358, 285010, 265019, 18108351, 264681, 264286, 264685, 21906765, 21906766, 21906768, 21906789, 55811957, 35695917, 265020, 265021, 60170815, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 55182323, 87168518, 60432113 66714117, 264606, 264563
2713	88003004 (5425, 5428)	Novel Protein sim. GBank gi2477513 (AC002398) - F25865_3 [Homo sapiens]	UNCLASSIFIED	264693
2714	13528218 (5427, 5428)	Novel Protein sim. GBank gi432196 gi AAD158971 - (AF007430) Smerca1-related protein [Mus musculus]	UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gi2477513 (AC002398) - F25865_3 [Homo sapiens]	UNCLASSIFIED	264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003008 (5431, 5432)	Novel Protein sim. GBank gi2477513 (AC002398) - F25865_3 [Homo sapiens]	glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264369, 264693, 264556, 264563
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi332704 gi BAA315911 - (AB014516) KIAA0616 protein [Homo sapiens]		264593, 264558
2718	79604062 (5435, 5436)	Novel Protein sim. GBank gi746495 (U23515) - weakly similar to gastrin zinc finger protein [Caenorhabditis elegans]	UNCLASSIFIED	264693
2719	88180423 (5437, 5438)			29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gi 335873 (U46896) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	18108374, 60424176, 264489, 561922335, 21906765, 21906766, 35696423, 22278997, 265020, 265022, 265006, 265008, 264992, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108366, 6042489, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 68712502, 52644045, 264909, 264908, 264828, 18108354, 22278995, 35696286, 264259, 29331822, 29331824, 68714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906768, 265021, 33657109, 263969, 80431526, 264629, 55811576, 65274791, 35696855, 264631, 264637, 60170394, 55182323, 22279000
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gi 492863 (gi AD304092.1) AF151855 CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023	35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2722	91639807 (5443, 5444)	Novel Protein sim. GBank gi 3212997 (gi AC23434.1) - (AC004997) match to ESTs AA667999 (NID-g262700), AA165465 (NID-g1741481), Z45871 (NID-g51505), and TB4026 (NID-g712314); similar to various tre-like proteins including: AF040654 (PID-g2746883), D13644 (PID-g2104571), AL02114,.....	Contains protein domain (PF00566) - oncogene TBC domain	264508, 264509, 264906, 264909, 264910, 55812038, 264766, 264687, 264629, 264636, 264486
2723	87387732 (5445, 5446)		UNCLASSIFIED	
2724	87639583 (5447, 5448)	Novel Protein sim. GBank gi 468088 (gi AD27730.1) AF132955 CGI-21 protein [Homo sapiens]	ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gi 3169705 (AC004780) - F17122_1 [Homo sapiens]	UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86980599 (5451, 5452)	Novel Protein sim. GBank gi 3342738 (AC005328) - IR26660_1, partial CDS [Homo sapiens]	MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi 71327139 p39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (ARIL HYDROLASE)	Contains protein domain (PF00849) - RNA pseudouridylate synthase	- synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 56714117, 29331826, 29331827, 35696052, 29331828, 33656970, 264509, 66712502, 264910, 33657402, 60433438, 264758, 55612038, 21906754, 33657084, 55611386, 265018, 285019, 264767, 21906765, 21906767, 21906769, 55611957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486281, 27485282, 27486285, 33657349, 55611576, 35696423, 35695955, 264630, 60431850, 264636, 56182323, 87166518, 60432113, 22279000, 264584, 264585
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3860433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein, cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55611957, 35695955, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408093 emb CAB16300 - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55611957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3860433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein, cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55611957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 56528486, 264556, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 17232399 p10168 YAU8_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265006, 267558, 267162, 264448, 264288, 29148627, 21906769, 87166518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3860433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein, cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264488, 18108358, 56182435, 264689, 35696423, 55611957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87166518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264369, 264567
2733	87353060 (5465, 5466)	Novel Protein sim. GBank gi 4519821 p b BAA75670.1 - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00710) - bZIP transcription factor	UNCLASSIFIED	29331825, 264508, 264909
2734	94140286 (5467, 5468)			transcriptador	60424178, 52644507, 56182575, 264259, 29331828, 264910, 264910, 60433556, 265019, 55611150, 264661, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5468, 5470)	Novel Protein sim. GBank g 3850589 (AC005278) - ESTs g0121276, g0145403, and g01A586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278986, 60432289, 29331827, 29146498, 264108, 264909, 264112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247855 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264680
2738	85731008 (5475, 5476)	Novel Protein sim. GBank g 25858501 b BAA22886 - (D38350) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264488, 265009, 264766, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank g 5420337 emb CAB46679.1 - (A24349) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank g 3417386 emb CAA76495 - (Y15187) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 60432233, 33657402, 55812038, 87168474, 285010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 5274727, 22279002, 264564
2741	86047518 (5481, 5482)	Novel Protein sim. GBank g 3242764 (AC005154) - similar to protein U9828 (P1D3851305) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21906769, 265020, 60170815, 264691
2742	87646844 (5483, 5484)	Novel Protein sim. GBank g 4758472 e NP_004472.1 pGALN - UDP-N-acetyl-alpha-D-glactosamine: polypeptide N-acetylglucosaminyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00052) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264905, 264758, 55812038, 264389, 28148627
2743	87627891 (5485, 5486)	Novel Protein sim. GBank g 4468337 emb CAB37992 - (A031432) GJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264906, 264908, 265006, 60433438, 264607, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264683, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank g 3880433 emb CAA91399 - (Z65521) similar to mitochondrial RNA splicing NSR4 like protein: cDNA EST EMBL.C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264485, 264369, 264288

2745	87740125 (5488, 5490)	Novel Protein sim. GBank g1402575pb/AA018826] - (AFC039803) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35698286, 264509, 264905, 264907, 264908, 264909, 264910, 264911, 264912, 265008, 264758, 264801, 265017, 264604, 264763, 264288, 264886, 264769, 264693, 35698423, 35695855, 264634, 264636, 264583, 264584, 264585
2746	95418601 (5491, 5492)	Novel Protein sim. GBank g14758738[INP_004680, IpnMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 264907, 264908, 264909, 52644045, 265006, 60170831, 264596, 55812038, 265018, 264683, 264288, 21908765, 21908767, 21908768, 21908769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank g14557803[INP_000262, IpnNPC1 - Niemann-Pick disease, type C1		glycoprotein	264569, 52644507, 18108394, 22278995, 35698286, 22278997, 22278999, 52645080, 29331824, 56182191, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811388, 87188474, 265010, 87188559, 264603, 265019, 264780, 264688, 264768, 21908769, 35695917, 60170815, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35696423, 35695855, 264556, 55182323, 18108385, 264482
2748	91214883 (5495, 5496)	Novel Protein sim. GBank g14191272[embCAA00984] - (A012295) apaG protein [Rizobium etli]	Contains protein domain (PF00549) - F-box domain.		65274572, 29331828, 264412, 264511, 265019, 264760, 264767, 264768, 264769, 21908768, 21908769, 265020, 27486262, 55526488, 87188518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264468, 52644507, 18108398, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank g11872408 (U74297) - PIUS (Cyclophilin)	UNCLASSIFIED		
2751	87057465 (5501, 5502)	Novel Protein sim. GBank g13041859 (AC004534) - OG-2	Contains protein domain (PF00046) - Homeobox domain	homeobox	29331822, 29331824, 265017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank g13041859 (AC004534) - OG-2 (PID:g157528) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5506)	Novel Protein sim. GBank gl 3651648 (AF098301) - neural F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278968, 29331822, 29331824, 29331825, 29331826, 285007, 284553, 58612038, 33108994, 18106351, 284286, 36181562, 21906767, 21906768, 265021, 264693, 18106374, 65274791, 264632, 36182323, 22279002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gl 535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	22278968, 68714117, 29331827, 35686052, 29331828, 264906, 264908, 264909, 265011, 265017, 265018, 265019, 264286, 21906768, 21906767, 265022, 35651023, 264693, 36182323, 18106382, 22279002
2755	88001472 (5509, 5510)	Novel Protein sim. GBank gl 2996653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcript factor
2756	11465908 (5511, 5512)	Novel Protein sim. GBank gl 1173339 (U30473) - putative src-like adapter protein, non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP. Method: conceptual translation supplied by author [Homo sapiens]	UNCLASSIFIED	264564
2757	95361590 (5513, 5514)	Novel Protein sim. GBank gl 3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]	Contains protein domain (PF00017) - Src homology domain 2	9563542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gl 2072220 (U94863) - p40 [Borna disease virus]	struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank gl 2072220 (U94863) - p40 [Borna disease virus]	struct	65274572, 35686286, 68714117, 29331828, 264606, 36182435, 21906754, 58611897, 264629, 264636, 36182323, 22279002
2760	78824788 (5519, 5520)	Novel Protein sim. GBank gl 4914573 (emb CAB43685.1) - (AL050390) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gl 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00023) - nuclease	22278968, 29331822, 29331830, 265010, 265019, 264286, 21906768, 21906769, 265020, 36182323, 22279002, 264563
2762	87592698 (5523, 5524)	Novel Protein sim. GBank gl 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00098) - PAS domain	18106394, 22278968, 264906, 264909, 265006, 265007, 264797, 265010, 265011, 265017, 265019, 18106351, 26444564683, 264696, 264768, 265020, 265021, 265022, 264891, 18106382, 264693, 18106385, 36557109, 18106386, 18106370, 18106381, 18106382, 18106394, 18106388, 87168518
2763	87539968 (5525, 5526)	Novel Protein sim. GBank gl 3511122 (AF060603) - zinc finger protein [Homo sapiens]	transcript factor	264389, 35969423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gl 2050643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGFG family of carbohydrate kinases	93648842, 264259, 29331822, 29331825, 29331826, 29331828, 35656970, 264605, 264907, 29331830, 265006, 265009, 21906754, 265019, 264446, 21906768, 27486262, 56182323, 36526486, 87168518, 264487

2765	94315106 (5528, 5530)	Novel Protein sim. GBank gji4689672[embjCAA17884.2] - (AL020218)/prediction:(method: - prediction:(method: - match)=(desc: [Drosophila melanogaster])		264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87168559, 264600, 265016, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56161562, 21906764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22279000, 22279002, 264563, 264482
2768	94315109 (5531, 5532)	Novel Protein sim. GBank gji4441611[embjCAB46854.1] - (A388555)/hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 80433358, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264835, 264555, 264558, 264557, 264638, 264558, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gji079451[prjA55463 - Tropomodulin, skeletal muscle - chicken]	struct	264412, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gji4441322[embjCAB46721.1] - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]	UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 25331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264767, 18108357, 264769, 264689, 21906766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264587

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gll4689132gblAAD27775.1(AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens])	Contains protein domain (PF00117) - Ribosomal protein S7pS5e	ribosomalprot	264488, 22278995, 56984075, 22278996, 35696288, 22278998, 22278999, 264239, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264682, 264365, 264298, 18108354, 52644229, 264695, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 63274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2778	87791557 (5551, 5552)				56182575, 22278998, 22278999, 264239, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 55811386, 265017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811576, 264555, 56526485, 22279000
2777	79818728 (5553, 5554)			UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264893, 264760, 264628
2779	87649728 (5557, 5558)	Novel Protein sim. GBank gll4680711gblAAD27745.1(AF13287 - (AF132870) CGI:36 protein [Homo sapiens])		UNCLASSIFIED	22278897, 264239, 29331824, 66714117, 35696052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gll758524[refNP_004625.1]pHGK1 - HPX/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29116489, 63274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gll468932gblAAD21223 - (AF068502) ubiquitin specific protease USP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182455, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gll4505013[refNP_002310.1]pLRN1 - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	63274872, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 26440045, 265009, 264908, 264909, 52644045, 265009, 264907, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264768, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264683, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016629 (5585, 5586)	Novel Protein sim. GBank glj72831[sp]p39188[ALU1_ HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]	tm7	264909, 264628, 263978, 263981
2784	87614360 (5587, 5588)			264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5589, 5570)	Novel Protein sim. GBank glj2134933[sp]j55890 - collagen response mediator protein - human	UNCLASSIFIED	22278999, 284908, 264758, 265018, 284769, 21906765, 21906768, 21906769, 265020, 264564
2786	87408542 (5571, 5572)	Novel Protein sim. GBank glj2073564 (J08223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCNZ [Drosophila melanogaster]	kinase	264905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank glj5174507[ref]NP_060020. [lpMA1] - paraneoplastic neuronal antigen	UNCLASSIFIED	264768, 21906765, 21906766, 55811957, 22278999, 284093, 60170615, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 284100, 264105, 264908, 263977, 55811576, 284635, 284637, 60433438, 80432113, 265017, 265019, 22279002, 55811150, 284369, 264288
2788	86090644 (5575, 5576)	Novel Protein sim. GBank glj3252826 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264103, 21906769, 264693
2789	85491275 (5577, 5578)	Novel Protein sim. GBank glj2495729[sp]Q92556[Y281_ HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)]	struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264908, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2790	87602784 (5579, 5580)	Novel Protein sim. GBank glj5101772[emb]CAB46135.1] - (AJ242378) p821 [Homo sapiens]		21906764, 18108368
2791	86083195 (5581, 5582)	Novel Protein sim. GBank glj2811266 (AC002550) - Unknown gene product [Homo sapiens]		22278996, 22278997, 284259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264908, 66712502, 29331830, 264909, 60432228, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264766, 52644229, 21906765, 21906766, 265020, 265021, 33657023, 263974, 18108374, 65274791, 35695855, 284636, 264556, 264558, 56182323, 83373044, 18108365, 56526486, 60432113, 22279000, 264567
2792	95083763 (5583, 5584)	Novel Protein sim. GBank glj2854163[sp]AAC02381.1] - (AF045642) No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	264259, 60432289, 66712502, 950509, 264636
2793	87425476 (5585, 5586)		UNCLASSIFIED	264689, 265022, 264691, 18108368, 284567
2794	85794830 (5587, 5588)		UNCLASSIFIED	

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gi 545146 ref NP_003348.1 pUBE2, ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBCA5)	Contains protein domain (PF00179) Ubiquitin-conjugating enzyme	-ubiquitin	65274572, 56182575, 35698286, 22278988, 22278989, 60432049, 264259, 29331822, 29331825, 80714111, 60432269, 29331826, 29331827, 35698092, 29331828, 265007, 90712502, 56182433, 2944511, 293356, 264512, 264910, 60432268, 265018, 60433436, 33109594, 85659542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906781, 21906789, 55811957, 265020, 265021, 265022, 26441150, 33657023, 264693, 65274620, 33657109, 35699423, 55811576, 65274791, 56182323, 55526486, 60432113, 22279002, 264482, 264583, 294494, 294587
2796	94848857 (5591, 5592)	Novel Protein sim. GBank gi 480851 gb AD27715.1 AF13294 - (AF13294) C91-06 protein [Homo sapiens]		UNCLASSIFIED	11005394, 65274572, 56182575, 56994075, 22278989, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35698092, 264509, 264908, 264907, 264908, 60712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264581, 264592, 60433398, 264594, 264585, 55812600, 264598, 21900794, 60174539, 91160674, 265010, 265011, 265017, 335138448, 55811150, 264762, 18106155, 264686, 264682, 264389, 264283, 264635, 264766, 264687, 56181582, 264765, 264688, 21906785, 21906766, 21906787, 21907788, 21906789, 55811957, 35695971, 265020, 265021, 60170015, 52644150, 264692, 33657023, 18108382, 264693, 65274620, 33657109, 33657162, 27466285, 33657349, 18108374, 35699423, 65274791, 35695959, 264596, 264597, 56182323, 264598, 60170394, 8337304, 65274727, 87168518, 22279000, 264583, 264584, 264586, 264587
2797	95110790 (5593, 5594)	Novel Protein sim. GBank gi 483557 gb AD31040.11 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278985, 22278986, 22278987, 29331827, 29146499, 264509, 264906, 56182435, 264797, 21900794, 265010, 265017, 265018, 264981, 264682, 264683, 264686, 21906785, 21906787, 21906788, 21906789, 29148629, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264583
2798	86198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264486, 264490, 264259, 26448, 20381149, 20281152, 264596, 264597, 264598, 264599, 264483, 264485, 264587

2799	86090651 (5597, 5599)	Novel Protein sim. GBank g 3252825 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	22278986, 22278997, 22278998, 22278999, 60432049, 264259, 29331826, 35696052, 29331828, 264909, 60433356, 33657402, 33109954, 87166474, 264448, 52644229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 60432113, 22279000
2800	88316481 (5599, 5600)	Novel Protein sim. GBank g 4240301[gb]BA74929.1 - (AB020713) KIAA0906 protein [Homo sapiens]	glycoprotein	264488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264786, 264886, 60170615, 264691, 264692, 27486285, 264628, 264629, 264636, 264557, 264596, 264559, 87168518, 264584, 264566, 264567
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain	265007, 264687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank g 2337865 (AC002464) - organic cation transporter-50% similarity to JC4884 (P1D-g21-3892) [Homo sapiens]	transport	264448, 35695855
2803	79577446 (5605, 5606)		UNCLASSIFIED	264639
2804	57111131 (5607, 5608)	Novel Protein sim. GBank g 559368[gb]AAD2029.1(AC00658) - (AC006585) hypothetical protein [Arabidopsis thaliana]	peptidase	264566
2805	8739486 (5609, 5610)		Contains protein domain (PF01585) - G-patch domain	264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	8789951 (5611, 5612)	Novel Protein sim. GBank g 1168973[gb]P44403[CLPB_HAEN - CLPB PROTEIN]	UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331828, 29331827, 29146496, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gj4468310mbjCAB378911 - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]	UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656870, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433438, 52646317, 2106754, 33109954, 33957084, 52644296, 67168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264667, 52644229, 21905765, 21905766, 21905767, 21906788, 21906789, 35695917, 285021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27466261, 27466262, 27466264, 27466265, 56955763, 18108370, 18108372, 18108374, 18108376, 2639770, 18108377, 35696423, 35695955, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95339111 (5615, 5616)	Novel Protein sim. GBank gj55418631embjCAB51071.11 - (AL096857) hypothetical protein [Homo sapiens]	MHC	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	89003530 (5617, 5618)	Novel Protein sim. GBank gj2772561 (AC004002) - similar to ciliary dynein beta heavy chain, 78% Similarity to P23098 (P1D.g118965) [Homo sapiens]	ATPase_associated	18108351
2810	87259032 (5619, 5620)			
2811	91235845 (5621, 5622)			
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gj3284553 (AC005189) - match to ESTs H97758 (NID.g1118643) and A0895546 (NID.g162873) [Homo sapiens]	UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29148629, 29148784, 264693
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gj424027jdbjBAA74915.11 - (AB020699) KIAA0892 protein [Homo sapiens]	UNCLASSIFIED	264106
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gj3348791 (AC005620) - R33590.1 [Homo sapiens]	UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811366, 265017, 265018, 265019, 265019, 264683, 265020, 87168518, 60432113
2815	79774521 (5629, 5630)		Contains protein domain (PF00170) - transcription factor	65274572
2816	95338229 (5631, 5632)	Novel Protein sim. GBank gj5420389embjCAB46580.11 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264907, 264909
2817			UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264750, 264681, 264766, 264769, 264689, 21905765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi1203846 (U56966) - coded for by C. elegans cDNA y30b3.5, coded for by C. elegans cDNA y30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 335695917, 33657109, 263978, 264634, 264636, 264639, 264594, 264565, 264566, 264486, 264567
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gi154986 (U13149) - possible apoprotein-associated protein [Peromyscus citellus]	Contains protein domain (PF00023) - Anky repeat	UNCLASSIFIED	56712502
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gi1492773gblAA034147.1AF15209 - (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52644365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi1399144lspip02747C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264638
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi12242671dqlpAA20820 - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433346, 33657402, 265011, 264760, 21906765, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi1399144lspip02747C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi1399144lspip02747C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264760
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gi3855683lamb3CAA22020 - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 335656970, 52644045, 52646317, 33657094, 52644286, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695955, 52644332, 18108385, 87168518, 264484

2827	85320518 (5653, 5654)	Novel Protein sim. GBank g 399144 sp p02747C10C_HUMAN - COMPLEMENT C1q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	- complement	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331822, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 264522, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 21906754, 265011, 264600, 264288, 264788, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264639, 264558, 83373044, 18108335, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91229615 (5655, 5656)	Novel Protein sim. GBank g 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	- phosphatase	29331822, 35698052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264686, 55811957, 18108370, 18108374, 55810764, 35698423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank g 4680689 gb AA02734.1 AF13295 - (AF132959) CGI:25 protein [Homo sapiens]			22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906765, 21906768, 21906769, 29148629, 52844150, 264693, 33857109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486
2830	88087106 (5659, 5660)	Novel Protein sim. GBank g 2488667 ep Q6200 NP1, MOUSE - NEUREXOPHILIN 1			265008, 265019, 264639, 22279002
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264686, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank g 5262815 emb CAB45747.1 - (AL080158) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank g 2224567 gb BA020772 - (AB020231) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank g 4589532 gb BA076788.1 - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank g 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	Transcript factor	264259, 264412, 265010, 264762, 264764, 263974, 264559, 264559, 264559

2837	87768482 (5673, 5674)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 22278697, 22278698, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gJ973378 (U31263) - core protein [Hepatitis C virus]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gJ157515 (U64999) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]	UNCLASSIFIED	264555
2840	87774655 (5679, 5680)	Novel Protein sim. GBank gJ224032[db]BA207901 - (AB002330) KIAA0332 [Homo sapiens]	UNCLASSIFIED	264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gJ334218 (AC004131) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2850	87623636 (5699, 5700)	Novel Protein sim. GBank gJ520387[emb]CA846679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 18108397, 264250, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567

2851	87820546 (5701, 5702)	Novel Protein sim. GBank g 4321619bp AA015788.1 - (AF051089) seven transmembrane domain orphan receptor. [Mus musculus]		UNCLASSIFIED	264905, 264807, 56182435, 264758, 55811366, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35695855, 264556, 18108385, 264587, 264381
2852	86987023 (5703, 5704)	Novel Protein sim. GBank g 1257379 (U88308) - similar to drosophila membrane protein PATCHED SP-18502 (P1258645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784530 (5705, 5706)	Novel Protein sim. GBank g 2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]			55182575, 55811150, 264680, 27160262, 27486265, 264632, 56182323, 55262486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank g 2795825 (AC004021) - keich protein, ring canal component involved in cytoplasmic bridges, 77% Similarity to A45773 (P1Dg107906) [Homo sapiens]			35696286, 26331824, 26331826, 26331828, 264908, 264768, 264693, 22279002, 264482
2855	94723556 (5709, 5710)	Novel Protein sim. GBank g 15004010 BAA13219 - (D68983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]			22278994, 26331822, 26331824, 26331825, 264906, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093358 (5711, 5712)	Novel Protein sim. GBank g 3264583 (AC005189) - match to ESTs H97758 (NIDg118643) and AA085546 (NIDg162873) [Homo sapiens]			21906766, 22278997, 265022, 26331822, 26331826, 27486262, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank g 3041855 (AC004537) - similar to tumor suppressor p53ING1; similar to AF044076 (P1Dg265920) [Homo sapiens]			22278995, 35696286, 26331824, 26331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank g 628359 P3327ME16_HUMAN - DNA-BINDING PROTEIN MEL-16 (ZINC FINGER PROTEIN 144)			264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 26331826, 26331827, 26331828, 264509, 264905, 264906, 26331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264784, 264765, 264288, 264389, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263881, 18108391, 264558, 18108385, 22279002, 264554, 264566, 264486, 264567
2859	90937675 (5717, 5718)	Novel Protein sim. GBank g 4325320 g AA017331.1 - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	264511, 264768, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2860	87532599 (5719, 5720)	Novel Protein sim. GBank g 446618 mb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial RNA (5-Methylaminomethyl-2-thiouridylic) Methyltransferases) (isoform 1) [Homo sapiens]	UNCLASSIFIED	264259, 26331822, 26331824, 26331825, 26331826, 26331827, 26331828, 264510, 264511, 33106954, 18108351, 264683, 264765, 241399, 264686, 21906785, 264691, 264692, 264693, 18108388, 22279002, 264482
2861	86699507 (5721, 5722)	Novel Protein sim. GBank g 3941730 (AF108083) - BSA [Homo sapiens]		264369, 264692
2862	87569365 (5723, 5724)	Novel Protein sim. GBank g 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein	UNCLASSIFIED	264691, 264693
2863	91220421 (5725, 5726)	Novel Protein sim. GBank g 3249038 (AC004473) - Contains similarity to goliath protein g 697204 from D. melanogaster, [Arabidopsis thaliana]	struct	56594075, 35696286, 22278998, 26331822, 26331824, 35696052, 26331828, 264106, 264511, 55812038, 33657094, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35696917, 265020, 265022, 33657023, 33657109, 33657349, 264629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank g 1107945 ref JAS5463 - Tropomodulin, skeletal muscle - chicken	struct	264259, 264810
2865	95312191 (5729, 5730)	Novel Protein sim. GBank g 436840 (L19048) - MSA-2 [Plasmodium falciparum]		22278995, 21906764, 264482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank g 585703 sp Q07065 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein	65274572, 22278996, 22278998, 22278999, 264259, 26331824, 26331827, 26331828, 60433438, 21906754, 265018, 264448, 264764, 52644150, 83373044
2867	86968001 (5733, 5734)	Novel Protein sim. GBank g 4580997 gb AA024571.1 AF12108 - (AF121081) CAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED	264488, 264768, 21906768, 22278998, 265022, 264259, 264508, 264905, 264907, 264511, 264910, 264635, 264636, 264637, 265011, 265017, 265018, 265019, 264583, 264088, 264586, 264764, 264369, 264567, 264486, 264288, 264766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gi1292668[emb CAA63923] - (X94232) t-Cell activation protein [Homo sapiens]	18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52644045, 264828, 265006, 265007, 265008, 265009, 264591, 60432229, 264593, 60433356, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108368, 27486251, 27486262, 27486264, 27486265, 18108370, 18108374, 35896423, 35695655, 264632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED
2870	84404574 (5739, 5740)		UNCLASSIFIED
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gi1530263[gb AAD41995.1]AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gi112205[pir B39066 - proline-rich protein 15 - rat	263981
2873	88094252 (5745, 5746)		UNCLASSIFIED
			264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264587, 264909, 264486, 264766, 18108391

2874	94313549 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52641156, 52646365, 56182275, 22278984, 22278995, 56894075, 35686286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35686052, 29331828, 33656870, 66712502, 52644045, 265007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 265018, 265019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88063726 (5748, 5750)	Novel Protein sim. GBank gij2781385 (AC004010) - similar to Leucine-rich transmembrane proteins; 41% similarity to U42767 (P101735918) [Homo sapiens]	Contains protein domain (PF000560) - glycoprotein Leucine Rich Repeat	22278996, 22278997, 22278999, 29331826, 29331828, 29146489, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gij2979530 (AC004449) - R33683, 2 [Homo sapiens]	Contains protein domain (PF00167) - Ig	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gij470208(gmb)CAB41846.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]	Fibroblast growth factor	52646385, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35686052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank gij387677(gmb)CAB030671] - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR G587531) [Caenorhabditis elegans]	UNCLASSIFIED Uncharacterized protein family UFP0034	264488, 264259, 26331822, 29331826, 264905, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264568, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2879	87869122 (5757, 5759)	Novel Protein sim. GBank gi4895145[gb AD32752.1] - (AF123734) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Urad-DNA glycosylase	UNCLASSIFIED	18108339, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi4680703[gb AAD2774.1]AF13296 - (AF132966) CGI-32 protein [Homo sapiens]			264488, 5264635, 52646842, 22278994, 35696286, 22278998, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644296, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906769, 35695917, 52645129, 33657109, 33657182, 2748262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264836, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 284563, 264483, 264567, 264486
2881	87650538 (5761, 5762)	Novel Protein sim. GBank gi733271 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED		22278998, 29331822, 52644045, 21905765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi1118112 (U11559) - No definition line found [Caenorhabditis elegans]			264488, 22278996, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264565
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gi4868098[gb AAD31087.1]AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87794643 (5767, 5768)				265018, 264634
2885	83095306 (5769, 5770)	Novel Protein sim. GBank gi2224697[db AA208322] - (AB02376) KIAA0378 [Homo sapiens]	UNCLASSIFIED		264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - Sush1 domain (SCR repeat)	complement/recept	604332049, 264229, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi3882323[db BA34521.1] - (AB018344) KIAA0801 protein [Homo sapiens]	UNCLASSIFIED		18108335, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi4500015[refNP_003447.1]p2NF2 - zinc finger protein 205	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcript/factor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)	Novel Protein sim. GBank g185405[emb]CA558337] - (X63413) U88 [Human herpesvirus 6]		UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288, 264591, 264766
2890	87703853 (5779, 5780)	Novel Protein sim. GBank g1387750[emb]CA601508] - (Z79064) predicted using GeneFinder, similar to collagen; cDNA EST EMBL.D65865 comes from this gene; cDNA EST EMBL.D69451 comes from this gene; cDNA EST EMBL.D66026 comes from this gene; cDNA EST EMBL.D69658 comes from this gene...		UNCLASSIFIED	264591, 264766
2891	88094428 (5781, 5782)	Novel Protein sim. GBank g1387750[emb]CA601508] - (Z79064) predicted using GeneFinder, similar to collagen; cDNA EST EMBL.D65865 comes from this gene; cDNA EST EMBL.D66026 comes from this gene; cDNA EST EMBL.D69451 comes from this gene; cDNA EST EMBL.D69658 comes from this gene...		UNCLASSIFIED	264591, 264766
2892	95419745 (5783, 5784)	Novel Protein sim. GBank g14929759[gb]AA034140.1[AF15190] CGI-145 protein [Homo sapiens]		UNCLASSIFIED	264591, 264766
2893	87798014 (5785, 5786)	Novel Protein sim. GBank g15668015[gb]AA046135.1] - (AF080171) zinc finger protein ZNF232 [Homo sapiens]		UNCLASSIFIED	264591, 264766
2894	87755985 (5787, 5788)	Novel Protein sim. GBank g13824708[emb]CA484646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL.D70269 comes from this gene; cDNA EST EMBL.D76135 comes from this gene; cDNA EST EMBL.D73147 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264259, 265009, 26433438, 52644296, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank g13824708[emb]CA484646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL.D70269 comes from this gene; cDNA EST EMBL.D76135 comes from this gene; cDNA EST EMBL.D73147 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF01437) - Plectin repeat		29331824, 265007, 264762, 264636, 264553
2896	87732122 (5791, 5792)	Novel Protein sim. GBank g14885549[emb]NP_005456.1[PPK8G - protein kinase B gamma]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	18108382, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146498, 264906, 264908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264557
2897	95413057 (5793, 5794)	Novel Protein sim. GBank g14902872[emb]NP_001296.1[PCLOD - Clostridium perfringens enterotoxin receptor 1]		UNCLASSIFIED	60424179, 56182575, 22278998, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182455, 265009, 264910, 60710831, 60431735, 60433356, 60433438, 65274444, 55811396, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)			UNCLASSIFIED	22278995, 264604, 18108385, 264566

2859	803570 (5797, 5798)	Novel Protein sim. GBank g 4581470 jmo CAB40137.1 - (Y18483) SLC7A8 protein [Homo sapiens]	UNCLASSIFIED	264764, 21906764, 264682
2860	94233338 (5795, 5800)	Novel Protein sim. GBank g 4759272 jef NP_004614.1 pTTC4 - tetrapeptide repeat domain 4	glycoprotein	65274572, 56182575, 35696286, 60432048, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 36182435, 265006, 265007, 265008, 265009, 60433356, 264758, 265018, 264784, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264682, 264683, 32833986, 2646311, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank g 4759272 jef NP_004614.1 pTTC4 - tetrapeptide repeat domain 4	phosphatase	22278995, 22278997, 22278999, 60432048, 29331822, 29331824, 29331825, 29331827, 35696052, 35696070, 264910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank g 2414615 jmo CAB16354 - (Z89259) hypothetical protein [Schizosaccharomyces pombe]		264683, 264681
2903	87606733 (5805, 5806)	Novel Protein sim. GBank g 10793318 jpf S52241 - XLCL2 protein - African clawed frog		264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108331, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86456072 (5807, 5808)	Novel Protein sim. GBank g 5633923 jpf AA046885.1 AF14367 - (AF14367) multispanning nuclear envelope membrane protein nutrin [Homo sapiens]	UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263987, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449826 (5809, 5810)	Novel Protein sim. GBank g 726837 jpf P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)	Novel Protein sim. GBank g 4689286 jpf AA027831.1 AF12185 - (AF12185) sorting nexin 8 [Homo sapiens]	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33108954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264683, 35695955, 60432113, 264566

2907	91211383 (5813, 5814)	Novel Protein sim. GBank g11707079 (U80451) - contains strong similarity to a DNA-like domain (PS-P500636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - DnaJ domain	52644507, 56182575, 56181666, 22278995, 56994075, 35696286, 50432046, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811386, 265019, 264682, 264389, 56181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2908	80414246 (5815, 5816)	Novel Protein sim. GBank g12673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]	helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2909	87420225 (5817, 5818)		eph	264259, 87768474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank g14539335jemb(CAB37483.1) - (AL035539) putative protein [Arabidopsis thaliana]		22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank g14468187jemb(CAB38415.1) - (AL031588) dJ1163J1.3 (novel protein similar to mouse 899) [Homo sapiens]	glucosylase	52646365, 18108397, 22278995, 22278997, 22278998, 22279099, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank g14929637jgbJAA034079.1(AF15184) CGI-54 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat	52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 68712502, 33109954, 264780, 264683, 264688, 264686, 265021, 264683, 18108368, 263976, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank g1854065jemb(CAA55337) - (X83413) U88 [Human herpesvirus 8]	UNCLASSIFIED Contains protein domain (PF00096) - Zinc finger, C2H2 type	52644507, 52644156, 52646842, 55182275, 35696286, 22279097, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87768474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)			264557

2915	86001972 (5829, 5830)	Novel Protein sim. GBank gi 5174485 ref NP_006030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - l-eph Lectin C-type domain	264569, 264448, 264687, 264768, 21906766, 5264684, 21906767, 21906766, 5618275, 29148629, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264783, 264448, 264683, 264566, 18108354, 264389, 264288, 264766
2916	95337790 (5831, 5832)	Novel Protein sim. GBank gi 5104851 ref BAA80165.1 - (AP000061) 305aa long hypothetical dTDP-4- dehydrohamose reductase [Aeropyrum pernix]	dehydrogenase	52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 86658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gi 169065 ref CAA19260.1 - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690229 (5835, 5836)	Novel Protein sim. GBank gi 539218 ref S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641487 (5837, 5838)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		66714117, 66715502, 263981

2920	87769523 (5639, 5840)				35696286, 22276997, 264259, 52645080, 29331824, 29331826, 29331827, 264428, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695955, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 877168518, 60432113
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gi4450013 gb AA024202.1 UR3194 - (UR3194) TPAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22276997, 264259, 52645080, 29331824, 29331826, 29331827, 264428, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695955, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 877168518, 60432113
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gi4450013 gb AA024202.1 UR3194 - (UR3194) TPAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF01074) - kinase		35696286, 22276997, 264259, 52645080, 29331824, 29331826, 29331827, 264428, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695955, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 877168518, 60432113
2923	95337789 (5845, 5846)	Novel Protein sim. GBank gi4433268 emb CAB2838.2 -(Z83844) d3J7E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain		35696286, 22276997, 264259, 52645080, 29331824, 29331826, 29331827, 264428, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695955, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 877168518, 60432113
2924	87791967 (5847, 5848)	Novel Protein sim. GBank gi2130595 pf S7254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36		35696286, 22276997, 264259, 52645080, 29331824, 29331826, 29331827, 264428, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695955, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 877168518, 60432113
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gi2388888 emb CAB11718 -(Z98980) actin associated protein [Schistosoma caracas pome]	UNCLASSIFIED		35696286, 22276997, 264259, 52645080, 29331824, 29331826, 29331827, 264428, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695955, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 877168518, 60432113

2828	95343003 (5851, 5852)	Novel Protein sim. GBank g1j283032ipj1522456 - hydroxyproline-rich glycoprotein - perinatal leucine			29331828, 265011, 264768, 264689, 264764, 264288, 264630, 264637
2828	20452179 (5855, 5856)			UNCLASSIFIED	264559
2829	91622920 (5857, 5858)	Novel Protein sim. GBank g1j413320(emt)(CAA06919) - (A-006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 265009, 33109954, 52644298, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35659517, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264466
2830	95302755 (5859, 5860)			UNCLASSIFIED	58182575, 56181686, 35696286, 22278998, 22278996, 22278999, 264259, 29331825, 60432289, 26331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264782, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170815, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2831	94312693 (5861, 5862)	Novel Protein sim. GBank g1j3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW-Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906766, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27486285, 35696423, 35695855, 264555, 87168518, 60432113, 264566
2832	79632623 (5863, 5864)				264906, 264807
2833	91720776 (5865, 5866)	Novel Protein sim. GBank g1j3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644228, 21906765, 21906766, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264555, 264566, 264567

2934	86576025 (587, 5868)				22278997, 22278998, 29331824, 33657402, 264691, 27486262, 264628, 87186518, 22279000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21906754, 265018, 265019, 264448, 264769, 21906764, 21906765, 265021, 264692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank g14153862 (AC005085) - determined by GENSCAN prediction and spliced EST; match to EST R84328 (NID942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2937	94653096 (5873, 5874)	Novel Protein sim. GBank g15174402[le]NP_008101.1pCD2B - CD2 antigen (cytoplasmic tail-binding protein 2		UNCLASSIFIED	56894075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433358, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21906765, 29148784, 65274791, 264558, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264567
2938	95410773 (5875, 5876)	Novel Protein sim. GBank g13319990[le]b[CAAT6720] - (Y117267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 68714117, 29331827, 35696052, 264107, 264905, 86712502, 52644045, 56182435, 264511, 265008, 265009, 60432228, 33657402, 60433438, 55812038, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21906765, 21906767, 21906768, 55811957, 35659197, 265020, 60170515, 264690, 264691, 264692, 33657023, 264693, 56274620, 33657109, 18108370, 18108374, 263976, 35696423, 35694855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22279002
2939	87766522 (5877, 5878)	Novel Protein sim. GBank g13879900[le]b[CAAG9900] - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b1.5 comes from this gene; cDNA EST yk4625d.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292b...	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686

2940	95011103 (5878, 5880)			UNCLASSIFIED	22278986, 29331822, 29331824, 26674117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264969, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566, 264567
2941	21423370 (5881, 5882)	Novel Protein sim. GBank g 6413872 db JAA323091 - (AS007824) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264567
2942	87430203 (5883, 5884)	Novel Protein sim. GBank g 1172845 sp P46623 RB25_P46BIT - RAS-RELATED PROTEIN RB25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank g 492853 jgi JAD34087.1 AF15185 - (AF15185) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29146488, 265008, 264593, 60433356, 60434338, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank g 4678232 emb CA641190.1 - (AL49860) 1-acylenol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - ATPase-associated Regulator of chromosome condensation (RCC1)		5694075, 22278998, 60432048, 264259, 29331822, 29331824, 60424969, 60432289, 29331826, 29331828, 264905, 264907, 52844045, 264909, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 264691, 33657023, 33657024, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35696421, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56526486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank g 728531 sp P29189 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 55696052, 264908, 265006, 60433356, 55812038, 264759, 55811366, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 264687, 56181562, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2946	94371315 (5891, 5892)	[Novel Protein sim. GBank gi 5441952 gb AA043195.1 AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]	UNCLASSIFIED	264488, 264259, 264508, 264509, 264906, 264907, 264909, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264754, 264288, 264684, 264769, 265021, 264692, 33657109, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108380, 264638, 264639, 83373044, 264565, 264566, 264486, 264567
2947	87362552 (5893, 5894)	[Novel Protein sim. GBank gi 3540281 gb AAC34383.1 - (AF058116) Al-1 related protein [Fugu nortipes]	UNCLASSIFIED	22278995, 22278986, 22278997, 22278999, 28146498, 264508, 29331830, 265007, 265008, 265009, 60432229, 21906754, 265010, 265017, 265019, 264786, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	[Novel Protein sim. GBank gi 5668514 gb AA056554.2 - (AF001533) mitogen-induced [Mus musculus]		52646642, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264783, 264684, 264288, 264685, 264688, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22278997, 264663, 264567
2949	88175545 (5897, 5898)	[Novel Protein sim. GBank gi 2132923 gb J567133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)]	UNCLASSIFIED	22278996, 22278997, 60432285, 29331826, 29331827, 29331828, 35696052, 29146099, 264104, 264107, 264905, 68712502, 264908, 60433396, 60433438, 87168559, 264764, 52644229, 86181562, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 35698423, 263981, 264558, 60432113, 22279002
2950	95086870 (5899, 5900)	[Novel Protein sim. GBank gi 468102 gb CA6291Y0.6, CAEEL - PUTATIVE AMINOPEPTIDASE ZK333.6 IN CHROMOSOME III	Contains protein domain (PF00083) - peptidase Cytochrome aminopeptidase family	264488, 35696286, 264259, 35696052, 264907, 265007, 284910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108382, 18108370, 18108379, 35696423, 65274791, 35698855, 264556, 86526486, 264489
2951	87392357 (5901, 5902)	[Novel Protein sim. GBank gi 4688902 emb CAB1450.1 - (AJ238248) centaurin beta2 [Homo sapiens]		264693

2552	9832952 (5903, 5904)	Novel Protein sim. GBank g j596663 emb CAB51.05.1 - (AL096881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAL/TRIO domain.	254687, 52645156, 21906766, 21906769, 22278996, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 284508, 264905, 20281149, 264906, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433356, 264639, 264756, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2553	88083275 (5903, 5906)	Novel Protein sim. GBank g l19622 sp P10658 SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPiP)	Contains protein domain (PF00260) - UNCLASSIFIED Amino transferases class-V	254482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2554	88088288 (5907, 5908)	Novel Protein sim. GBank g l488526 jef NP_005251 lgGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	254482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2555	87698426 (5908, 5910)	Novel Protein sim. GBank g j3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	254482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2556	85789745 (5911, 5912)	Novel Protein sim. GBank g l689254 gb AA027830.1 AF121857 sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	254482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2557	90933301 (5913, 5914)	Novel Protein sim. GBank g l503023 jef NP_000089.1 PCP12 - carnitine palmitoyltransferase II precursor	cadherin	254482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2558	87440014 (5915, 5916)	Novel Protein sim. GBank g l424022 jdb BA74907.1 - (AB020691) KIAA0854 protein [Homo sapiens]		254482, 18108351, 264448, 264288, 18108356, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264756, 52646317, 21906754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264887, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822

2959	95109420 (5917, 5918)	Novel Protein sim. GBank g j5986221 (U33005) - Tct1 [Mus musculus]	Contains protein domain (PF00568) - Oncogene TBC domain	263394, 2227897, 264259, 60432049, 29331826, 29331828, 35696052, 29331830, 66712502, 26182435, 265006, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486295, 18108374, 65274791, 35695855, 83373044, 56529486, 60432113, 35698286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2960	87420091 (5919, 5920)		UNCLASSIFIED	UNCLASSIFIED
2961	95413416 (5921, 5922)	Novel Protein sim. GBank g j598646jmb CAB05177.2] - (Z82268) predicted using GeneFinder, similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	2227897, 2227898, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265006, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108395, 87168518, 22278002, 264554, 264567
2962	87912700 (5923, 5924)		UNCLASSIFIED	UNCLASSIFIED
2963	95313464 (5925, 5926)	Novel Protein sim. GBank g j420223(dj BAA74850.1) - (AB020574) KIAA0887 protein [Homo sapiens]	Contains protein domain (PF001010) - Helix-loop-helix DNA-binding domain	35698286, 2227897, 264902, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264696, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486, 18108392, 56594075, 2227898, 2227899, 29331822, 29331825, 29331826, 29331827, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264697, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486291, 264639, 55810754, 35696423, 264555, 264636, 264637, 264557, 264558, 264563, 264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388
2964	94324617 (5927, 5928)		UNCLASSIFIED	UNCLASSIFIED

2965	80384762 (5929, 5930)	Novel Protein sim. GBank gi 485447 refNP_005452.1 KRM1 - Kreisler (mouse) maf-related leucine zipper homolog		Transcript factor	264259, 29331826, 264508, 264509, 264905, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33857402, 265011, 264760, 264762, 264764, 264288, 264895, 264766, 264692, 33857109, 264628, 264829, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264567, 18103391, 60432289, 264682, 264448
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi 526275 emb C4845690.1 - (Xenopus laevis) [Xenopus laevis] Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]			
2967	94658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 65658542, 264762, 264764, 265021, 264556, 18108381, 264564, 264486
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi 49297159 p A034118.1 MAF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		264687, 52645156, 21060765, 52646365, 21060767, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264638, 264690, 52644150, 264259, 33857023, 52645080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21060754, 33857182, 29331827, 29331828, 35696052, 27486262, 87168518, 87168474, 265010, 87168559, 285018, 22279000, 265019, 22279002, 264563, 18108351, 264906, 264907, 264448, 18108352, 264566, 264389, 264288, 66714842, 22278996, 22278998, 22278999, 90432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21060754, 265011, 87168559, 265018, 265019, 264448, 264288, 264389, 52644229, 21060766, 21060768, 21060769, 29148794, 265020, 265021, 52644150, 264691, 33857109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi 30247439 p C24734THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	
2970	88088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004759) - fos37502.1 [Homo sapiens]	Contains protein domain (PF00048) - Homeobox domain	homeobox	

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gij728635p39194JALU7 SQ WARNING ENTRY III!	HUMAN - III ALU SUBFAMILY	Im7	264488, 56182575, 35696286, 56994075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21906754, 87168559, 265018, 265019, 18108351, 264689, 21906765, 21906767, 21906768, 265020, 265021, 60170815, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264564, 264567
2972	86525943 (5943, 5944)	Novel Protein sim. GBank gij728635p39194JALU6 SP WARNING ENTRY III!	HUMAN - III ALU SUBFAMILY	kinase	265017, 35695917, 265021, 33657109, 22279902, 264563
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gij2746789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gij786117 (L18134) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 36182575, 56181686, 22278955, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 32645080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21906754, 55811386, 52644296, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108359, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695783, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22279900, 264482, 264487
2975	96325213 (5948, 5950)	Novel Protein sim. GBank gij380812[emb3CAA19508] - (AL023339) similar to HECT-domain (ubiquitin-transferase); - cDNA EST y440610.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85058542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	87711202 (5951, 5952)	Novel Protein sim. GBank gij587913[gbjAA046874.1JAF16093] - (AF160934) BcDNA LD14189 [Drosophila melanogaster]		transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gij528275[emb3CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2278	87332059 (5955, 5956)	Novel Protein sim. GBank g1746549 (U2352) - No definition line found [Caenorabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264250, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433366, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2279	91725256 (5957, 5958)	Novel Protein sim. GBank g1526275 [Jem0]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement	264486, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482	
2280	86296600 (5959, 5960)			265005, 21906767, 263981, 22279000	
2281	87376330 (5961, 5962)			264629, 264564	
2282	95303875 (5963, 5964)	Novel Protein sim. GBank g1492976 [gb]AA034144.1AF15190 - (AF151907) CGI-49 protein [Homo sapiens]	UNCLASSIFIED	22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002	
2283	91725258 (5965, 5966)	Novel Protein sim. GBank g1526275 [Jem0]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		60424178, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002	
2284	94138487 (5967, 5968)	Novel Protein sim. GBank g12393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z69297 (P1D.g1130619) [Homo sapiens]	ATPase-associated		
2285	87099072 (5969, 5970)	Novel Protein sim. GBank g1103160 [p1]S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)	UNCLASSIFIED	264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113	
2286	86284861 (5971, 5972)			55811957, 264566	
2287	86455934 (5973, 5974)		UNCLASSIFIED	264369	

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gi 4679028 sp AA027002.1 - (AF071207) HSPC021 [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331826, 60432289, 35696052, 29331828, 264107, 264903, 264907, 264908, 69712502, 264828, 264905, 56182435, 265006, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264368, 264288, 264685, 5264229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486282, 18108370, 18108372, 18108374, 55910784, 65274791, 35695955, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567, 22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21906765, 21906767, 21906768, 18108374
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi 13671 sp P23964 ALU_F WARNING ENTRY IIII	kinase	264563
2990	87330444 (5978, 5980)	Novel Protein sim. GBank gi 2829836 sp P97346 RHOD_MOUSE - RHOD-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00271) - Ras family	285007, 264512, 18108351, 264288, 264689, 285020, 264691, 33657023, 33657109
2991	94325351 (5981, 5982)		UNCLASSIFIED	
2992	85425164 (5983, 5984)		UNCLASSIFIED	
2993	94325353 (5985, 5986)		UNCLASSIFIED	
2994	94136634 (5987, 5989)	Novel Protein sim. GBank gi 2496549 sp Q50658 YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02	transport	264259, 265019, 264689, 18108385, 264488, 29331822, 265017, 264781, 21906769, 65274791, 263981, 264565, 22278994, 22278995, 56994075, 22278997, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264683, 35695955, 83373044, 18108385, 22279000, 264565, 264566, 264905, 264907, 265019, 18108351, 264683
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		65274572, 35696026, 264259, 29331824, 35696062, 29146499, 264506, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264786, 264788, 264689, 35695917, 60170615, 33657023, 264692, 264634, 264565, 18108381, 18108392, 18108388, 264484
2996	91013788 (5991, 5992)	Novel Protein sim. GBank gi 2438912 (AC002201) - similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	

2007	87627140 (5993, 5994)	Novel Protein sim. GBank g145896.2 (b)AA716848.11 - (A023227) KIAA1004 protein [Homo sapiens]	homeobox	2654488, 56182575, 264259, 6671417, 29331826, 35696032, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 5264536, 22278997, 264508, 264906, 18108371, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
2008	88085381 (5995, 5996)	Novel Protein sim. GBank g1054756 (emb)CAA222521 - (AL03014) CDNA EST Y42509.3 comes from this gene; CDNA EST Y42509.3 comes from this gene; cdna EST EMBL AF79323 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	2654488, 56182575, 264259, 6671417, 29331826, 35696032, 264508, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 5264536, 22278997, 264508, 264906, 18108371, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
2009	94847055 (5997, 5998)	Novel Protein sim. GBank g115408 (P)P18353 (C)C19_CAEEL - CUTICLE COLLAGEN 19	UNCLASSIFIED	2654488, 56182575, 264259, 6671417, 29331826, 35696032, 264508, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 5264536, 22278997, 264508, 264906, 18108371, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
3000	95093770 (5999, 6000)	Novel Protein sim. GBank g1163174 (U32575) - similar to yeast Scdip, Swiss-Prot Accession Number P32644; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]	UNCLASSIFIED	2654488, 56182575, 264259, 6671417, 29331826, 35696032, 264508, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 5264536, 22278997, 264508, 264906, 18108371, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
3001	88078454 (6001, 6002)	Novel Protein sim. GBank g12078470 (AC002073) - Putative gene. Censin predictions confirmed by EST splicing; coded for by human CDNA AA122029 (NM_01678046), D31562 (NM_0644442), AA158721 (NM_01733015), R59640 (NM_0630333) and F13062 (NM_070311) [Homo sapiens]	calthopsis	2654488, 56182575, 264259, 6671417, 29331826, 35696032, 264508, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 5264536, 22278997, 264508, 264906, 18108371, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
3002	87718167 (6003, 6004)	Novel Protein sim. GBank g13599478 (AF085185) - Myosin-1A [Caenorhabditis castellanii]	UNCLASSIFIED	2654488, 56182575, 264259, 6671417, 29331826, 35696032, 264508, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 5264536, 22278997, 264508, 264906, 18108371, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639

3003	86648079 (6005, 6006)	Novel Protein sim. GBank g11754989 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01381) - collagen Collagen triple helix repeat (20 copies)	254312, 264393, 264564, 264567, 264486
3004	80066976 (6007, 6008)	Novel Protein sim. GBank g12224629[gb]BAA20802 - (A002342) KIAA0344 [Homo sapiens]	Contains protein domain (PF01360) - oxygenase	29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794443 (6009, 6010)	Novel Protein sim. GBank g168069[gb]A027719.1[AF 13294] CGI-10 protein [Homo sapiens]	Monooxygenase	265011, 265019, 21906766, 21906767, 21906768, 265020, 33657023, 33657249, 60170394, 22279002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank g13930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - MHC Ank repeat	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	90936065 (6013, 6014)	Novel Protein sim. GBank g12565032 (U80739) - CAGH1A [Homo sapiens]	Transcription factor Zinc finger, C2H2 type	52544507, 52564516, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)	Novel Protein sim. GBank g13127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - synthase AMP-binding enzyme	264905, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank g14927370[gb]AA033084.1[AF06797] DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01823) - UNCLASSIFIED Protein of unknown function	52646842, 56182575, 22278695, 22278698, 264259, 29331825, 29331826, 29331827, 29331828, 35696002, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109984, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264780, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264559, 18108385, 18108388, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank g14927370[gb]AA033084.1[AF06797] DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01823) - UNCLASSIFIED Protein of unknown function	264686, 264687, 21906767, 21906769, 55811957, 22278695, 356959917, 22278696, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695955, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323697 (6021, 6022)	Novel Protein sim. GBank g19052319[gb]AA033501.1[AF 11883] citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	356956032, 56184335, 264758, 21906754, 265018, 264760, 264782, 18108351, 264692, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)	Novel Protein sim. GBank g19052319[gb]AA033501.1[AF 11883] citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	263972

3013	91238799 (6025, 6026)	Novel Protein sim. GBank g13702286 (AC005787) - H33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, C-beta repeat	transcriptfactor	264488, 263994, 35696286, 22278997, 264259, 29331824, 60424269, 60714117, 35696062, 264905, 264906, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567
3014	7987763 (6027, 6028)	Novel Protein sim. GBank g13373374mb1(CAA93081) - (Z68879) Similarity to Yeast Ch12p protein (PIR Acc. No. S54453); cDNA EST EMBL-D27950 comes from this gene; cDNA EST EMBL-D27949 comes from this gene; cDNA EST EMBL-D33447 comes from this gene; cDNA EST EMBL-D33316 comes from...		ATPase_associated	264760
3015	86995468 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759845 (6031, 6032)	Novel Protein sim. GBank g1176819bp14733JC99_ YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52648842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486282, 27486264, 33657349, 27486265, 35695763, 35695955, 877168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank g1456958jdb1AA76851.11 - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 877168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 877168518, 264404, 60432113, 22279500, 264567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank gji1219332 (AC004020) - Unknown gene product [Homo sapiens]		onco gene	284558 284569, 52644507, 18108394, 65274572, 56192575, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265009, 60432229, 284593, 60433356, 55812038, 21900754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21900766, 21900768, 21900769, 52644150, 264680, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gji1414809 (AF061529) - <i>rp</i> [Mus musculus]	Contains protein domain (PF00415) - ATPase-associated Regulator of chromosome condensation (RCC1)		284485, 263994, 35696286, 264259, 264508, 264805, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 284764, 264288, 264389, 264766, 264687, 284688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 284485 264769, 264629, 264482
3022	87118500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264566
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gji165925ip132323JAGA_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	284488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52640405, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21900767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264556, 22279000
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21900769, 55811957, 35695917, 264680, 264555, 264559 284593, 55811576
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gji195671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III [Saccharomyces cerevisiae]			

3026	87643662 (6051, 6052)	Novel Protein sim: GBank g1024052[pp19792](KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264480, 29331825, 264111, 265007, 60170831, 265010, 87186559, 265019, 21906765, 29148627, 263967, 20281149, 20281069, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim: GBank g1029647[gb]A034084_1(AF151814 - (AF151847) CGI-89 protein [Homo sapiens])	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60430406, 264259, 29331822, 29331824, 60714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486261, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim: GBank g1028052[emb](CAA186501 - (A1022599) hypothetical protein [Schizosaccharomyces pombe])	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264690, 264693, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim: GBank g1075776[emb](CAA18782) - (A1022727) dJ8019.1 (olfactory receptor-like protein [HsBM1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	im7	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002
3031	91677953 (6061, 6062)	Novel Protein sim: GBank g10430567[gb]A022105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	

3032	94130124 (6043, 6064)	Novel Protein sim. GBank gi 101951 (U37429) - similar to M. musculus MER3 and other AHC/TSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	- lythase	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87188474, 87188559, 265019, 264288, 21900769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87188518
3033	95308321 (6085, 6086)	Novel Protein sim. GBank gi 503157 (J161NP_005712.1) pACTR - ARP3 actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - Actin	- struct	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21900754, 265010, 265019, 264681, 264369, 264768, 21900764, 21900768, 35695917, 33657023, 264528, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)			UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264782, 264786, 264637, 264638, 264486, 264636
3035	91220682 (6069, 6070)	Novel Protein sim. GBank gi 3738207 (emb CA21282) - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]		UNCLASSIFIED	
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi 7283759 (P39194) ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII (AF131766) Similar to Ene-VASP like protein [Homo sapiens]		kinase	264907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi 406559 (gi A020040) - (AF131766) Similar to Ene-VASP like protein [Homo sapiens]			265017
3038	85421807 (6075, 6076)	Novel Protein sim. GBank gi 5360103 (gi A042865.1) (AF15509) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	22278996, 22278997, 264259, 264905, 265007, 265009, 60433566, 21900754, 265018, 265019, 18108351, 264687, 21900765, 265020, 265021, 65274620, 27486282, 264638, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi 475128 (emb CA842094.1) - (AJ238711) ZRP protein [Rattus norvegicus]		UNCLASSIFIED	35696286, 29331828, 264100, 264110, 264511, 265007, 21900754, 265011, 264681, 264683, 264687, 21900768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264564, 18108391, 264632, 264558, 18108382, 18108385, 264567
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi 484278 (emb CA843247.1) - (AL050037) hypothetical protein [Homo sapiens]		UNCLASSIFIED	
3041	86312357 (6081, 6082)	Novel Protein sim. GBank gi 387607 (emb CA804122.1) - (281505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28023 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...		UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33659970, 33109954, 21900754, 87188559, 264600, 264683, 21900765, 21900768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi 790236 (U21156) - sarcolinmal associated protein 2 [Oryctolagus cuniculus]		glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank, gi 85405 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264905, 66712502, 56182435, 55811386, 52644286, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850, 22278986, 22278998, 22278995, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108368, 18108370, 60170394
3044	87646182 (6087, 6088)	Novel Protein sim. GBank, gi 404922 (AF42276) - α 51 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiquitin/COX5 methyltransferase family		
3045	94127598 (6089, 6090)	Novel Protein sim. GBank, gi 458686 dbj BAAT76859.1 - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 265005, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486282, 18108370, 264628, 18108374, 35695955, 264630, 264632, 264635, 264563, 264564, 264566
3046	8608247 (6091, 6092)			UNCLASSIFIED	22278998, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 52646317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	85089924 (6093, 6094)			UNCLASSIFIED	264488, 22278998, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264786, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695955, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank, gi 4588034 gb AA025962.1 AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		264102, 29148784
3049	86239955 (6097, 6098)	Novel Protein sim. GBank, gi 5454158 ref NP_066286.1 pVARS - vely-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21906768, 265020, 33657109, 35695955, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank, gi 458686 dbj BAAT76843.1 - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906766, 265002, 264693, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750589 (6101, 6102)				22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank, gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN	dehydrogenase		264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi3947613[eml]CAA19465.1] - (AL023828) cDNA EST EMBL M89008 comes from this gene. cDNA EST y22253.3 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181666, 22278995, 35686286, 22278998, 264259, 60432267, 265008, 265009, 60433438, 21906754, 265010, 97166593, 264603, 265016, 265019, 264763, 264764, 264283, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35984423, 264633, 56182323, 22279000, 264593
3054	60943510 (6107, 6108)	Novel Protein sim. GBank gi107621[prj]S0755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35686286, 35696052, 70331030, 264588, 264609, 264512, 264910, 265017, 264604, 264766, 265020, 33857109, 264628, 35695855, 265036, 264584, 264586, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi468085[igp]AAU27717.1[AF13294 - (AF132942) CG-08 protein [Homo sapiens]		transport	60424179, 65274572, 56182375, 35696286, 22278998, 60432289, 35696052, 56182435, 265008, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 97166593, 265019, 18108351, 264683, 264286, 264569, 264689, 21906768, 55811857, 35695917, 60170915, 33857023, 65274620, 33857109, 35695753, 60431526, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264585
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi172837[9p]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII]		glycoprotein	264488, 264589, 18108394, 55816842, 22278997, 22278998, 22278999, 264259, 60714117, 26531826, 25331827, 35696052, 264508, 264569, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33857402, 55812038, 264596, 264788, 265010, 265011, 265017, 265019, 264780, 18108351, 264782, 264783, 264784, 264288, 264786, 264897, 18108357, 264788, 264789, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264991, 264893, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 63373044, 18108385, 22279000, 22279002, 264563, 264564, 264595, 264596, 264486, 264587

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gji3978119(embj)CA88801 - (Z4908) similar to GTP-binding protein, cDNA EST EMBL.M89111 comes from this gene, cDNA EST EMBL.D277709 comes from this gene, cDNA EST EMBL.D277708 comes from this gene, cDNA EST EMBL.D73788 comes from this gene, cDNA EST Y4353,...		struct	264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264787, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	79646226 (6115, 6116)	Novel Protein sim. GBank gji456803(ajb)AA025962, JAF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]		UNCLASSIFIED	264693
3059	87639425 (6117, 6118)	Novel Protein sim. GBank gji456803(ajb)AA025962, JAF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]		UNCLASSIFIED	22278959, 22278986, 22278997, 22278998, 22278999, 264480, 264489, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264788, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740964 (6121, 6122)			UNCLASSIFIED	264112, 52644286, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gji445690(ajb)AA020653 - (AF070577) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gji2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gji4240315(ajb)BA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	52646365, 52646842, 65274572, 26182575, 56181688, 22278985, 22278986, 22278987, 22278999, 264259, 604332049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60433229, 60433438, 55812038, 52644286, 265018, 264682, 264288, 264686, 264788, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gji565874(ajb)AA045980, JAC00506 - (AC005067) Supported by Human EST H08032.1 (NID,g872854), mouse EST AA87042.1 (NID,g2965487), and gencan [Homo sapiens]		UNCLASSIFIED	264095, 29331854, 60424289, 66714117, 264100, 264907, 265007, 264581, 60432229, 264593, 265011, 265019, 18108351, 264786, 264787, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank g 4884268 emb CABA3245.1 - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 66712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank g 4686258 p AA027832.1 AF121859 sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		264488, 264489, 35696286, 22278996, 56994075, 264299, 29331822, 29331825, 35696032, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265019, 264780, 264782, 264448, 264763, 264764, 264288, 264389, 264788, 264788, 264687, 264769, 264689, 21906765, 21906767, 21906769, 35695917, 265020, 265021, 264534, 52944150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264835, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)	Novel Protein sim. GBank g 3878119 emb CAA88680 - (Z4908) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01926) - struct GTPase of unknown function		22278996, 56994075, 22278996, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109854, 87168474, 87168559, 265017, 264448, 264764, 264683, 264765, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482
3069	95412753 (6137, 6138)	Novel Protein sim. GBank g 3878119 emb CAA88680 - (Z4908) similar to GTP-binding protein; cDNA EST			264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109854, 87168474, 87168559, 265017, 264448, 264764, 264683, 264765, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank g1387778[emb]CA1805571 - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...	synthase	264488, 22278984, 22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264491, 2914620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712002, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264810, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18106351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18106370, 18106377, 55811576, 35695955, 264634, 264635, 18106381, 60170394, 56182323, 264558, 83373044, 18106385, 18106387, 56526486, 264404, 264553, 264565
3071	94325573 (6141, 6142)	Novel Protein sim. GBank g14502425[pe]NP_001709.1pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Thoredoxin	264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35698052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644266, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695955, 26464630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22278900, 22279002, 264563, 264564, 264565, 264566, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 284555, 56182323, 60432113, 264564
3072	95115892 (6143, 6144)	Novel Protein sim. GBank g11263289 (U47856) - fibron-4 (Araeus diadematus)	transcriptfactor	264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35698052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644266, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695955, 26464630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22278900, 22279002, 264563, 264564, 264565, 264566, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 284555, 56182323, 60432113, 264564

3073	86147248 (6145, 6146)	Novel Protein sim. GBank g1134401sp P232528CORE_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN [B] (SPR-B)) (14.9 KD PANICORNULIN)		UNCLASSIFIED	264789
3074	880093351 (6147, 6148)	Novel Protein sim. GBank g13418847 (AC004982) - similar to yeast hypothetical protein ylk4, similar to P38164 (P1D3586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108398, 18108370, 18106374, 264567
3075	88009352 (6149, 6150)	Novel Protein sim. GBank g14557349 e NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	8874277 (6153, 6154)	Novel Protein sim. GBank g1302395 sp Q00808 HET_1_PODAN - VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27486264, 33657349, 35695973, 35695555, 264639
3078	88009355 (6155, 6156)	Novel Protein sim. GBank g13900850 (AC004994) - similar to KIAA0600, similar to d1026-456 (PID33043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank g1387541 0 emb CAB02876 - (Z31052) Similarly to Yeast ABC1 protein (SW/ABC_1_YEAST); cDNA EST X22988.3 comes from this gene; cDNA EST X22988.3 comes from this gene [Caenorhabditis elegans]	Transport		29331824, 29331826, 264758, 55811368, 265017, 55811190, 52644228, 21906768, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002
3080	95288274 (6159, 6160)	Novel Protein sim. GBank g1525722 p p A11265.1 - (AF117887) protein arginine methyltransferase [Mus musculus]	Interferon		264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 60714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264682, 264448, 264753, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695973, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88004864 (6161, 6162)	Novel Protein sim. GBank g1728831 sp P39189 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265011, 265018, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88035756 (6165, 6166)	Novel Protein sim. GBank gij1683241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906774, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22278000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gij47674 (prijA37475 - probable structural component p38 - borna disease virus)	UNCLASSIFIED	22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 264906, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264565, 264566, 264567, 264486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gij2565057 (U80741) - CAGH44 [Homo sapiens]	UNCLASSIFIED	265011, 264681
3086	87769842 (6171, 6172)	Novel Protein sim. GBank gij3394189 (AC005602) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263967, 263974, 55810764, 263981, 18108385, 264487
3087	87462888 (6173, 6174)			52646365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21900754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695655, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3353304 (AF001549) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4689146 (pjjAA027782.1) (AF07704) - lambda-3-hydroxyacyl-CoA dehydrogenase crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase	18108397, 65274572, 56182575, 36181868, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264780, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank g[135-4050 (U47024)] - MEM3 [Mus musculus]	UNCLASSIFIED	60424179, 52645156, 65274572, 36182575, 56181688, 22278995, 35696286, 36694075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264906, 264908, 52844045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21906754, 33109954, 52646317, 55811386, 52644286, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264389, 18108357, 264788, 52644229, 56181562, 21906754, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 80170615, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486265, 35695763, 18108374, 18108378, 55810784, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22278000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank g[8873932[emb]](CAB01659) - (Z79596) Similarity to Bovine aspartyl beta hydroxylase (TFR.G162694); cDNA EST EMBL.D27916 comes from this gene; cDNA EST EMBL.D27915 comes from this gene; cDNA EST EMBL.D64881 comes from this gene; cDNA EST EMBL.D68139 comes f.....	UNCLASSIFIED	35696286, 26331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264768, 264769, 264769, 264683, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gi1710758[sp]t590[R52, HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (L1REP3 PROTEIN)]	Contains protein domain (PF00333) - ribosomal prot ribosomal protein S5	264488, 60242176, 18105396, 22278995, 56994075, 52278996, 35666286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 284508, 284509, 284905, 284906, 284907, 29331830, 284908, 284909, 2844113, 28464510, 284511, 265006, 284512, 265007, 265008, 284910, 265009, 60170831, 284591, 264592, 60431735, 284593, 284594, 60433438, 284595, 284758, 21906754, 265010, 265011, 284601, 284602, 265017, 284603, 284604, 265018, 284605, 265019, 284760, 284762, 264681, 18108351, 264763, 284682, 284448, 284754, 284683, 284288, 284369, 284765, 284756, 284688, 284767, 284687, 284768, 284759, 284688, 21906764, 284689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 29148784, 35655917, 265020, 265021, 284534, 60170615, 284690, 284691, 284692, 65274620, 33657109, 27486282, 284628, 284629, 18108374, 263978, 18108377, 35696423, 284630, 284631, 284632, 284634, 284635, 284555, 284636, 284637, 284556, 284638, 284557, 284558, 284639, 60170394, 18108385, 284559, 29331824, 35696052, 284905, 284506, 60432229, 60431735, 284684, 284369, 284288, 284766, 21906767, 35696423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gi1502587[emb]CAB44347.11 - (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED	
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gi400734[sp]31044[FBP, RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)]	Contains protein domain (PF01161) - collagen Phosphatidylethanolamine-binding protein	18108398, 284259, 60432289, 29331827, 284511, 284763, 284288, 284767, 265022, 284691, 284693, 65277791, 56182323, 284584, 284585

3095	94848162 (6189, 6190)	Novel Protein sim. GBank gi 487759 gb AA031421.1 AF12444 - (AF12444) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56185575, 22278995, 35666286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264784, 264369, 264288, 264686, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33857023, 264693, 263972, 18108376, 55811576, 35696423, 264692, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264565, 264487, 18108391
3096	87736128 (6191, 6192)	Novel Protein sim. GBank gi 388222 dbj BA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566
3097	8824895 (6193, 6194)	Novel Protein sim. GBank gi 46628 emb CAB37981 - (AL022395) 4J273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002
3098	80258024 (6195, 6196)	Novel Protein sim. GBank gi 303603 dbj BA02145.1 - (D12621) cytochrome P-450LTV [Homo sapiens]	cyto450		264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gi 108376 gpl B48013 - proline- rich proteoglycan 2 precursor, parotid - rat	UNCLASSIFIED		29331825, 60432289, 35696055, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	79602134 (6201, 6202)		UNCLASSIFIED		264906, 264693, 264628, 264630, 264632

3102	91220862 (6203, 6204)	Novel Protein sim. GBank gli5035706(gb AAD41781.1 AF28536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	1st/2nd	35696266, 22278996, 22278999, 26331827, 35696052, 264906, 264512, 265008, 60170831, 60433569, 33108954, 18108351, 264684, 264689, 21908787, 60170515, 264692, 33657023, 264638, 22279000, 264482, 264584, 35695917, 264565
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gli464564(isp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17)	UNCLASSIFIED		
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gli5032207(e NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6)	UNCLASSIFIED		264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 26331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264752, 264764, 264288, 264768, 264768, 264687, 264769, 21906768, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695955, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373944, 264404, 22278902, 264563, 264565, 264566, 264486, 264487
3106	95361416 (6211, 6212)	Novel Protein sim. GBank, gli1938574 (U87190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 26331822, 264906, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 56812038, 265017, 265018, 264683, 264686, 264687, 264768, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182233, 18108385, 18108388, 22279000, 264483
3107	95343272 (6213, 6214)	Novel Protein sim. GBank, gli3341441(em CAA76851) - (V17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696266, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432288, 29331827, 29331828, 33656970, 264105, 264512, 265008, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906768, 265021, 21906769, 21906769, 21906769, 264691, 33657109, 27486261, 27486265, 18108370, 263927, 18108374, 55811576, 18108385, 55826486, 264482, 264487, 56182433, 264268, 264690, 264694
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gli5032207(e NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6)	UNCLASSIFIED		

3118	94655848 (6235, 6236)	Novel Protein sim. GBank gij380563[emb]CA601444.1] - (278018) predicted using GeneFINDER, similar to serine/threonine kinase; cDNA EST Y353010.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	gij	52645156, 52646842, 5274572, 56182975, 22278995, 56994075, 22278996, 35666296, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 66714117, 29331826, 29331827, 35666052, 29331828, 2849005, 264908, 29331830, 52644045, 36182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644286, 87168474, 37168559, 255017, 265018, 264605, 265019, 264762, 264448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264680, 52644150, 264691, 33657023, 264693, 33657108, 33657348, 264628, 18108370, 60431528, 18108374, 3596423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264468, 265005, 264288
3119	85726796 (6237, 6238)		Contains protein domain (PF00328) - Helix and phosphate		
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gij5019819[g]AC37863.1[AF143152] putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gij4501877[mlNP_001088.1]pACRI; acrosin			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35666052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)	Novel Protein sim. GBank gij2439517 [AC002563] - putative RHO/RAC effector protein, 95% similarity to P48205 (P1D:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	UNCLASSIFIED	264638
3123	86083003 (6245, 6246)			kinase	16108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486255, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87786899 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gij4980826[g]AC035412.1[AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermidoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase		56181626, 264259, 66714117, 60432889, 29331826, 29331827, 264807, 264808, 264828, 265009, 60433356, 33657402, 60433438, 264756, 18108351, 264288, 2948627, 29148628, 33657023, 33657109, 18108352, 56526486

3128	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264480, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264359, 264685, 28148629, 33657023, 264693, 33657109, 18106374, 55811576, 18108385, 60432113, 22279002, 35696286, 22278996, 22278998, 29331826, 264908, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank.gj2828280(jmb)(CAI16694.1) - (AL021687) putative protein [Xenopus laevis]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank.gj385828 (AF090133) - lin-7A [Rattus norvegicus]	Contains protein domain (PF05565) - POZ domain (Also known as DHR or GLP).	mi5c_channel	22278996, 264259, 52644045, 265008, 21906754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank.gj3135273 (AC003058) - hypothetical protein [Xenopus laevis]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264784, 264369, 264289, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264654, 264566, 264636
3130	14893960 (6259, 6260)	Novel Protein sim. GBank.gj329465 (AF064553) - NSD1 protein [Mus musculus]			
3131	95351468 (6261, 6262)	Novel Protein sim. GBank.gj1848277 (U06136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331821, 264907, 56182435, 264694, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264786, 21906769, 55811957, 285020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27468261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168516, 264654

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gll680647gblAAD27713. (AF:1323) CGI:03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	Ubiquitin	52644507, 52646842, 52646305, 65274572, 56102575, 22278994, 22278995, 35096286, 5694075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170931, 60432229, 60433356, 33657402, 55812038, 52646317, 21906754, 52644296, 85656542, 87168559, 265017, 265018, 265019, 264448, 264286, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486285, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56528486, 87168518, 60432113, 22276002
3133	87279414 (6265, 6266)	Novel Protein sim. GBank gll547613refNP_003738.1p1TNKS - TANKYRASE		polymerase	22276994, 22278996, 264905, 265006, 265007, 87168559, 264780, 21906767, 18108374, 22276000, 22278002, 264563 264593, 264369, 264685, 264628, 264566
3134	84449816 (6267, 6268)	Novel Protein sim. GBank gll1729827spIP54633ITALA_DICDI - FILOPODIN (ITALIN HOMOLOG)		struct	22278996, 264095, 29331826, 33657402, 18108348, 263974
3135	85389358 (6269, 6270)	Novel Protein sim. GBank gll3033476 (AF012927) - fibrinogen-binding protein [Streptococcus equi]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278996, 264259, 264428, 265006, 265008, 60433438, 265019, 264784, 264288, 264769, 264689, 265020, 27486382, 263972, 65274791, 264557, 264558
3136	84445839 (6271, 6272)	Novel Protein sim. GBank gll827101pIIS41092 - probable carrier protein c2 - Caenorhabditis elegans		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265006, 21906754, 87168474, 265011, 87168555, 265017, 265018, 265019, 18108351, 264682, 264789, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264485
3137	85257947 (6273, 6274)	Novel Protein sim. GBank gll3342730 (AC005331) - R31341_1 [Homo sapiens]			

3144	953636328 (6287, 6288)	Novel Protein sim. GBank gl 4834468 em CA843322.1 - (AL050229) hypothetical protein [Homo sapiens]			264488, 18108395, 22278986, 35686285, 22278987, 22278988, 29331820, 29331827, 35686052, 29331828, 264106, 265006, 265007, 265008, 33657402, 8658542, 265011, 18108351, 264446, 264958, 21906765, 21906766, 21906767, 265020, 265021, 52844150, 27466261, 19108370, 18108374, 35686423, 56182323, 83373044, 22278990, 22279002, 264367, 22279003, 29331824, 29146498, 20281100, 265006, 59812038, 265010, 21906766, 29146827, 21906768, 29148784, 264892, 33637023, 33637103, 35685763, 263961, 56182323, 97166519
3145	86511657 (6289, 6290)	Novel Protein sim. GBank gl 3879109 em CA603330 - (Z81116) Similarity to Human endosomal protein P162 (TRQ13073); cDNA EST ENMLZ14487 comes from this gene; cDNA EST ENMLZ14450 comes from this gene; cDNA EST ENMLD27011 comes from this gene; cDNA EST ENMLD27015 comes from 1...	UNCLASSIFIED		264258, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264446, 264958, 21906766, 265021, 264892, 33637108, 18108374, 35686423, 35685855, 60432113, 264954
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gl 21357476 ipr I569890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - struct pH domain		56181686, 35686286, 60432049, 264259, 56182181, 29331825, 60432289, 35685902, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264446, 264288, 265022, 33637023, 33637108, 60431528, 55274791, 264631, 56182323, 264404, 22279002
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gl 3874279 em CA607315.1 - (Z39225) predicted using GeneHancer; cDNA EST YK319612.3 comes from this gene; cDNA EST YK319612.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - UNCLASSIFIED haloacid dehalogenase-like hydrolase		35686286, 35686052, 264511, 86585842, 97168474, 264764, 35686423, 264355, 264658, 264657, 264558, 63373044, 95226486, 60432113
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gl 52523256 AD40051.1 (AF08310 - (AF083108) sirinun type 3 [Homo sapiens])	UNCLASSIFIED		29331822, 35686052, 264108, 29148629, 18108391
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gl 4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01383) - eph FYVE zinc finger		264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35685855, 56182323, 264639
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gl 3376454 em CA76883 (Y117850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Transferrase Gluthathione S-transferases		29331822, 265008
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gl 172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00086) Zinc finger, C2H2 type		21906754, 87168555, 264605, 21906768, 52844150, 27486264, 35686423, 22279000
3152	86589108 (6303, 6304)		UNCLASSIFIED		

3153	95317298 (6305, 6306)	Novel Protein sim. GBank g1469504 (g1469504:2705.1)(AF14395) corom- 3 [Mus musculus]	Contains protein domain (PF00400) WD domain, G-beta repeat	struct	264488, 2646365, 35696286, 22278997, 22278997, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 3657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264692, 264754, 264288, 264369, 264758, 21908765, 21908766, 21908767, 21908768, 21908769, 29148784, 265021, 265022, 60170815, 53641150, 264680, 264692, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 50432113, 22279000, 22279002, 22278998, 264259, 26331824, 66712502, 356508, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374, 29331826, 264509, 264907, 264908, 264510, 264511, 264512, 33657402, 264691, 264693, 33657023, 18108370, 264534, 264639, 18108385, 264553, 264488
3154	87718573 (6307, 6308)	Novel Protein sim. GBank g1469504 (g1469504:2720.1)(AF13294) CG1-11 protein [Homo sapiens]	ATPase associated		56182575, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696092, 52644045, 265007, 265009, 60170831, 50432228, 60433356, 21908754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21908765, 21908768, 21908769, 35695817, 265020, 265022, 264692, 18108370, 35696423, 58182323, 22278998, 18108396, 264259, 29331825, 35696052, 29148498, 87168559, 265017, 264448, 264288, 264691, 18108385, 52645129, 35696423, 52644332
3155	87762394 (6309, 6310)	Novel Protein sim. GBank g1726857 (g1726857:194)(U7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY fill)	UNCLASSIFIED		264448, 263974
3156	87737449 (6311, 6312)	Novel Protein sim. GBank g1563007 (g1563007:1)(AC00601 - (AC006017) N- acetylglucosaminyltransferase, similar to Q10473 (P1CJ709595) [Homo sapiens])	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	
3157	88259577 (6313, 6314)	Novel Protein sim. GBank g1530606 (g1530606:1895.1)(AF15677 - (AF15677) ASB-3 protein [Homo sapiens])	Contains protein domain (PF00023) - Arx repeat	kinase	
3158	80034118 (6315, 6316)	Novel Protein sim. GBank g1530606 (g1530606:1895.1)(AF15677 - (AF15677) ASB-3 protein [Homo sapiens])	UNCLASSIFIED		56182575, 22278999, 29331824, 264408, 60433356, 264758, 265010, 87168559, 264448, 18108354, 264758, 21908768, 265020, 264691, 264692, 33657109, 18108374, 35696423, 264555, 60170394, 22279000
3159	94124114 (6317, 6318)	Novel Protein sim. GBank g15531272 (g15531272:1)(CA850897.1 - (AJ243800) WSC4 homologue [Noveromyces lactis])	Contains protein domain (PF00023) - Arx repeat		22279000
3160	80221068 (6319, 6320)	Novel Protein sim. GBank g13030525 (AF064447) - sex- determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Arx repeat	struct	18108351, 264555, 264556, 264557, 264558, 264559

3161	8807411 (832, 6322)	264468, 22278905, 22278907, 22278908, 264259, 29331822, 6043298, 29331828, 52644045, 265017, 265018, 264448, 264288, 21906764, 21906767, 265020, 18108374, 264636, 264566		
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U2OS)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberosus sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis,Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases,Tuberous sclerosis, Scleroderma, Obesity,Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmune disease,allergies, immunodeficiencies,transplantation, Graft versus host,

264508	5PH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	5PH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (UISMC)		
264487	5RH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	5RH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	5RH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	5RH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	5RH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	5RH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	5RH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	5RH.22 (Placenta)	Placenta	Infertility, birth defects
264567	5RH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	5RH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	5RH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	5RH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	5RH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	5RH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	5RH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft vesus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft vesus host

264767	5RH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	5RH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	5RH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	5RH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	5RH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	5RH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	5RH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	5RH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	5RH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	5RH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx98		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UtMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain- hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSk)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1 TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1 TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1 Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	mQEA Baits		
263973	RRQEA B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: 1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

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 420
 ctgtgggaga cctaccgtga cgaggatgcc accctcgtcg aggtcaaccc gatgatcaag
 480
 accggcgatg gacgcacatc ggctatcgac ggcaagatga ctgttgacaa caacgcaccc
 540
 ttccgccagc ctgaccgcgc cggcttggtg gatcgcgccca ccaccgaccc gctcgagttg
 600
 cgtgcccggc agctcgggtc caactacgtc aagcttgacg gcaacgtcgg cgtcatcgga
 660
 aacggtgctg gtctggtcat gagcaccctt gactgcgttg cgtacgcccg tgagaaactc
 720
 ccgggatctc cagctccccg taacttcctc gacatcgggt gcggcgccctc ggccgagatc
 780
 atggccaacg gccttgacct catcatgagt gacgagcagg tgcgttcctg gttcgtcaac
 840
 gtctttggcg gtatcaccgc ctgtgaccag gtggcgcttg gtatcaaggg cgctctcgag
 900
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 960
 gagggcagaa agattctcga ggaattc
 987

<210> 4
 <211> 329
 <212> PRT
 <213> Homo sapiens

<400> 4
 Glu Leu Gly Thr Pro Val Val Ala Val Lys Ala Gln Val Lys Val Gly
 1 5 10 15
 Gly Arg Gly Lys Ala Gly Gly Val Lys Ile Ala Lys Ser Pro Ala Glu
 20 25 30
 Ala Ala Gly Arg Ala Glu Ala Ile Leu Gly Met Asp Ile Lys Gly His
 35 40 45

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Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
  50          55          60
Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Tyr Leu Ala
  65          70          75          80
Met Cys Ser Arg Glu Gly Met Asp Ile Glu Thr Leu Ala Lys Glu
          85          90          95
Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val
          100          105          110
Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
          115          120          125
Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr
          130          135          140
Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
          145          150          155          160
Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp
          165          170          175
Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg
          180          185          190
Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn
          195          200          205
Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
          210          215          220
Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
          225          230          235          240
Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Ala
          245          250          255
Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
          260          265          270
Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
          275          280          285
Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
          290          295          300
Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala
          305          310          315          320
Glu Gly Arg Lys Ile Leu Glu Glu Phe
          325

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<210> 5

<211> 622

<212> DNA

<213> Homo sapiens

<400> 5

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  120
gaacatagct tgtcataaca tctctgcagg gttctcccaa acccctttct gcttggcaac
  180
agctgacatc acacctagct gtaagtcctt gtagatcgca aattactttt tggagactgg
  240
gggtagcagg ggcattgggg taatagcctt ctagcccttt ttgagggaaa cacatgggtg
  300

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aggctatttt ggggctggga agtggggggc tgggtgtcccc tggatggctg tgcgtggcctc
 360
 tggctgcaag ggagaggggc acaggcaagg acatgacccc cgtaaccctc gagccccctc
 420
 cagaaattta accagagcct gtccctcctt tcttgctgc ccccaacatc tcacaatccc
 480
 tcctgtgatg gcagatgtct ccatctactc tacagacacc tgcaactatc attcccttga
 540
 tccgtggtaa ttaggagggg actcctctgt gaagaaccgc ttctaccatc ctctttttaga
 600
 aactctttct ccactgggat cc
 622

<210> 6
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Ser Leu Pro Val Pro Leu Ser Leu Ala Ala Arg Gly Gln His Ser
 1 5 10 15
 His Pro Gly Asp Thr Arg Pro Pro Leu Pro Ser Pro Lys Ile Ala Ser
 20 25 30
 Pro Met Cys Phe Pro Gln Lys Gly Leu Glu Gly Tyr Tyr Pro Asn Ala
 35 40 45
 Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu
 50 55 60
 Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly
 65 70 75 80
 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
 85 90 95
 Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn
 100 105 110
 Pro Met Ala Arg Arg Glu Thr Val Leu
 115 120

<210> 7
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 7
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 agaaaaccca cactctctct cccctcccca gtggctgtgg ctttctcagg gacaatagga
 120
 tgaatgggct ttcagtgtgg ggacagcaaa acatgcacta gggcccagag tggcagttct
 180
 ctggtgtgtg agagtgcctg ccacaggcct tggccagagc ccgtgaggga gtgggtgtgtg
 240
 aaaggccacc tccacgtggg taagcgtgag gacttggact tctctggcac tgagatggga
 300
 cctcctgcct gtggggagtca tctggccacc accctggggc cagtaaaggt tggagctaga
 360

agggtcgtcc tccctgactt gagctctgag ggctttgcct gccagccag agcggcaagg
 420
 cacaggggac cctcggggac gcccatggcc accctgggga agacagggct cctcacgcgt
 480

<210> 8
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Gly Phe Gln Cys Gly Asp Ser Lys Thr Cys Thr Arg Ala Gln Ser
 1 5 10 15
 Gly Ser Ser Leu Gly Val Glu Ser Ala Cys His Arg Pro Trp Pro Glu
 20 25 30
 Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg
 35 40 45
 Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
 50 55 60
 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
 65 70 75 80
 Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
 85 90 95
 Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly
 100 105 110
 Lys Thr Gly Leu Leu Thr Arg
 115

<210> 9
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 9
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 ctctgtctgct actttacaat gatccgttct tccccctctc ctctcctggtc aacagctggc
 120
 tcccagggat gctggatgac ctctttcagt ccattgttct gtgcgcctct gctcgtctct
 180
 ggctgtgcgt gtaccacggg attcgtgtcc agggagaaag aaagtgttta actttctatt
 240
 tgccataaatt ctctattgtt ggactattgt ggttggtctc tgttacgcta ggaatatggc
 300
 aaacagttaa cgaattacat gatccaatgt accagtatcg agttgatacc ggaatttttc
 360
 agggaatgaa ggtcttcttc atggtggtgg cagcgtgtga cattctgtac ctcttgttct
 420
 tgatagtg
 428

<210> 10
 <211> 138
 <212> PRT

<213> Homo sapiens

<400> 10

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Met Arg Asp Trp Gly Ile Glu Gln Lys Trp Met Ser Val Leu Leu Pro
 1           5           10           15
Leu Leu Leu Leu Tyr Asn Asp Pro Phe Phe Pro Leu Ser Phe Leu Val
 20           25           30
Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
 35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
 50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
 65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
 85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
100           105           110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
115           120           125
Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
130           135

```

<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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gaatgttgca ggcaaaactca agaccgggtgg ccttggtgaa ggtccaggtc agctcggcgg
120
acttgccccg ctcgaccagc acgctgttgg ggctcgtcatg cttcatgcgc cccatcatgc
180
catgccccat ggccggcgtgg tccatcttgc ccatgcgggt ggccgctgagc atgccgctgg
240
cttgcatctt gagcatttct ttctggtgtt cggcgtgcat cgccgcgatca cccagattga
300
attcgtgcag taactggcct ttgttgacca gcacaaagcg cacggtctca cggcgtttta
360
catccagagc cttggggcgaa aaggaaatgt cctgcagggt gacttccacg gtgcgcgtgg
420
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453

```

<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Met Leu Gln Ala Asn Ser Arg Pro Val Ala Leu Val Lys Val Gln Val
 1           5           10           15
Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

```

[illegible]

```
<210> 13
<211> 2034
<212> DNA
<213> Homo sapiens
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400> 13						
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ggcgtggcca	agcaggacac	ggtgcgcgctg	gccttctgct	ccggggagcct	gcgggtcctc	
120						
tgggacctac	catgctggcca	ttttctccca	tgtgtcaaac	acatggggttc	agccagcgaa	
180						
gattccatgg	gacctcctcg	tgtgggacgt	gtgctcccca	ccacaaatgg	aacgttcctc	
240						
gtttgcactc	ggagggggtg	gtggctcctgc	tggctggagc	agcctggggc	cagaggaagc	
300						
cgtatcaacc	ggctctgcag	cgtctcagcg	agggtgccct	ggagtaccta	gccaacctgg	
360						
accgagcccc	agacccccacg	gtcaggaaggg	acgccttttc	caccgacatc	ttcagcgcct	
420						
acgatgtttc	cttcccatcag	tggctgcaga	gtcgagaagc	caagctccgt	cttgccgtgg	
480						
tggaggctct	ggggcctatg	agccatctgc	tgccagtgga	gaggctggaa	gagcagctgc	
540						
ccaagctcct	ccttgggatt	ctcgccctct	acaagaagca	cgcagagacc	ttctacttgt	
600						
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660						
ccagcttgga	tgcctctctg	gctgcactgc	actcccagat	ctgtgtgcct	gtggagtcct	
720						
caagccccc	ggtgatgagt	aaccagaagg	aggtgctgcg	ctgcttcact	gtgctggcct	
780						
cgagctcgcc	tgaccgccta	ctggcctctc	tgtgtcccag	gctggacacc	accaatgaga	
840						
ggaccctcgt	gggcacccctg	caggggggcca	aacatgtcat	caactcaact	gctgctcaaa	
900						
tggaagataa	aaagcccttt	atcctgtctt	ccatgaggct	tcctctccctg	aacaccaaca	
960						

gcaaggtgaa gcgggacagt gtgcaggtga ttagcgccca tggcccacca cggtacacgt
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 1080
 gagcaggagg ctgagaagcc agggcccgcc agcaaggacc ccaaggccga cagcgtgcgg
 1140
 gccatcagcg tgcgcaccct ctacctggtc agcaccaccg tggacaggat gagtcacgtc
 1200
 ctctggccat acctgtctca gtctctcacc cctgtgcgct tcaactggggc cctgactccg
 1260
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 1320
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 1380
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 1440
 ctcagtggtc tgcacccaaa cattcaccct ttgctgggtc agcattggga aacgactgtc
 1500
 ccgctgctgc tggggctacgt ggatgagcac acagaagaga cctgccaca ggaggagtg
 1560
 gaggagaagc tgttgatggt gagggccggg gtacggccca tcttgggctc taagggtgtg
 1620
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 1680
 gggttggtcg gggagccaag gatcaggcag catcaaggct gaagacccca gcagccttgc
 1740
 agcgggggccc ttgctgtgac aaggcaccgg ccctctagca gtgcagcccc caagcgtcgg
 1800
 gggaacacct tcacctgcc tggtagacca actgtggcat ggctgtcccc tgagggttg
 1860
 ctctgccgcc cccggcctcc gctggaaggc ggtctgcagc ccctgcagcc acagcacatg
 1920
 gggatgtgcc caggtccag ccagccctgt gaggggtcgg gctcccagcc cctcagtggc
 1980
 atcttggcct gcagttcctg cgagacaccc tggccatcat ttctgacaac gcgt
 2034

<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

Ile	Val	Gln	Gln	Cys	Ala	Leu	Pro	Pro	Glu	Gln	Glu	Pro	Glu	Lys	Pro
1				5					10					15	
Gly	Pro	Gly	Ser	Lys	Asp	Pro	Lys	Ala	Asp	Ser	Val	Arg	Ala	Ile	Ser
			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
			35				40					45			
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55				60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
	65				70				75					80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

```

      85              90              95
Ala Ser Leu Pro Ser Pro Tyr Ala Val Thr Gly Arg Leu Leu Val Val
      100              105              110
Ser Ser Ser Pro Tyr Leu Gly Asp Gly Arg Gly Ala Ala Ala Leu Arg
      115              120              125
Leu Leu Ser Val Leu His Pro Asn Ile His Pro Leu Leu Gly Gln His
      130              135              140
Trp Glu Thr Thr Val Pro Leu Leu Leu Gly Tyr Leu Asp Glu His Thr
      145              150              155              160
Glu Glu Thr Leu Pro Gln Glu Glu Trp Glu Glu Lys Leu Leu Met Val
      165              170              175
Arg Ala Gly Val Arg Pro Ile Leu Gly Leu Lys Val Leu Ser Gly Leu
      180              185              190
Gly Gly Ala Gly Val Ala Glu Ala Gly Pro Pro Ala Ser Thr Ser Pro
      195              200              205
Arg Gly Leu Ala Gly Glu Pro Arg Ile Arg Gln His Gln Gly
      210              215              220

```

<210> 15
 <211> 363
 <212> DNA
 <213> Homo sapiens

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<400> 15
naccgcttgc tggctcgcca cggcaaggcg catgtcggct gcgatatctg caagccggcg
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gtgggttcga tcttgcctc gtgctggaac cagccgatca tggaccggcg gttggtgccg
120
ttgcaggaca ccaatgacac cttcatggcc aacatgcaga agaacggtag ctattcgatc
180
atccccgcga tcgcggcgcg cgagatcacc cgggacaaac tgatcgccct cggcgcggtg
240
gcgaagaaat acgatctgta caccaagatc accggcgccc agcggatcga cctgttcggc
300
gcccagttgc acgaattgcc gcagatctgg ggcgagctgg tggatgcggg attcgagacc
360
ggt
363

```

<210> 16
 <211> 121
 <212> PRT
 <213> Homo sapiens

```

<400> 16
Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
1      5      10      15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
20     25     30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
35     40     45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
50     55     60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

```

```

65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
      85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
      100              105              110
Leu Val Asp Ala Gly Phe Glu Thr Gly
      115              120

```

```

<210> 17
<211> 682
<212> DNA
<213> Homo sapiens

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<400> 17
gaattccatt ttgtggagta agaggtgact ggggtatagg gtacaaccca tagccatcca
60
tgttcatctt tgttttgaat ataattggct agaagatata catatatcta tgtaacttcc
120
tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
180
agaaaacagag cagctggaca agaggacagg tataggggaat aagggaagaag ccagtaaggg
240
aggaaaagacc ctccgtgaca aaggggcagg gaacagaact caaacattta atggcaggta
300
accagggtta gaattggtaaa ttgaaagggt aatataaagg gagaatgggt aaatgaattt
360
tctgaaatta attgctgtgt ttatagtttt tagccatgca tcggaatcac ctccaggactc
420
cactccaat caattatata tctgggggag gaccaaggcg ttggtatttt tcagaagctc
480
cactgggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
540
tgttgcagag gagcttcctt gggaaatgtc acacacagaa catcaatctt ccttccccac
600
tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctggttccc
660
tgctgtctca caaatcgaa ga
682

```

```

<210> 18
<211> 110
<212> PRT
<213> Homo sapiens

```

```

<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1      5      10      15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
      20      25      30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
      35      40      45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
      50      55      60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```

```

65              70              75              80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
              85              90              95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
              100              105              110

```

```

<210> 19
<211> 515
<212> DNA
<213> Homo sapiens

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<400> 19
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60
ccccctctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
120
cgtctgcagt gcagtcttgg gctataagaa acactggggc actcaatacc tcccccttt
180
tggcccttct cctcctctgg tccatgggtg gggttggggg gagcccagtt tcagcaccag
240
cagctgggag ccataccaca ctcatTTTTT agttctggct gtgggagccc ctccccacag
300
tttcagttcc ccaagcccca ggcctgagtt ttttttattg caaaagctgg ttgtgtgtgt
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgtgtg aggtgtccag tctgaagaa tgcctgggat acttctctcaa gcagttcctt
480
ctcacagctc cctggctgct ccgcatgtca gatct
515

```

```

<210> 20
<211> 130
<212> PRT
<213> Homo sapiens

```

```

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1          5          10          15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
20          25          30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
35          40          45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Trp Ser Met
50          55          60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65          70          75          80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
85          90          95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
100         105         110
Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
115         120         125
Lys Ser

```

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
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 60
 tagacgcggg gcctatgggt gcggaggacc atggagtga gcgagtaaga ctatgatgat
 120
 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg
 180
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
 240
 atacaatgac tgcttgacct gatgggttca caattgagca attggagctt acacgatctc
 300
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctgggtcaag
 360
 aattaaagca agttgtccaa ggcattccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
 1 5 10 15
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
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 ctgggcctgt tcgcgctgct gctgtcctgc tcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggcttc
 180
 ggggacctgg tgagcagcca gcacgccgcc taccggaacc aggggctcta ccgcctgggc
 240
 aacttctctt tcattcctgt cggtgtgtgc tgcatttact cgctcttcaa cgctcatctcc
 300
 atcctcatca agcagggtgt caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg
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 cgctgctgcc cggtcctctg cgcgcc
 385

<210> 24
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 24
 Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
 1 5 10 15
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
 20 25 30
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
 35 40 45
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
 50 55 60
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
 65 70 75 80
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
 85 90 95
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
 100 105 110
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
 115 120 125

<210> 25
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 25
 ccattgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagttctg
 60
 agggaggggag ttcccagctc tgtatttttg aagggtcagt ctgtgtgctt ggaccagtga
 120
 ggagcccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggagggaag ctgggtcgaat gcactgtgta ttggaggca gaaccagcag agggctctct
 240
 gggttgagtg tagggcaaaa gaaaaaag gcaccaagcc tgggtgctgg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgagctcga atatccatgc agcgcgcgcg aggatggaga gagcgatgga gcaactcaac
 60
 cgccctgacgc gctcgctgcg ccgcgcgcgc accgtggagt tgcccaggga taatgaaact
 120
 gctgtttata cattaatgcc aatggttatg gctgatcaac acagggtctgt ttctgaaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtgaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

```

65              70              75              80
His Ile Ala Ala Asn Cys Gly Ser Val Glu Cys Leu Val Leu Leu Leu
85
Lys Lys Gly Ala Asn Pro Asn Tyr Gln Asp Ile Ser Gly Cys Thr
100              105              110

```

```

<210> 29
<211> 375
<212> DNA
<213> Homo sapiens

```

```

<400> 29
ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
60
gagagctatt tgagcgccgt gacgccgctg agtcccaaa agattcgta gctgccccgc
120
tacaatatca cgatcaagcg cgctcgtaac atgacgggca agggccgcac gccgagctgg
180
tactcgctcg tcgtggctgg caatggctcg ggccctcggt gctatggcga aggcaaaagt
240
actaacatca gccgcgcgaa caaaaaggcg ttccacgcgc cggtgaaaaa catggacttg
300
gtatcggtcc accggtegaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
360
tgggggcgcta cgcgt
375

```

```

<210> 30
<211> 125
<212> PRT
<213> Homo sapiens

```

```

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1              5              10              15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20              25              30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35              40              45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50              55              60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65              70              75              80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85              90              95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100              105              110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115              120              125

```

```

<210> 31
<211> 375
<212> DNA
<213> Homo sapiens

```

<400> 31
 accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
 60
 ggggacgaggc acttacgagc ctgcgcgtca gggatgcttc ctggggccctt gagagtgccag
 120
 agattccttg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct
 180
 ccgcgcctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc
 240
 ctgcagagtg cacaaacctt gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
 300
 cactccccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
 360
 tggcctgcat tgttt
 375

<210> 32
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp
 1 5 10 15
 Gln Trp Gln Pro Ile Gly Ser Gly Cys Lys Asp Val Ser Cys Ser
 20 25 30
 Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala
 35 40 45
 Arg Asn Arg Gln Glu Pro Pro Phe Glu Leu Ala Gly Arg Glu
 50 55 60
 Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp
 65 70 75 80
 Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg
 85 90 95
 Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr
 100 105 110
 Ser Ile Ser Glu Gln Ser
 115

<210> 33
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 33
 ccattgagcc caaccgttgg cgataaagtc cgttttagcg ataccaattt atgggcaacc
 60
 attgaacaag atttattaac caaagggtgat gagtgtaaat ttgggtggcg taaaagtgtg
 120
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
 180
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaaag cgatattggg
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac
 300
 gtcacgccaa acatgattat cgggtgctagc acagaagtac ataacgggtgc a
 351

<210> 34
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
 1 5 10 15
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
 20 25 30
 Lys Phe Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
 35 40 45
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
 50 55 60
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
 65 70 75 80
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
 85 90 95
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
 100 105 110
 Val His Asn Gly Ala
 115

<210> 35
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 35
 nnctagctg caccaccacc tgttcacgca ggcagagcgg ccaccctca tggagaaga
 60
 ggaatccact gtattgggca caggcttccct gctggacctt ggcaagcagg tgcttggtg
 120
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct
 180
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatc agggcggcga
 240
 gagtgcctct caccacgtcc tccactggct cagggtccat ggctcggcgc cgggcgcgct
 300
 ccgacgcttg gtcggggcgg cggggccggg cgcgcaccgc cctcccttca cgcgt
 355

<210> 36
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 36
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1             5             10             15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20             25             30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35             40             45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Gly Thr Pro Gly
      50             55             60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65             70             75             80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85             90             95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100             105             110
Thr Ala Ser Leu His Ala
      115

```

```

<210> 37
<211> 492
<212> DNA
<213> Homo sapiens

```

```

<400> 37
acgcgtggcc ttcgtctgcc accaggacgc actcagcccc accgggttcc cggaccgcgc
60
gcaaccatga caagggcgat gttgtgatct ggggtggatc cttctccgac atgctcgagg
120
gatcggtatc ctccggcgta gtcacggtgc ttgccgaggg cggctatcgc ccaagggtcc
180
tcgccgacga cgtctgctgc ggggttgacgt ggatcactac cggtcagctc gacgggtgctc
240
ggcgtcgggt gcgcgctggt ctgcacgtgc tggcaccctc gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca tacctcgccc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgtcgct cagcccccatt
480
gtcatccgcg gg
492

```

```

<210> 38
<211> 127
<212> PRT
<213> Homo sapiens

```

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1             5             10             15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20             25             30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35             40             45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65      70      75
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85      90      95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100      105      110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115      120      125

```

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

```

<400> 39
aacgaaggtt cgcgtacgcgc tctgaaagcc ctgcgtaaag agcgttcoga tcgccgggaa
60
gtgatgngca cgcctaaaaat gcagggtggc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc gaaaaacaac tggtagagcaa cttctctgcy
180
caagtcacgc gtggtgataa aattgcgctg attgccccga acggttgtgg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gcogtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga cgcgtacggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

```

<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

```

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1      5      10      15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
20      25      30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
35      40      45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
50      55      60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65      70      75      80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
85      90      95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
100      105      110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
115      120      125
Gln Glu Val Met Val Asn Gly Arg Val

```

130

135

<210> 41
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 41
 gaattcaagt ggacacaggg tccacgcccc cgtctcaccg ataagagcta caagcacaaac
 60
 tactatgacg agcgggtttc gctcgaagag cgtcttgagc gcaactgtggc taaggatttc
 120
 gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgctgat gggtaaggat
 180
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcggttac
 240
 taccctcgatt tccgcgttca cgcggtgaat tccctgggg atccgtaccc gatccatc
 300
 gacgcgacct ttgtgccgct tcgtccgggg ctcctcatca acaaccgaa tcgtccactg
 360
 ccgcaggagc agaggaagat ctccgagggc aatgactggc agatcgttga tgcgtgctcag
 420
 ccggcgccacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
 480
 ttgttacttg atccgaagac ggtcatctgc gaggcttcgg aagttcatca gatggagcag
 540
 atggacaagc tgggtatgaa cgtcatcccg gtgccttcc gtgacgcgta cccattcggt
 600
 ggaggtctcc actgcgccac agctgatgta tatcgcaag gtacctgtga ggactacttc
 660
 ccgaatcagg tcgacgaccc gaccttgggt tgagaaaacc ccgtgggtcat gtcagtactg
 720
 acggatctcg gtggctcggt acggaactta cgttgcctgt taccggggcg ccgggtctga
 780
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
 840
 aacgtcaaac aggaagttcc aggcgtcggt acgatgaacc agaaagtggg attcgtgtcc
 900
 atgcttcttt ctgcaacggg tatggggttg gtgggtactt tcgggcgtct cagcactcct
 960
 gtggatccca cgacgggagc taagtacatc atcgggtgatt ttttggccac tggtaggatg
 1020
 atagtcgggg tcctgggatt tctgcttatt atcgtcatc ttgaaaaatg gtctgagctc
 1080

<210> 42
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 42
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
 1 5 10 15
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu


```

      20      25      30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
      35      40      45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
      50      55      60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
      65      70      75      80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
      85      90      95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
      100      105      110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
      115      120      125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
      130      135      140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
      145      150      155      160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
      165      170      175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
      180      185      190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
      195      200      205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
      210      215      220
Asp Asp Pro Thr Leu Val
      225      230

```

<210> 43
 <211> 358
 <212> DNA
 <213> Homo sapiens

```

<400> 43
gggccccca catagtggac acaggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc cagcacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtccc
240
agatcctgaa ggaagtgcag agcccagagg ggaatgatctc gctgaggggac acagctgcct
300
ccctccgcct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

```

<210> 44
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

```

1	5	10	15
Leu Gly His	Arg Gly Cys Leu	Pro Ala Ala Pro	Gly Arg Ala Val Asp
	20	25	30
Thr Thr Ala	Trp Ser Ala Val	Pro Gly His Cys	His Ala His Arg Cys
	35	40	45
Pro Leu Arg	Met Asp Leu Gly	Phe Arg Ile Arg	Val Ala Tyr Gln Arg
	50	55	60
Glu Ser Gln	Ile Leu Lys Glu	Val Gln Ser Pro	Glu Gly Met Ile Ser
	65	70	75
Leu Arg Asp	Thr Ala Ala Ser	Leu Arg Leu Glu	Arg Asp Thr Arg Gln
	85	90	95
Leu Pro Leu	Leu Thr Ser Ala	Leu His	
	100	105	

<210> 45

<211> 905

<212> DNA

<213> Homo sapiens

<400> 45

gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcgggtttc
 60
 gcggctcctg gaatcccaga gcagtatggt ggcgacgggt cggatgcatg tgcgtccgca
 120
 ataatactgg aagaggtcgc tcgagtcctgt gcgtcgtcgt ccaccgtcat atcgcccaat
 180
 gagcttggta cgcgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
 240
 tctgaagtgg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggg tgatgctgga
 300
 tcagatccag ctgcacttaa gtgtcagacc gacgaagatg gggacagttt cgtcctgaat
 360
 ggcgttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttcgggtt
 420
 actgacccag acgatccgcg ccacagaatc agcgcgttga tggtccatgc agatgacccg
 480
 ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa
 540
 gtggttttca agaatacgcg tatccccaag gaacagagtaa ttggccgtcg agggcacggt
 600
 ctgagtggtg ctctaggtac gcttgataac tctcgtgtct cgattgtctg tcaagcagtg
 660
 ggaattgtcc aaggagcttt agacattgcc acggattacg tccaagaagc caagcagttt
 720
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
 780
 ttggaggcgg cgcgagcgct gacatactct gcagctgatc gtatggggcg ccagactgac
 840
 gatgtgagtt acttcggcgc ggcgcccaaa tgtttcgctt ccgacacagc gatggcagtg
 900
 tgcac
 905

<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46
 Val Asn Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
 1 5 10 15
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Asp
 20 25 30
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
 35 40 45
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
 50 55 60
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
 65 70 75 80
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
 85 90 95
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
 100 105 110
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
 115 120 125
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
 130 135 140
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
 145 150 155 160
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
 165 170 175
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
 180 185 190
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
 195 200 205
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
 210 215 220
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
 225 230 235 240
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
 245 250 255
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
 260 265 270
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
 275 280 285
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
 290 295 300

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47
 aagcttgtag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcattcta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctgggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcggtta
 240
 gatttcgaaa aaggactcac caaatcccag ggtcgacgag aagagtccat acccgctggc
 300
 gaagacgccca gcacgtataa cagacttatg aaagcgctgc gccaacgccca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His
 1 5 10 15
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg
 20 25 30
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala
 35 40 45
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys
 50 55 60
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly
 65 70 75 80
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg
 85 90 95
 His Asp Val Ile Lys Ser Gly Lys Leu Ala
 100 105

<210> 49
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 49
 tgatcatgat gctggcatgg actattctgg tcctgttccc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgct tccttctgta tcatcaaat ttcctctctc actgagtctc
 120
 ttgcattccc ttggaagcat gctgtactat gtcccatcct taaagaactc cccctgtctg
 180
 cacattaccc tctgccagct ggctcatttt tctgtctccc ttacaggga aactcttcaa
 240
 aaagtatatc ccacctcctt ccatctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctccctttg
 309

<210> 50
 <211> 101
 <212> PRT

<213> Homo sapiens

<400> 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1             5             10             15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
      20             25             30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
      35             40             45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
      50             55             60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
      65             70             75             80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
      85             90             95
Val Leu Pro Pro Phe
      100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

```

agatctttga agaattgccca cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggccctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgctggc attccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt ctgtacttct atgtgccctt
300
caaaatcttc tggttctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggccctctgt ttcatttatg tgacctccca
480
tcagggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1             5             10             15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
      20             25             30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

          35              40              45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
  50              55              60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
  65              70              75              80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
          85              90              95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
          100              105              110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
          115              120              125

```

<210> 53

<211> 474

<212> DNA

<213> Homo sapiens

<400> 53

```

accggtacac ctacgtcacc cgtaaaaacc gacgcaatac cgggatcgcc tcgtcctcaa
  60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgcct aatggccaaa
  120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
  180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
  240
gcatcgcgta agctgtctcg cctgcgcgcg gattcatccc ccgtgcgggtt acgtaaccgt
  300
gaccaagtcg acggggcgctc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
  360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctgggtgaagc
  420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgcatatggc gggc
  474

```

<210> 54

<211> 101

<212> PRT

<213> Homo sapiens

<400> 54

```

Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
  1              5              10              15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
          20              25              30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
          35              40              45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
          50              55              60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
          65              70              75              80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
          85              90              95
Ala Lys Ser Ser Trp

```

100

<210> 55
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 55
 ccatggccca ggacagcggg catatcggct acgactacgg tacaccgggtg gcgccacagt
 60
 tcggcgcgagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccggtggg
 120
 tgggtgttcga ccatgtgcgt tgcacccacg acacettctt gatcgacgtc ttctcacc
 180
 agcccgatgc caccgcgcag cagggtcaatg ccgacaaccc gactacgtc gggcggttca
 240
 gccgcacatgg catgggcctg gtggatgaca agggccggtg cattaccag ggcgtatcgc
 300
 gcgcgttgaa tgcggcgcg cgcaccaagg cgctgaacct gggaccgagt gacgcggcgc
 360
 agttatcggg gaggcgta
 378

<210> 56
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
 1 5 10 15
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
 20 25 30
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
 35 40 45
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
 50 55 60
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
 65 70 75 80
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
 85 90 95
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
 100 105 110
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
 115 120 125

<210> 57
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 57
 agacccccc gacacagatc aggagtcgtc atgtccagaa agaagaaggc cggcatcctc
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggtgcc
 120
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
 240
 atctctggaa ctagccgtga caaggtcaat cacatgatta tcgacggcga ggaacggggt
 300
 atggctcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcgggtg gcaccgcca gaacgcgt
 388

<210> 58
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 58
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
 1 5 10 15
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
 20 25 30
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
 35 40 45
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
 50 55 60
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
 65 70 75 80
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
 85 90 95
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
 100 105 110
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Thr Ala Lys Asn
 115 120 125
 Ala

<210> 59
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggtaccatcg gagctcgaca agaaatggtt ggggtgaagtc gtggcttctg ctccaccag
 60
 tgccctcatg ggtagccca cctgaatata ttcatgcctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcattctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct
 240
 cagaccgcgt ggacaagacc aagatgaaa tggaacacga ggccttggtg gaagggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcggtg cagacgggtga
360

tgctttcaga agcccgagg agcgtcttgg gggcagtgtc gaaggttggtg ctgtaca
417

<210> 60

<211> 101

<212> PRT

<213> Homo sapiens

<400> 60

Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
1 5 10 15

Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
20 25 30

Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
35 40 45

Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
50 55 60

Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
65 70 75 80

Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
85 90 95

Lys Val Val Leu Tyr
100

<210> 61

<211> 304

<212> DNA

<213> Homo sapiens

<400> 61

agatcttcac agccttagac ttttttcattg ggtgccttac agttttggag gtccttatcc
60

gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
120

tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
180

ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagttc
240

tcccctagac cggggcccatg gccaggcctg accacagagc tcccattgcc ttctctgcac
300

gcgt

304

<210> 62

<211> 92

<212> PRT

<213> Homo sapiens

<400> 62

Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
1 5 10 15

```

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
20                25                30
Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
35                40                45
Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
50                55                60
Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
65                70                75                80
Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
85                90

```

```

<210> 63
<211> 577
<212> DNA
<213> Homo sapiens

```

```

<400> 63
cgcgctcaagg ggggtctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgag
60
ctgacgggtgc tagctgggtg gctcaccccta gccgggcgta tcagtgtcgg ggaactcgtc
120
accgtggtgc ggctggccca aaccctcggc cctccgctgc gagcactggg cgctgacacc
180
gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
240
ccggcagcct ggcagatcca ccccgacgac ggtgcccgca ccacaccggg tgatggcccc
300
gtggagttgc acatcccggg caggggatttc cagcttgacg tcgccggcgg caccatgtg
360
ggtatcatgg cgcctcaatc ggtctgtgac gccttgggcg aggcgataga ccacgggtcc
420
gagaccgtct tgaatggggg tcccgcagat cgcctcaacc ctgcccaacg gcgtcgtctg
480
gtgctgtgtg ctccccgctc ccccgaaactg ttcgacgata ctgcccgctg gaacatcgtg
540
cttgacagcc agacgactgt cgccaggctg aatgcat
577

```

```

<210> 64
<211> 192
<212> PRT
<213> Homo sapiens

```

```

<400> 64
Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
1      5      10      15
Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
20     25     30
Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
35     40     45
Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
50     55     60
Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
65     70     75     80

```

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                    105                    110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                    120                    125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                    135                    140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145                    150                    155                    160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                    170                    175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                    185                    190

```

<210> 65

<211> 339

<212> DNA

<213> Homo sapiens

<400> 65

```

gtcgaccgcg ccttggggtc gctcgaaggg gccagcctgg accagggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgcc gggcaactag tgggcaccat ggcctccgag
120
cgcccttgccg taccccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggtctgtct taacgacgcc gtaaagaaag gcggcatgat ggcctgcccc
300
cgcgtcggcg gtttgtctgg ctccttcac cggggtccc
339

```

<210> 66

<211> 113

<212> PRT

<213> Homo sapiens

<400> 66

```

Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
1      5      10      15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
20     25     30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
35     40     45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
50     55     60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65     70     75     80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
85     90     95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
100    105    110

```

Ser

<210> 67
 <211> 446
 <212> DNA
 <213> Homo sapiens

<400> 67
 tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc
 60
 cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga
 120
 caaggggtcc ttgcacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca
 180
 gggagtcggg cccgccctag ccttcctcga ttcagcgtgg ggagcccgaga tccacgtgga
 240
 gacaacaggg tgtcccagtg ccgtggctctg gaatccacgc tcctcgtcga cacatgccga
 300
 taacccgaca gccacggcat ggccgcgattt cgtatgcgtc gagaccgggg cctgcaagga
 360
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga tttagcgtcga
 420
 aacgttgtga tcgctgcatg gatatt
 446

<210> 68
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Trp His Thr Tyr Leu Arg Val Ala Asp Ala Ala Gln Ala Arg Val
 1 5 10 15
 Arg Gly Val Arg Gly Ala Ser Trp His Asn Phe Ala Thr Gly Asp Lys
 20 25 30
 Gly Ser Phe Asp Ala Asn Glu Leu Ala Val Thr Pro Asp Thr Asp Thr
 35 40 45
 Val Ile Gln Gly Val Gly Pro Ala Leu Ala Leu Leu Asp Ser Ala Trp
 50 55 60
 Gly Arg Gln Ile His Val Glu Thr Thr Gly Cys Pro Ser Ala Val Val
 65 70 75 80
 Trp Asn Pro Arg Ser Ser Ser Thr His Ala Asp Asn Pro Thr Ala Gln
 85 90 95
 Ala Trp Arg Asp Phe Val Cys Val Glu Thr Gly Ala Cys Lys Asp Asn
 100 105 110
 Ala Val Ile Val Ala Pro His Ser Asp Leu Thr Met Ser Thr Arg Ile
 115 120 125
 Ser Val Glu Thr Leu
 130

<210> 69
 <211> 552
 <212> DNA

<213> Homo sapiens

<400> 69

nnaagggttaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
 60
 ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccgag atgccaaaa
 120
 agtcctccaa gattgccagc ttcacccca aaggggggaa gctcaacagt gccagaagg
 180
 agncctatgg cccttccct cagtgaata ccaaaaccag gaatgaaaag catgcccggg
 240
 aaatccccaa gtgcccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
 300
 agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttctctcttc
 360
 agcctggcgt cctcagaagg aaaaggccca ggagggacca cctgaacca cagcatcagc
 420
 agccagactg tcagtgggtc tgctgggacc acccagacca caggaagcaa tnnaccgtca
 480
 gtgttcagct acctcagccc cagcagcaat acaaccatcc caactgcc acggttgac
 540
 ctttcctgta ca
 552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

Xaa	Arg	Val	Arg	Arg	Lys	Ala	Arg	Thr	Leu	Gln	Arg	Glu	Pro	Leu	Cys
1				5					10					15	
Arg	Arg	Gly	Trp	Pro	Ser	Arg	Arg	Ser	Gln	Lys	Lys	Thr	Pro	Val	Glu
			20					25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35					40					45			
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
	50					55					60				
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
	65				70					75				80	
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
			85						90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
		100						105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys
		115					120					125			
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
		130				135					140				
Ser	Gly	Ser	Val	Gly	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser	
		145			150				155				160		
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
				165					170					175	
Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
				180											

<210> 71
 <211> 316
 <212> DNA
 <213> Homo sapiens

<400> 71
 cgcgttgaaa tggcggtcga acttaaacgt ttacatattg actccgtgcc attaaacatt
 60
 ttgaatcctg ttaaaggagac tccatttgaa agcaacgaag ctttacgtcc tttaaatatac
 120
 ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatacg aactgcaggt
 180
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtgg cctaaacggg
 240
 atcatgggtg gtggctactt aactactggc ggtcggtcac ctcaagacga tctccaaatg
 300
 attcaagact tggagt
 316

<210> 72
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 72
 Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val
 1 5 10 15
 Pro Leu Asn Ile Leu Asn Pro Val Lys Gly Thr Pro Phe Glu Ser Asn
 20 25 30
 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg
 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
 50 55 60
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
 65 70 75 80
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
 85 90 95
 Asp Leu Gln Met Ile Gln Asp Leu Glu
 100 105

<210> 73
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 73
 nntaccggca agatcctggc cgaagggtgac gtcgagggtt ctgaggctat cgactttgct
 60
 gcttggtatg tcgaccgagc cgaggagctc gagggcgctc acgggtgcccc gtttggtgccg
 120
 ccacgagtga ccgtcgtcac cccgccgtgg aacttcgccc tgtctattac cgccggatcc
 180

acccttgcgc ctctggccgc cggatcgta gtactactca agcccgctcc acaggcccgc
 240
 cactgtgctg ccgtcatctc tgaatgcctg tgggaggctg ggatccccgc ggagttctg
 300
 cagctcgctg atgttgagga aaatgaggct ggtaaacacc tggtagacca ccccgaggtc
 360
 gatcgggtca tcctcacggg aggt
 384

<210> 74
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 74
 Xaa Thr Gly Lys Ile Leu Ala Glu Gly Asp Val Glu Val Ser Glu Ala
 1 5 10 15
 Ile Asp Phe Ala Ala Trp Tyr Val Asp Arg Ala Glu Leu Leu Glu Gly
 20 25 30
 Val Asp Gly Ala Gln Phe Val Pro Pro Arg Val Thr Val Val Thr Pro
 35 40 45
 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala
 50 55 60
 Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg
 65 70 75 80
 His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro
 85 90 95
 Arg Asp Val Leu Gln Leu Val Asp Val Glu Glu Asn Glu Ala Gly Lys
 100 105 110
 His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly
 115 120 125

<210> 75
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 75
 gaattcgtct cggaatacac gctggaaaaat tcggccgaga tgccgggggt gcgctcanac
 60
 cgcattgagg cgctggccga gctctatgcc gatcccaaga ccagggtgggt gagcttctgg
 120
 accatgggct tcaaccagca caccgcggc gtctggtgca acaatctcgt ctacaacatc
 180
 cacctgctga ccggaaaaat ctgcagccc ggcaacagcc cgttctcgt gaccgggagc
 240
 ccattggcct gcggcacggc gcgcgaggtc ggtaccttct cgcacgcct gcccgccgac
 300
 atggtgggtca ccagcaaggc gcaccgcgac atcgccgaga agatctggca gctgccggaa
 360
 ggaccagtc cgcacaagcc cggctaccac gccgtgtctg agagc
 405

<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 76
 Glu Phe Val Ser Glu Tyr Thr Leu Glu Asn Ser Ala Glu Met Ser Gly
 1 5 10 15
 Val Arg Ser Xaa Arg Ile Glu Ala Leu Ala Glu Leu Tyr Ala Asp Pro
 20 25 30
 Lys Thr Arg Val Val Ser Phe Trp Thr Met Gly Phe Asn Gln His Thr
 35 40 45
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
 50 55 60
 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
 85 90 95
 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
 100 105 110
 Glu Lys Ile Trp Gln Leu Pro Glu Gly Pro Val Pro Asp Lys Pro Gly
 115 120 125
 Tyr His Ala Val Leu Gln Ser
 130 135

<210> 77
 <211> 5816
 <212> DNA
 <213> Homo sapiens

<400> 77
 gagcggcgcc ctgctctggc cgttgetccc gctcctgetc ctgctgctgt cggcgcgggga
 60
 cggcgtgcgc gcccgcgagc ctccaggcccc gggttacttg attgcagctc cctctgtttt
 120
 tcgcgcgggc gtggaggaag tcatacagcgt gaccatcttt aactctccaa gggaagtca
 180
 ggtccaggct cagctgggtg cccagggtga gccggtggtg cagagccagg gagccatcct
 240
 ggataaagg acaatcaaac tcaaggtgcc caccggcctc cggggccaag cgcttctgaa
 300
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 360
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<210> 78

<211> 799

<212> PRT

<213> Homo sapiens

<400> 78

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Thr	Ala	Ser	Ile	Ile	Gly	Asp	Val	Met	Gly	Pro	Thr	Leu	Asn	His	Leu	35	40	45
Asn	Asn	Leu	Leu	Arg	Leu	Pro	Phe	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	50	55	60
His	Phe	Ala	Pro	Asn	Val	Phe	Val	Leu	Lys	Tyr	Leu	Gln	Lys	Thr	Gln	65	70	75
Gln	Leu	Ser	Pro	Glu	Val	Glu	Arg	Glu	Thr	Thr	Asp	Tyr	Leu	Val	Gln	85	90	95
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Ala	Phe	Gly	Glu	Arg	Asp	Ala	Ser	Gly	Ser	Met	Trp	Leu	Thr	Ala	Phe	115	120	125
Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Ser	Phe	Ile	Phe	Val	Asp	Pro	130	135	140
Arg	Glu	Leu	Ala	Ala	Ala	Lys	Ser	Trp	Ile	Ile	Gln	Gln	Gln	Ala		145	150	155
Asp	Gly	Ser	Phe	Leu	Ala	Val	Gly	Arg	Val	Leu	Asn	Lys	Asp	Ile	Gln	165	170	175
Gly	Gly	Ile	His	Gly	Ile	Val	Pro	Leu	Thr	Ala	Tyr	Val	Val	Val	Ala	180	185	190
Leu	Leu	Glu	Thr	Gly	Thr	Ala	Ser	Glu	Glu	Glu	Arg	Gly	Ser	Thr	Asp	195	200	205
Lys	Ala	Arg	His	Phe	Leu	Glu	Ser	Ala	Ala	Pro	Leu	Ala	Met	Asp	Pro	210	215	220
Tyr	Ser	Cys	Ala	Leu	Thr	Thr	Tyr	Ala	Leu	Thr	Leu	Leu	Arg	Ser	Pro	225	230	235
Ala	Ala	Pro	Glu	Ala	Leu	Arg	Lys	Leu	Arg	Ser	Leu	Ala	Ile	Met	Arg	245	250	255
Asp	Gly	Val	Thr	His	Trp	Ser	Leu	Ser	Asn	Ser	Trp	Asp	Val	Asp	Lys	260	265	270
Gly	Thr	Phe	Leu	Ser	Phe	Ser	Asp	Arg	Val	Ser	Gln	Ser	Val	Val	Ser	275	280	285
Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Tyr	Thr	Leu	Leu	290	295	300
Gly	Asp	Val	Ala	Ala	Ala	Leu	Pro	Val	Val	Lys	Trp	Leu	Ser	Gln	Gln			

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Arg	Asn	Ala	Leu	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Cys	Val
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Leu	Gln	Ala	Leu	Ala	Glu	Tyr	Ala	Ile	Leu	Ser	Tyr	Ala	Gly	Gly
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Asn	Leu	Thr	Val	Ser	Leu	Ala	Ser	Thr	Asn	Leu	Asp	Tyr	Gln	Glu
				355				360				365		Thr
Phe	Glu	Leu	His	Arg	Thr	Asn	Gln	Lys	Val	Leu	Gln	Thr	Ala	Ala
				370				375				380		Ile
Pro	Ser	Leu	Pro	Thr	Gly	Leu	Phe	Val	Ser	Ala	Lys	Gly	Asp	Gly
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Cys	Leu	Met	Gln	Ile	Asp	Val	Thr	Tyr	Asn	Val	Pro	Asp	Pro	Val
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Lys	Pro	Ala	Phe	Gln	Leu	Leu	Val	Ser	Leu	Gln	Glu	Pro	Glu	Ala
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Gly	Arg	Pro	Pro	Pro	Met	Pro	Ala	Ser	Ala	Ala	Glu	Gly	Ser	Arg
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Asp	Trp	Pro	Pro	Ala	Asp	Asp	Asp	Asp	Pro	Ala	Ala	Asp	Gln	His
				450				455				460		His
Gln	Glu	Tyr	Lys	Val	Met	Leu	Glu	Val	Cys	Thr	Arg	Trp	Leu	His
465					470				475					480
Gly	Ser	Ser	Asn	Met	Ala	Val	Leu	Glu	Val	Pro	Leu	Leu	Ser	Gly
				485					490					495
Arg	Ala	Asp	Ile	Glu	Ser	Leu	Glu	Gln	Leu	Leu	Leu	Asp	Lys	His
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Gly	Met	Lys	Arg	Tyr	Glu	Val	Ala	Gly	Arg	Arg	Val	Leu	Phe	Tyr
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Asp	Glu	Ile	Pro	Ser	Arg	Cys	Leu	Thr	Cys	Val	Arg	Phe	Arg	Ala
				530				535				540		Leu
Arg	Glu	Cys	Val	Val	Gly	Arg	Thr	Ser	Ala	Leu	Pro	Val	Ser	Val
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Asp	Tyr	Tyr	Glu	Pro	Ala	Phe	Glu	Ala	Thr	Arg	Phe	Tyr	Asn	Val
				565					570					Ser
Thr	His	Ser	Pro	Leu	Ala	Arg	Glu	Leu	Cys	Ala	Gly	Pro	Ala	Cys
				580					585					590
Glu	Val	Glu	Arg	Ala	Pro	Ala	Arg	Gly	Pro	Gly	Trp	Phe	Pro	Gly
				595				600				605		Glu
Ser	Gly	Pro	Ala	Val	Ala	Pro	Glu	Glu	Gly	Ala	Ala	Ile	Ala	Arg
				610				615				620		Cys
Gly	Cys	Asp	His	Asp	Cys	Gly	Ala	Gln	Gly	Asn	Pro	Val	Cys	Gly
625					630				635					640
Asp	Gly	Val	Val	Tyr	Ala	Ser	Ala	Cys	Arg	Leu	Arg	Glu	Ala	Ala
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Arg	Gln	Ala	Ala	Pro	Leu	Glu	Pro	Ala	Pro	Pro	Ser	Cys	Cys	Ala
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Glu	Gln	Arg	Leu	Pro	Ala	Ser	Ser	Ser	Ser	Thr	Tyr	Gly	Asp	Asp
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              740              745              750
Thr Pro Ala Pro Gln Arg His Ser Gly Arg Val Val Gly Ala His Arg
              755              760              765
Pro Gly Leu Leu Ser Pro Val Phe Val Tyr Ser Pro Ala Phe Gln Ser
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Gly Gly Glu Glu Gly Leu Trp Met Ser Asn Thr Cys Thr Leu Arg
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<210> 79
 <211> 346
 <212> DNA
 <213> Homo sapiens

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<210> 80
 <211> 101
 <212> PRT
 <213> Homo sapiens

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Lys Ala Glu Tyr Leu Ala Ala Thr Ser Tyr Arg Asp Phe Leu Leu Lys
20         25         30
Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
35         40         45
Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
50         55         60
Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
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Ser Glu Glu Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
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Pro Asp Gly Asn Ala
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<210> 81
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 81

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<210> 82

<211> 79

<212> PRT

<213> Homo sapiens

<400> 82

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Met	Xaa	Val	Cys	Met	Cys	Val	Cys	Thr	Cys	Xaa	Cys	Val	Pro	Val	Cys
				20					25					30	
Met	Cys	Pro	Cys	Ala	Cys	Leu	Cys	Cys	Val	Cys	Ala	Cys	Met	Cys	Ala
				35					40					45	
Cys	Leu	Cys	Val	Xaa	Val	Cys	Val	Arg	Ala	Cys	Val	Cys	Thr	Cys	Val
				50					55					60	
His	Val	His	Val	Cys	Ala	Pro	Val	Cys	Met	Ser	Val	Cys	Thr	Arg	
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<210> 83

<211> 411

<212> DNA

<213> Homo sapiens

<400> 83

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 411

<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
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 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
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 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
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<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 85
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 240
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<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly
 20 25 30
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
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Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
      65              70              75              80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85              90              95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100             105             110

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<210> 87

<211> 355

<212> DNA

<213> Homo sapiens

<400> 87

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      120
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      180
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      240
gtgggtactcg atatcacatc taaaccgccg gccaccatcg agtgggaatg agccccgtct
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<210> 88

<211> 96

<212> PRT

<213> Homo sapiens

<400> 88

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      1              5              10              15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20              25              30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35              40              45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50              55              60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
      65              70              75              80
Val Val Leu Asp Ile Thr Ser Lys Pro Ala Thr Ile Glu Trp Glu
      85              90              95

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<210> 89

<211> 351

<212> DNA

<213> Homo sapiens

<400> 89

ATTORNEY DOCKET NO.: 15966-543

nacgcgtcaa caccaggcta cgggtgggtat gatcatgata agggctggga cccgcaggag
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 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca
 120
 ggtgattgga taaggccaga ggggtgggcy ggggttctgcc cctgctgaag cctggtgggg
 180
 cccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg
 240
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgactgaacc
 300
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c
 351

<210> 90
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 90
 Ser Leu Val Gly Pro Arg Ser Val Ile Trp Asp Arg Asn Asn Thr Ser
 1 5 10 15
 Ala Leu Gly Leu Leu Asp Val Ala Gln Ala Leu Glu Gln Asn His Ser
 20 25 30
 Leu Lys Ser Met Pro Leu Pro Leu Asn Asp Val Thr Gln Ala His Arg
 35 40 45
 Ser Arg Pro Glu Leu Thr Thr Arg Ala Val His Gln Ile
 50 55 60

<210> 91
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 91
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 acgtcgaagc ccagcagggc ctccctgcagg tccctggggc agccagcaca cacaaagtcc
 120
 cggaaggggc tgtagactcc ctgccagcgg ctttccgggg gaaggcaccc acgcccagct
 180
 gcctcttgca ggtactgctc gggctctggt ggagggcagc cgtgtccagc acaccctgtg
 240
 tgtgcagctc tctccctgcc ccaactgccga acgagccctc caggtgaag ccattggggg
 300
 acgtgacctt gcccttcccc atgaggt
 327

<210> 92
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 92
 Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

ATTORNEY DOCKET NO.: 15966-543

1	5	10	15
Ser Phe Gly	Ser Gly Ala Gly Arg	Gly Leu His Thr Gln	Gly Val Leu
	20	25	30
Asp Thr Ala Ala Leu	Pro Pro Asp Pro	Ser Ser Thr Cys Lys Arg Gln	
	35	40	45
Leu Gly Val Gly Ala Phe	Pro Gly Lys Ala Ala	Gly Arg Glu Ser Thr	
	50	55	60
Ala Pro Ser Gly Thr Leu Cys	Val Leu Ala Ala	Pro Gly Thr Cys Arg	
	65	70	75
Arg Pro Cys Trp Ala Ser Thr	Cys Arg Ala Pro	Gly Ser Cys Val Gly	
	85	90	95
Leu Arg Ile Thr Cys Pro Ala	Arg Gly Pro Thr		
	100	105	

<210> 93
 <211> 394
 <212> DNA
 <213> Homo sapiens

<400> 93
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 atgctcgaat gggacggcgg acatgagcaa tagggcgcca aagcacagcg agaggaaaggc
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 ggcgcgctct gcggcctcgc ggaatgaagga ggggtggtcg cgcaagagac gccccgcgcc
 180
 ttttgtaccg ataaatccc ggcgccacct gatcgtgacc gagggtacga aaacggaacc
 240
 gctctatttc gaggetatca ggttgcgtgt caacaaccgt tatcacggcc agtgggtgac
 300
 aatggaagtt gtcgttaccg gcaagcatatc caggggactt ctcgatcgtg cagtcactct
 360
 ggcggaagaa agtgccacag gattcactca cgta
 394

<210> 94
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 94
Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
1 5 10 15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
20 25 30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
35 40 45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
50 55 60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
65 70 75 80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
85 90 95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95
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 120
 ccaaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
 180
 cagtggtcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc
 240
 tggggctctg cttggccata ggcaactgcac attgtgccac ctgctcatca cctcctctag
 300
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag
 360
 gctgagcatg gagctcacc catgccatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccattggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttctc
 480
 aatctctgtt cccaccacat ttcattaggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
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 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
 100 105 110
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
 115 120

<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97
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 tcgcggtgcc ttgcgcgcgg gctggtaggt ggagaagccg cgcgagtacg ccgcgtagag
 120
 cgacatcgtg tctgagacgt cgaagctcag gccagcttt ggcgctccagg cgcgctcggg
 180
 cggtccgccc tcttgcggca attgattcag cgcaatcccg gccatcacat gccacgcctt
 240
 gtccagggtc atgaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 98
 Met Ala Ser Gly Asp Leu Phe Pro Gly Asn Val Phe Ser Pro Arg Val
 1 5 10 15
 Pro Phe Pro Ser Ser Asp Ile Thr Pro Asn Ile Glu Arg Leu Ser Asn
 20 25 30
 Ser Pro Leu Arg Ser Ser Arg Ala Tyr Ala Gln Asp Phe Met Thr Leu
 35 40 45
 Asp Lys Arg Trp His Val Met Ala Gly Ile Ala Leu Asn Gln Leu Pro
 50 55 60
 Gln Glu Gly Gly Pro Thr Glu Arg Ala Trp Thr Pro Lys Leu Gly Leu
 65 70 75 80
 Ser Phe Asp Val Ser Ser Asp Thr Met Ser Leu Tyr Gly Ala Tyr Ser Arg
 85 90 95
 Gly Phe Ser Thr Tyr Gln Pro Ala Arg Lys Ala Pro Arg Ala Tyr Gly
 100 105 110
 Pro Ser Ala Ala Arg Pro Ser Lys Arg Glu
 115 120

<210> 99
 <211> 545
 <212> DNA
 <213> Homo sapiens

<400> 99
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 tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg
 120
 tcgatcccat cactcgggat ttgctggaat cectgggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcgggtcgca tcgattggct ctcccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggagggtac tcgatgatga ctgaacgttc
 300
 ccattccacg atcagggttaa ggtggccggc ggtggtggtt ctgcgtctcg ttccgctgct
 360
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccggttg ggccgggtga
 420
 aagcggccgt cgtcaacgag gacaaggccg tcaagggtgcg tggacaactg gttccgatgg
 480
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 540
 tcgac
 545

<210> 100
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 100
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 1 5 10 15
 Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
 20 25 30
 Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
 35 40 45
 Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
 50 55 60
 Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
 65 70 75 80
 Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
 85 90 95
 Ser Gly Ala Asp Ala
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<210> 101
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 101
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 120
 aagctgcggc ggggtactat ctcatcctcg ccacggatcc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatggtccag
 300
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
 360
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccg
 420

gtcgacattg tccacgcca agatgtccat aaggagatgg ccgacaagct ttgctctggc
 480
 gagatcacct gggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacgggtgat
 540
 atcgactttg cagccatcgt gaggctcctt gatgaagccg gggtcgatgg ttattacgtc
 600
 ctagagcagg acatcatga
 619

<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
 Thr Arg Ser Leu Thr Pro Ser Lys Leu Pro Gly Val Thr Ile Ser Ser
 1 5 10 15
 Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 103
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 gccattgggg ggagaccctt gccgtgggga aagacccttg ccattggggga gacccttgcc
 120
 actgggggga gacccttgcc gctgggggga gaccgagacc attgggggga gacccttgcc
 180
 atgggggaaa acccttgcca ttgggggaga ntacctgcca ttgggggaga tccttgccgt
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 tggggggaga tccttgctgt tggggggaga ntccctcctg taggggaaga ccctgcagg
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agtgggtggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp
1 5 10 15
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
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ccgggtcaac gagggtttgg cgcacggtcc actccgtggc gcccggggtg atgtgcaaca
120
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgctc cagtacccat
180
ccagcgcgcat gccccagcgg tcggcatccc agccgtggtc gccgtcgagc gccccagggg
240
cttcaatgtc gtcacggcg gccagttcca cccggcgga catctcgttg cggaccatga
300
ccgggaaggc gcgggaattc tcggtcagtt tcggcggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser
1 5 10 15
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His


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          35          40          45
Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro
  50          55          60

<210> 107
<211> 549
<212> DNA
<213> Homo sapiens

<400> 107
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60
gccgcttaat aaccgaccaa catgaaactc aagggtgccc ccttcctagc ggggaccttg
120
cacagacccc aaaataagggt gttttgtctc gccctcctca gttcacgtgg gcaccttgga
180
acactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gcactgtttt
240
cgctccttc gccctgttct cgtgactgac aggagcaggg gtcacaagca ggcagcccga
300
gagctctgct cacctggaaa agcatttttg tgtagcttaa atgtgaaggc ctcaggcagt
360
ggcctgttgt cctcctccac atgcgcccac cttcactctt tcatgtgact ggcctgtttt
420
tgaaggcaag gccctgttca cccttggtta ggccaggat gttctgcacc gaaaatggcc
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ctgccctctg cattggatgg ctagctctta gggtggttta ttttagcaaa taagcgttac
540
agggtaggc
549

<210> 108
<211> 108
<212> PRT
<213> Homo sapiens

<400> 108
Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
1      5      10      15
Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu
20     25     30
Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
35     40     45
Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
50     55     60
Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
65     70     75     80
Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
85     90     95
Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
100    105

<210> 109
<211> 748

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<212> DNA

<213> Homo sapiens

<400> 109

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 120
 gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcttc
 180
 agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
 240
 cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
 300
 gagtggttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
 360
 atgtctcaac ttttgcagtt gaaagatcga gaaaaaatg cagcaagaga ttcatggcag
 420
 aagaaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
 480
 ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
 540
 cggcttacgc aagagcttga agaattagag gagcaacatc agcaaagaca caaatcatta
 600
 aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
 660
 gctcttgaaa atcatttaca acagaagcat tctgcagagc ttcaatcact aaaagatgca
 720
 cacagagagt caatggaggg cttccgga
 748

<210> 110

<211> 157

<212> PRT

<213> Homo sapiens

<400> 110

Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
 1 5 10 15
 Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
 20 25 30
 Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
 35 40 45
 Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
 50 55 60
 Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
 65 70 75 80
 Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
 85 90 95
 Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
 100 105 110
 Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Gln Gln Arg
 115 120 125
 Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

130	135	140
Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg		
145	150	155

<210> 111
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 111
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 cgtgaaccgc tcgccccgca ggtcaacgac ttcgggatca ccgggttcga cggcattctc
 120
 tcggcttatn nacgccacca gcatncgact ttgggtgaga tcatcgcacc gttcggacat
 180
 ctggtcatga tcgacggaac gcactcatte gatctcatgg ccttcaagtc aaagtcgtta
 240
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 420
 gagtcggc
 429

<210> 112
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 112
 Ala Arg Pro Glu Ser Ala Gln Trp Cys Gln Asp Met Gly Ala Thr Gly
 1 5 10 15
 Ile Ile Asn His Arg Glu Pro Leu Ala Pro Gln Val Asn Asp Phe Gly
 20 25 30
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His
 35 40 45
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
 50 55 60
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
 65 70 75 80
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
 100 105 110
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
 115 120 125
 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly
 130 135 140

<210> 113
 <211> 382

<212> DNA

<213> Homo sapiens

<400> 113

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 120
 gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggacgct gaagggcttc
 180
 gcggtgctgg agtatgagac ggctgagatg gcggaggagg cacagcagca ggcggacggc
 240
 ctgtccctgg ggggcagcca cctgcgagtc tcttctgcg cccctgggac ccccgggcgc
 300
 agtatgctgg ccgctctcat cgttgcccag gccacggccc tcaatcgggg gcaggggagtc
 360
 ctccccgagc ccaacatcct gc
 382

<210> 114

<211> 125

<212> PRT

<213> Homo sapiens

<400> 114

Met	Leu	Gly	Ser	Gly	Arg	Thr	Pro	Cys	Pro	Arg	Leu	Arg	Ala	Val	Ala
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Trp	Ala	Thr	Met	Arg	Ala	Ala	Ser	Ile	Leu	Arg	Pro	Gly	Val	Pro	Gly
			20					25				30			
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
	35						40					45			
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50					55				60					
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65				70					75				80		
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85					90					95		
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
		100					105					110			
Arg	Arg	Ala	Gly	Leu	Ser	Ser	Pro	Ala	Ser	Val	Gln	Cys			
		115					120					125			

<210> 115

<211> 4798

<212> DNA

<213> Homo sapiens

<400> 115

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 120
 ccccatcctt cctccacca acctagaggg ttgtcttcgt aaatgctggc cctttccttc
 180

atggggtcca cectctgagt gtgtcatgaa ctcttccact tccttgccctt gggttcgtatt
240
gggtccctctg ccgcaggtca gagatttgga cagagcccttc tcctccatctc tcacagtcctc
300
cattttaccat tagatgccag gccccagacag ttgatgaaaa atgtaagaaa cggaccacaag
360
tataagaaaa agctagatct gtccatttta ttcttagttt ttggaagaga tgtggatatac
420
gagaaatatt actctactat tgaaaaaaat atatatcagt ctgattataa atgtcaactc
480
atactaagtc aatatcaggg aagcagtggtg gagaaggatg tggcaaactg gagattgctg
540
tttccataga aagagggcag ctaatgctta tctccagacc attgttatgc agtaatgtag
600
actccatttc accagattta attcttaagg agaaactgga aacttggtatt attatttgat
660
tattactttt ggcagttaat tttaaaaatc accgttttagg ccaaaacaac atgacatttg
720
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 4798

<210> 116

<211> 1062

<212> PRT

<213> Homo sapiens

<400> 116

Met Met Gly Thr Ser Gln Gly His Val Ala Arg Lys Ser Arg Asn Trp

1	5	10	15
Gly Leu Asn Pro	Ser Arg Leu Ser	Ile Pro Leu Ser	Ser Thr Pro
20	25	30	
Cys His Leu Ser	Pro Ser Ser Leu Ser	Phe Ser Val Ala	Glu Arg
35	40	45	
Lys Pro Pro Leu	Phe Asn Met Asn	Ala Met Ser Ala	Leu Tyr His Ile
50	55	60	
Ala Gln Asn Glu	Ser Pro Val Leu	Gln Ser Gly His	Trp Ser Glu Tyr
65	70	75	80
Phe Arg Asn Phe	Val Asp Ser Cys	Leu Gln Lys Ile	Pro Gln Asp Arg
85	90	95	
Pro Thr Ser Glu	Val Leu Leu Lys	His Arg Phe Val	Leu Arg Glu Arg
100	105	110	
Pro Pro Thr Val	Ile Met Asp Leu	Ile Gln Arg Thr	Lys Asp Ala Val
115	120	125	
Arg Glu Leu Asp	Asn Leu Gln Tyr	Arg Lys Met Lys	Lys Ile Leu Phe
130	135	140	
Gln Glu Ala Pro	Asn Gly Pro Gly	Ala Glu Ala Pro	Glu Glu Glu Glu
145	150	155	160
Glu Ala Glu Pro	Tyr Met His Arg	Ala Gly Thr Leu	Thr Ser Leu Glu
165	170	175	
Ser Ser His Ser	Val Pro Ser Met	Ser Ile Ser Ala	Ser Ser Gln Ser
180	185	190	
Ser Ser Val Asn	Ser Leu Ala Asp	Ala Ser Asp Asn	Glu Glu Glu Glu
195	200	205	
Glu Glu Glu Glu	Glu Glu Glu Glu	Gly Pro Glu Ala	Arg
210	215	220	
Glu Met Ala Met	Met Gln Glu Gly	Glu His Thr Val	Thr Ser His Ser
225	230	235	240
Ser Ile Ile His	Arg Leu Pro Gly	Ser Asp Asn Leu	Tyr Asp Asp Pro
245	250	255	
Tyr Gln Pro Glu	Ile Thr Pro Ser	Pro Leu Gln Pro	Pro Ala Ala Pro
260	265	270	
Ala Pro Thr Ser	Thr Thr Ser Ser	Ala Arg Arg Arg	Ala Tyr Cys Arg
275	280	285	
Asn Arg Asp His	Phe Ala Thr Ile	Arg Thr Ala Ser	Leu Val Ser Arg
290	295	300	
Gln Ile Gln Glu	His Gln Gln Asp	Ser Ala Leu Arg	Glu Gln Leu Ser
305	310	315	320
Gly Tyr Lys Arg	Met Arg Arg Gln	His Gln Lys Gln	Leu Leu Ala Leu
325	330	335	
Glu Ser Arg Leu	Arg Gly Glu Arg	Glu His Ser Ala	Arg Leu Gln
340	345	350	
Arg Glu Leu Glu	Ala Gln Arg Ala	Gly Phe Gly Ala	Glu Ala Glu Lys
355	360	365	
Leu Ala Arg Arg	His Gln Ala Ile	Gly Glu Lys Glu	Ala Arg Ala Ala
370	375	380	
Gln Ala Glu Glu	Arg Lys Phe Gln	Gln His Ile Leu	Gly Gln Gln Lys
385	390	395	400
Lys Glu Leu Ala	Ala Leu Leu Glu	Ala Gln Lys Arg	Thr Tyr Lys Leu
405	410	415	
Arg Lys Glu Gln	Lys Glu Glu Leu	Gln Glu Asn Pro	Ser Thr Pro
420	425	430	
Lys Arg Glu Lys	Ala Glu Trp Leu	Leu Arg Gln Lys	Glu Gln Leu Gln


```

      435              440              445
Gln Cys Gln Ala Glu Glu Glu Ala Gly Leu Leu Arg Arg Gln Arg Gln
450              455              460
Tyr Phe Glu Leu Gln Cys Arg Gln Tyr Lys Arg Lys Met Leu Leu Ala
465              470              475
Arg His Ser Leu Asp Gln Asp Leu Leu Arg Glu Asp Leu Asn Lys Lys
      485              490              495
Gln Thr Gln Lys Asp Leu Glu Cys Ala Leu Leu Leu Arg Gln His Gln
500              505              510
Ala Thr Arg Glu Leu Glu Leu Arg Gln Leu Gln Ala Val Gln Arg Thr
515              520              525
Arg Ala Glu Leu Thr Arg Leu Gln His Gln Thr Glu Leu Gly Asn Gln
530              535              540
Leu Glu Tyr Asn Lys Arg Arg Glu Gln Glu Leu Arg Gln Lys His Ala
545              550              555
Ala Gln Val Arg Gln Gln Pro Lys Ser Leu Lys Val Arg Ala Gly Gln
565              570              575
Arg Pro Pro Gly Leu Pro Leu Pro Ile Pro Gly Ala Leu Gly Pro Pro
580              585              590
Asn Thr Gly Thr Pro Ile Glu Gln Gln Pro Cys Ser Pro Gly Gln Glu
595              600              605
Ala Val Leu Asp Gln Arg Met Leu Gly Glu Glu Glu Glu Ala Val Gly
610              615              620
Glu Arg Arg Ile Leu Gly Lys Glu Gly Ala Thr Leu Glu Pro Lys Gln
625              630              635
Gln Arg Ile Leu Gly Glu Glu Ser Gly Ala Pro Ser Pro Ser Pro Gln
645              650              655
Lys His Gly Ser Leu Val Asp Glu Glu Val Trp Gly Leu Pro Glu Glu
660              665              670
Ile Glu Glu Leu Arg Val Pro Ser Leu Val Pro Gln Glu Arg Ser Ile
675              680              685
Val Gly Gln Glu Glu Ala Gly Thr Trp Ser Leu Trp Gly Lys Glu Asp
690              695              700
Glu Ser Leu Leu Asp Glu Glu Phe Glu Leu Gly Trp Val Gln Gly Pro
705              710              715
Ala Leu Thr Pro Val Pro Glu Glu Glu Glu Glu Glu Glu Gly Ala
725              730              735
Pro Ile Gly Thr Pro Arg Asp Pro Gly Asp Gly Cys Pro Ser Pro Asp
740              745              750
Ile Pro Pro Glu Pro Pro Pro Thr His Leu Arg Pro Cys Pro Ala Ser
755              760              765
Gln Leu Pro Gly Leu Leu Ser His Gly Leu Leu Ala Gly Leu Ser Phe
770              775              780
Ala Val Gly Ser Ser Ser Gly Leu Leu Pro Leu Leu Leu Leu Leu
785              790              795
Leu Pro Leu Leu Ala Ala Gln Gly Gly Gly Gly Leu Gln Ala Ala Leu
805              810              815
Leu Ala Leu Glu Val Gly Leu Val Gly Leu Gly Ala Ser Tyr Leu Leu
820              825              830
Leu Cys Thr Ala Leu His Leu Pro Ser Ser Leu Phe Leu Leu Leu Ala
835              840              845
Gln Gly Thr Ala Leu Gly Ala Val Leu Gly Leu Ser Trp Arg Arg Gly
850              855              860
Leu Met Gly Val Pro Leu Gly Leu Gly Ala Ala Trp Leu Leu Ala Trp

```

```

865                      870                      875                      880
Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg Trp
                        885                      890                      895
Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp
                        900                      905                      910
Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln
                        915                      920                      925
Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys
                        930                      935                      940
Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg
945                      950                      955                      960
Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg
                        965                      970                      975
Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser
                        980                      985                      990
Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala
995                      1000                      1005
Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu
1010                      1015                      1020
Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro
1025                      1030                      1035                      1040
Leu Pro Gly Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg
                        1045                      1050                      1055
Ala Leu Pro Pro Trp Arg
1060

```

```

<210> 117
<211> 471
<212> DNA
<213> Homo sapiens

```

```

<400> 117
naccgcttga cgatctgtct ggctgggtgta gtgatctgcg ctgtgggtgt cgctgatgac
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ctgctcgacc ttctgcctt ggccaaggca gctggccagg tattagcggc cggcacgtgc
120
gtcagggcg gagtgcgaat gttttggatc ccgctgccga actccatcat tgctttgggg
180
acgcctactt cgatcttggt gacggtgttc ttcatgtgtt tgtgcgccaa tgcgggtgaat
240
ttcattgatg gacttgacgg cctggcatcc ggtgtggtgg ccatcgggtc cttggcttcc
300
ttctcataca cctacctgct ggctcacgaa caggactttg ttgttgcgac gactaccagt
360
ctcattacgg ctgcgacggc gggcgccctgt ctcggttttt tgccccacaa ctggcatccg
420
gcgaggatgt tcatgggtga ttccggagct ctgctacttg gcttattgct a
471

```

```

<210> 118
<211> 157
<212> PRT
<213> Homo sapiens

```

```

<400> 118
Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly
 1           5           10           15
Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly
          20           25           30
Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
          35           40           45
Trp Ile Pro Leu Pro Asn Ser Ile Ala Leu Gly Thr Pro Thr Ser
          50           55           60
Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
          65           70           75           80
Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
          85           90           95
Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
          100          105          110
Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
          115          120          125
Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
          130          135          140
Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu
          145          150          155

```

```

<210> 119
<211> 302
<212> DNA
<213> Homo sapiens

```

```

<400> 119
ntcaaacatg agcagtcgtg gcggccgagg ccgcgggtggc tattatcgcg agctttatgg
60
tagccgaggt cgaggcagta aatctaataa aacttttcgca aaaaattcgg atgtctactc
120
tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa
180
gcttcatatg cgcccgatcc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc
240
ctttactttt tatctggatc atgcacaagc agaccatac gctgccccaa ataaggcacg
300
cn
302

```

```

<210> 120
<211> 98
<212> PRT
<213> Homo sapiens

```

```

<400> 120
Met Ser Ser Arg Gly Gly Arg Gly Gly Tyr Tyr Arg Glu Leu
 1           5           10           15
Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys
          20           25           30
Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
          35           40           45
Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

```

```

      50              55              60
Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr
65              70              75              80
Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys
      85              90              95
Ala Arg

```

```

<210> 121
<211> 318
<212> DNA
<213> Homo sapiens

```

```

<400> 121
ngcatggggg gccctgggac cgcacttggtg cccctttttt ttttagggaa aaaattgagc
60
cctaaaggat ttgccgcatt acaggaaggt tttttggtaa gtttgggggtt gtttctgtgc
120
tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
180
aaatttttag gctgtggcta ttacttcctt ttttttcttt tttttttttg ttttagagaca
240
gagtcctgnc tctgtgccag gctggagtga agtggcaca tctcagctca ctgcaacctc
300
tgcctcccag gttcaagc
318

```

```

<210> 122
<211> 89
<212> PRT
<213> Homo sapiens

```

```

<400> 122
Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
1              5              10              15
Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
20              25              30
Val Ser Leu Gly Leu Phe Leu Cys Val Arg Arg Ser Arg Ser Ser
35              40              45
Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
50              55              60
Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
65              70              75              80
Glu Ser Xaa Ser Val Ala Arg Leu Glu
      85

```

```

<210> 123
<211> 338
<212> DNA
<213> Homo sapiens

```

```

<400> 123
acgcgtctag ggtagaaatc aactccagta actgtcatc aacctcagca atgctgggga
60

```

cgggcagagg cagggcagct gtgtgccaca ttctgccag ggctggctcag gccccggctc
 120
 tcaccactcc tctccctgc tttgaacctg tggaacaaag ggccctgca ccccaactca
 180
 ttctctctttg ccacataagg gcctcaagtc atgtgtgccc ctctgcctgg gtgtctttt
 240
 ctccctctgc ttgggtcact gtacacacca ctggccactt tctcaggga agggccctca
 300
 ctgcccacac acctaaacat gccccctgct cctccata
 338

<210> 124

<211> 96

<212> PRT

<213> Homo sapiens

<400> 124

Met	Leu	Gly	Thr	Gly	Arg	Gly	Arg	Ala	Ala	Val	Cys	His	Ile	Pro	Ala
1				5						10				15	
Arg	Ala	Gly	Gln	Ala	Pro	Ala	Leu	Thr	Thr	Pro	Pro	Pro	Cys	Phe	Glu
			20						25				30		
Pro	Val	Glu	Gln	Arg	Ala	Pro	Ala	Pro	Gln	Leu	Ile	Pro	Leu	Cys	His
			35					40				45			
Ile	Arg	Ala	Ser	Ser	His	Ala	Val	Pro	Ser	Ala	Trp	Val	Ala	Phe	Ser
			50			55				60					
Pro	Ser	Ala	Trp	Val	Thr	Val	His	Thr	Thr	Gly	His	Phe	Pro	Gln	Gly
65					70					75				80	
Arg	Ala	Leu	Thr	Ala	His	Thr	Pro	Lys	His	Ala	Pro	Cys	Ser	Ser	Ile
				85					90					95	

<210> 125

<211> 280

<212> DNA

<213> Homo sapiens

<400> 125

ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc
 60
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
 180
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
 240
 gcttctgctg tcttggccca ttctggatag gcctgatcta
 280

<210> 126

<211> 92

<212> PRT

<213> Homo sapiens

<400> 126

Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

      1           5           10           15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20           25           30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35           40           45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50           55           60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
      65           70           75           80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85           90

```

<210> 127

<211> 444

<212> DNA

<213> Homo sapiens

<400> 127

```

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ctgcaaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcggttcacga ggggctgcgc cgagcacctg cccaacgcgc ggcacacctt gcacaagttc
180
cacgtcatcgc ggcacgccaa tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggtcg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccg ccgatctgga tgcctgcatc gccaggatgg ccactgtgcy caccgcgcgc
360
gcctgggtctt acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caacgtggca
420
cgcgacatgc tcaagcactg gtgc
444

```

<210> 128

<211> 148

<212> PRT

<213> Homo sapiens

<400> 128

```

Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
      1           5           10           15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20           25           30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35           40           45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50           55           60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
      65           70           75           80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85           90           95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

```

      100              105              110
Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu
      115              120              125
Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu
      130              135              140
Lys His Trp Cys
145

```

```

<210> 129
<211> 291
<212> DNA
<213> Homo sapiens

```

```

<400> 129
gaggaggagc gtaccgtccc cggtatagcc aagctcgaga agccgcaagc tatcgagaac
60
ttggacgaga ttattgacgt ctttgacgcc gtcattggtg ccggtggcga tatggccgtc
120
gagtgcccgcc tcgaggaagt tccgctgacg caaaagcaga tcacgcagaa ggctcggtta
180
caggctaagc ccgtcattgt ggccaccacg atgcttgagt cgatgatcca cgctccccgt
240
ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
291

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<210> 130
<211> 97
<212> PRT
<213> Homo sapiens

```

```

<400> 130
Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln
1      5      10      15
Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met
20      25      30
Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro
35      40      45
Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro
50      55      60
Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg
65      70      75      80
Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly
85      90      95
Ala

```

```

<210> 131
<211> 416
<212> DNA
<213> Homo sapiens

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```

<400> 131
tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag
60

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attccaccgg tgcctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
 180
 ggggcattgc ggaatgcggg ctacgaccgg ctgtcacgta ccnacctgc tgggnnaccg
 240
 cgcgggggtg acctgctggt acgggttact gccgacgtcg acgcggtgtt ggacatggtc
 300
 gtgcgggtga tcgtccgggc gtgcgcgtca agcctcgta tcattggcac caccgtcctt
 360
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggg
 416

<210> 132
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 132
 Ser Gly Ala Ser Val Ala Leu Met Gly Val Ser Ala Trp Leu Leu Ser
 1 5 10 15
 Arg Ala Ala Glu Ile Pro Pro Val Leu Tyr Leu Glu Ala Ala Val
 20 25 30
 Gly Val Arg Phe Phe Gly Ile Ser Arg Gly Val Phe Arg Tyr Ala Glu
 35 40 45
 Arg Leu Val Gly His Asp Leu Ala Leu Arg Met Gln Gly Ala Leu Arg
 50 55 60
 Met Arg Val Tyr Asp Arg Leu Ser Arg Thr Xaa Pro Ala Gly Xaa Arg
 65 70 75 80
 Arg Arg Gly Asp Leu Leu Val Arg Val Thr Ala Asp Val Asp Ala Val
 85 90 95
 Leu Asp Met Val Val Arg Val Ile Val Pro Ala Cys Ala Ser Ser Leu
 100 105 110
 Val Ile Ile Gly Thr Thr Val Leu Leu Cys Pro Arg Glu Gly
 115 120 125

<210> 133
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 133
 gccgttgcta tcgctgctgg tatgctgca gacgtcactg tttttgatat caatatcgct
 60
 gcgtgaaga gactcgccga catctaccag ggtcgtgttc acacagtagt atccaccgcg
 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttgtga tcggttctgt ccttattccg
 180
 ggtagttcta ccccgaaagt tgttactacc gatatgggtg ctccatgca gectgggtct
 240
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca cccaccact
 300
 tacgatgacc ccaatttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
 1 5 10 15
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
 taagatgtgg tcctgcccctg ttccctgaagg ggctgcagct ctgatggaaa atacagggat
 60
 ttacactcag ggctacagcc acgggggggct gagggccaag gctgcaatct cgggggaagg
 120
 ggaagtgtgg ttttctctgt ggattggaaa catcctcttg gaggcaaaga cttttctctg
 180
 atcttacaga cttcccggga ttttttagatt agaattattgg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
 300
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
 420
 atgacatctt gtcttcatgc tcgagagaga attacttcaac tgggtccact tggagtccca
 480
 gtgttcagac accaagcctg actgggaggg ttccgttttc ttaacacctt cccaccgccg
 540
 acttccaagt cccacgcgt
 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

```

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1             5             10             15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
      20             25             30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
      35             40             45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
      50             55             60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
65             70             75             80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
      85             90             95
Ile Ser Ser Gly
      100

```

<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

```

accggttgga tggcctgcag gccaaagcgt tccctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaaca gctggctgcg cacctgcttg aggtccaccc attgcgcata gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acagggtcttc gacaaaaaccg
180
gactgctggc gggtcgcaac gcgcatgata ggcagcgccct ggctggcgcc ctggtcgagc
240
cagcgcgctg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggata acggcaagtg
360
ccggcgctgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

```

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1             5             10             15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
      20             25             30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
      35             40             45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
50             55             60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

```

65              70              75              80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
              85              90              95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
              100              105              110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
              115              120              125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
              130              135              140

```

<210> 139

<211> 341

<212> DNA

<213> Homo sapiens

<400> 139

```

acgcgtcggt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgcgcgagc
60
ttgtgaacag cagaatcaag ccgctggtta atcttcctgg gagcttcata ggcgggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttcgagcct gtaacgactg aggggttcgga tggaaaaaca catgctccag gatgggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtacgcgcaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

```

<210> 140

<211> 113

<212> PRT

<213> Homo sapiens

<400> 140

```

Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1      5      10      15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
20     25     30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
35     40     45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
50     55     60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65     70     75     80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Phe Thr Ser Cys Gly
85     90     95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
100    105    110
Ala

```

<210> 141

<211> 324

<212> DNA

<213> Homo sapiens

<400> 141

gaattcctct tggatagctt cgggtaaatg ggtacagcaa atatcaggag cgcaaccgca
 60
 accctttactt actggtacat gaacaccatt tacattacag ctatcgtact caccctcagct
 120
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
 180
 gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcataact cctttgacca
 240
 tgcgtaataa atacgtccgt cattagtac acctgatggg gcgaacaaaa aagaacggca
 300
 gcagttatca ccgccatac gcgt
 324

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25					30			
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
		35					40					45			
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
		50					55				60				
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65					70					75				80	
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85						90					95	
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100						105						

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

nacgctgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
 60
 gcaccccagg agaagaactt cctgtacaaa tgcataggca ccacctggg tgcgtgcttca
 120
 agtaaggagg tggtaggaaa gcaccttcaa gagctgtctg agacggccag ataccaggag
 180
 gaggcagaac gcgaggcct cgctgtctgc ttccggatct gtgccatctc ccacctcgag
 240
 gacacgtgg cccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
 300

attctcaaca tttttaagga tcgaagtgg aacgaagtgg agaaggtgaa gagtgctctg
 360
 atcctgtgct atgggcacgt ggcggcccg gcccccgagg agctgggtgct ggccaaggta
 420
 gagtcagaca tctctccggaa catcntgcc gcacttcagc acnncaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagcccg ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaagga gagctggagg cacagatgat ggagttcatc
 600
 agggcagagc ccccgactc cttgaggaca cctattcgga agaaagccat gctcacctgc
 660
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccggggcga tgtgatccat
 720
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
 cagaagtccc tgtatctgga gacactgcac gccttgagg atctgctgac gagcctcctg
 840
 cagcggaaca tgacccccca aggcctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtcctcaa gaggtcacgt agcggcgctg gccttaggcc tgagcgccct cctcgtgcgc
 960
 tacttctcgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
 1020
 cccaggtacc tgtgcaatgg ccctggtgcc ctccacaac ctgggccttc tcactcgccct
 1080
 cttctcccca cgggtgctgg acctgtggcc tgccaccgc caggaggccg tggactgtgt
 1140
 ctactccctg ctgtacctcc agctcggcta tgagggtctc tccggggact accgcgatga
 1200
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
 1260
 cttccacacc tgccacagtg taggccagat tattgccaag cgctccccc cagcccttca
 1320
 cgcgt
 1325

<210> 144
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 144
 Xaa Ala Trp Ile Cys Gln Leu Ser Leu Glu Leu Cys Arg Gln Leu Pro
 1 5 10 15
 Cys Tyr Asp Glu Ala Pro Gln Glu Lys Asn Phe Leu Tyr Lys Cys Ile
 20 25 30
 Gly Thr Thr Leu Gly Ala Ala Ser Ser Lys Glu Val Val Arg Lys His
 35 40 45
 Leu Gln Glu Leu Leu Glu Thr Ala Arg Tyr Gln Glu Glu Ala Glu Arg
 50 55 60
 Glu Gly Leu Ala Cys Cys Phe Gly Ile Cys Ala Ile Ser His Leu Glu
 65 70 75 80
 Asp Thr Leu Ala Gln Leu Glu Asp Phe Val Arg Ser Glu Val Phe Arg

85										90					95				
Lys	Ser	Ile	Gly	Ile	Leu	Asn	Ile	Phe	Lys	Asp	Arg	Ser	Glu	Asn	Glu				
100										105					110				
Val	Glu	Lys	Val	Lys	Ser	Ala	Leu	Ile	Leu	Cys	Tyr	Gly	His	Val	Ala				
115										120					125				
Ala	Arg	Ala	Pro	Arg	Glu	Leu	Val	Leu	Ala	Lys	Val	Glu	Ser	Asp	Ile				
130										135					140				
Leu	Arg	Asn	Ile	Xaa	Pro	Ala	Leu	Gln	His	Xaa	Lys	Asp	Pro	Ala	Leu				
145										150					155				
Lys	Leu	Cys	Leu	Val	Gln	Ser	Val	Cys	Met	Val	Ser	Arg	Ala	Ile	Cys				
160										165					170				
Ser	Ser	Thr	Gln	Ala	Gly	Ser	Phe	His	Phe	Thr	Arg	Lys	Ala	Glu	Leu				
175										180					185				
Val	Ala	Gln	Met	Met	Glu	Phe	Ile	Arg	Ala	Glu	Pro	Pro	Asp	Ser	Leu				
190										195					200				
Arg	Thr	Pro	Ile	Arg	Lys	Lys	Ala	Met	Leu	Thr	Cys	Thr	Tyr	Leu	Val				
205										210					215				
Ser	Val	Glu	Pro	Ala	Leu	Asp	Glu	Gln	Ala	Arg	Ala	Asp	Val	Ile	His				
220										225					230				
Gly	Cys	Leu	His	Ser	Ile	Met	Ala	Leu	Leu	Pro	Glu	Pro	Lys	Glu	Glu				
235										240					245				
Asp	Gly	Gly	Cys	Gln	Lys	Ser	Leu	Tyr	Leu	Glu	Thr	Leu	His	Ala	Leu				
250										255					260				
Glu	Asp	Leu	Leu	Thr	Ser	Leu	Leu	Gln	Arg	Asn	Met	Thr	Pro	Gln	Gly				
265										270					275				
Leu	Gln	Ile	Met	Ile	Glu	His	Leu	Ser	Pro	Trp	Ile	Lys	Ser	Pro	Arg				
280										285					290				
Gly	His	Val	Ala	Ala	Arg	Ala	Leu	Gly	Leu	Ser	Ala	Leu	Leu	Val	Arg				
295										300					305				
Tyr	Phe	Leu	Glu	His	Leu	Arg	Val	Ser	Gly	Ala	Gln	Val	Asp	Thr	Arg				
310										315					320				
Phe	Pro	Ser	Glu	Pro	Arg	Ile	Leu	Cys	Asn	Gly	Pro	Gly	Ala	Leu	Pro				
325										330					335				
Gln	Pro	Gly	Pro	Ser	His	Arg	Pro	Leu	Leu	Pro	Thr	Val	Cys	Gly	Pro				
340										345					350				
Val	Ala	Cys	His	Pro	Pro	Gly	Gly	Arg	Gly	Leu	Cys	Leu	Leu	Pro	Ala				
355										360					365				
Val	Pro	Pro	Ala	Arg	Leu														
370										375					380				
Val	Pro	Pro	Ala	Arg	Leu														
385										390					395				

<210> 145

<211> 802

<212> DNA

<213> Homo sapiens

<400> 145

cggcgcgtcta ggtccggtc agtcgcgtgt tgtcgcgcgt agaacacgag gctgcgcaag
60
cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggtct
120
acatcacctt ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgtcggacaa
180
gacatcatgc cecatattct gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240

cagaggacga caccgatctg gcggacgccg cccgttcacg gcgcagatac ctcatctctg
 300
 tcatttggtg cgttatcgct gctgtctctg gactaggcat ttccgggtat cttgcgtggt
 360
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgttg tgaaccggtt atgtactggt
 420
 gtccgggtgt ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
 480
 tggagaagcg ctgggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccc
 540
 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg
 600
 tattgatctc cgttttatcg gctcctagca gccgtggtca acgtatcgct atcaagcgat
 660
 acaggactcg tcgttcgcat cgttggtgtg ctgctgggaa acaatcccag cgatctactc
 720
 ggctaccgcc agacagttca ctcaaacccc ctacgcggcg cgcagacatc aaatcccatt
 780
 ctcgatagac ggcccacacc ac
 802

<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

Met	Lys	Val	Tyr	Ile	Thr	Leu	Val	Lys	Ala	Cys	Thr	Thr	Ser	Val	Gly
1			5					10					15		
Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
		20					25				30				
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35				40					45				
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50				55					60					
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
	65				70				75				80		
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
			85					90					95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
		100					105					110			
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
	115					120					125				
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
	130					135					140				
Ile	Phe	Phe	Trp	Leu	Ala	Val									
	145				150										

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147

acgcgtgaaa acggtatgac tcttctggcc ttagtagatc tgtctaaaaa acccgatgag
 60
 ttacacagt gggcattagt agcccgcat gtctatgaca ttcctgggtc acgaaaagtt
 120
 attggtcaga aagtaccttg tgttgcatgt acggggctcg aaaaggtgct tcataaaaag
 180
 gattactggg atctagcaac acctatgcca attgctgggg gtacaacgga cgaacagtt
 240
 attgctgatg cagcagctac aatccccacc acggagtggg atatccttgc aagactacgt
 300
 ccacgcctag aagaggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
 360
 ccccccta
 368

<210> 148

<211> 117

<212> PRT

<213> Homo sapiens

<400> 148

Met	Thr	Leu	Leu	Ala	Leu	Val	Asp	Leu	Ser	Lys	Lys	Pro	Asp	Glu	Phe
1				5					10					15	
Thr	Gln	Trp	Ala	Leu	Val	Ala	Arg	Asp	Val	His	Asp	Ile	Pro	Gly	Leu
			20					25					30		
Arg	Lys	Val	Ile	Gly	Gln	Lys	Val	Pro	Cys	Val	Ala	Val	Thr	Gly	Ser
			35				40						45		
Glu	Lys	Val	Leu	His	Lys	Lys	Asp	Tyr	Trp	Asp	Leu	Ala	Thr	Pro	Met
			50			55					60				
Pro	Ile	Ala	Trp	Gly	Thr	Thr	Asp	Arg	Thr	Val	Ile	Ala	Asp	Ala	Arg
					70					75					80
Arg	Thr	Ile	Pro	Thr	Thr	Glu	Trp	Asp	Ile	Leu	Ala	Arg	Leu	Arg	Pro
				85					90					95	
Arg	Leu	Glu	Glu	Val	Arg	Lys	Gln	Arg	Asn	Asp	Val	Leu	Leu	Leu	Asn
			100					105					110		
Glu	Glu	Asp	Pro	Pro											
															115

<210> 149

<211> 407

<212> DNA

<213> Homo sapiens

<400> 149

nngctagcat ggaccctagt cacacaggca gccatacccg aggtcaaagt gacccatttt
 60
 cctaataatgg ccgctcagat ccaatacttt gaagattcgt ccgtgggttat atggcacgat
 120
 gcggtggatg gtagctgtga ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag
 180
 gggcctgaac agggctcaggc gcaccttttc gtgctccatc cctacgacaa gactcaagcg
 240
 tatattctga cgcgacgac tcagcattgg cgcacgtcga accgtggcga gacgtggcag
 300

tcattctcaa cgcctcatcc gcttacgacc ttgaaagcta tgcctctgga ctttcatccg
 360
 acgcatcatg actggatcct ttctacgggc caggcttgca cggtaaa
 407

<210> 150
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 150
 Xaa Leu Ala Trp Thr Leu Val Thr Gln Ala Ala Ile Pro Glu Val Lys
 1 5 10 15
 Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp
 20 25 30
 Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg
 35 40 45
 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
 50 55 60
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
 65 70 75 80
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
 85 90 95
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Lys
 100 105 110
 Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe
 115 120 125
 Thr Gly Gln Ala Cys Thr Val
 130 135

<210> 151
 <211> 448
 <212> DNA
 <213> Homo sapiens

<400> 151
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<211> 149
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 35 40 45
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp
 50 55 60
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser
 65 70 75 80
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp
 85 90 95
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
 100 105 110
 Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys
 115 120 125
 Ser Pro Pro Arg Gly Ala His Gly Lys Pro Ala Pro Gly Gly Arg Gly
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 Cys Met Asp Ile Arg
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 <212> DNA
 <213> Homo sapiens

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<210> 154
 <211> 69
 <212> PRT
 <213> Homo sapiens

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<400> 154
Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val
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Cys Val Cys Ile Cys Gly Gly Thr Gly Val Cys Pro Ser Val Cys Met
          20           25           30
Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val
          35           40           45
Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys
          50           55           60
Ser Cys Thr Arg Val
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<210> 155
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<212> DNA
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240
gaactgggca cctcgcaagc tacgccaccg cgatccatgc ccccgcccgt atcttccgcc
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344

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<212> PRT
<213> Homo sapiens

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          20           25           30
Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser
          35           40           45
Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln
          50           55           60
Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser
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Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu
          85           90

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<210> 157
<211> 6816
<212> DNA
<213> Homo sapiens

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420
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<210> 158
 <211> 1572
 <212> PRT
 <213> Homo sapiens

<400> 158
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 Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
 35 40 45
 Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
 50 55 60
 Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
 65 70 75 80
 Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
 85 90 95
 His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
 100 105 110
 Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
 115 120 125
 Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
 130 135 140
 Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
 145 150 155 160
 Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
 165 170 175
 Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
 180 185 190
 Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
 195 200 205
 Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
 210 215 220
 Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
 225 230 235 240
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
 245 250 255
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly

260 265 270
 Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
 275 280 285
 Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
 290 295 300
 Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
 305 310 315 320
 Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
 325 330 335
 Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
 340 345 350
 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
 355 360 365
 Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
 370 375 380
 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
 385 390 395 400
 Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
 405 410 415
 Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu
 420 425 430
 Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
 435 440 445
 Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
 450 455 460
 Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
 465 470 475 480
 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
 485 490 495
 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
 500 505 510
 Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu
 515 520 525
 Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
 530 535 540
 Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
 545 550 555 560
 Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
 565 570 575
 His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
 580 585 590
 Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
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 Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Glu
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 Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His
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 Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr

690	695	700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser		
705	710	715
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu		720
	725	730
Lys Ser Asn Ser Ser Leu Asp Lys His Gln Ser Ser Thr Leu Gly Asn		735
	740	745
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu		750
	755	760
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu		765
	770	775
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe		780
785	790	795
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		800
	805	810
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		815
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		830
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		845
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		860
865	870	875
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		880
	885	890
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		895
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		910
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Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		925
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		940
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Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		960
	965	970
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		975
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		990
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		1005
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		1020
1025	1030	1035
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		1040
	1045	1050
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		1055
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		1070
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		1085
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		1100
1105	1110	1115
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		1120

1125					1130					1135						
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1140					1145					1150						
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Met	Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	
1170					1175					1180						
Gln	Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	
1185					1190					1195					1200	
Asp	Ile	Tyr	Lys	Leu	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	
1205					1210					1215					1220	
Glu	Arg	Leu	Ala	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Ala	Tyr	Ser	Lys	
1220					1225					1230					1235	
Val	Thr	Glu	Val	Met	His	Ser	Gly	Arg	Arg	Leu	Leu	Gly	Thr	Tyr	Phe	
1235					1240					1245					1250	
Arg	Val	Ala	Phe	Phe	Gly	Gln	Ala	Ala	Gln	Tyr	Gln	Phe	Thr	Asp	Ser	
1250					1255					1260					1265	
Glu	Thr	Asp	Val	Glu	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr	
1265					1270					1275					1280	
Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg	
1285					1290					1295					1300	
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met	
1300					1305					1310					1315	
Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Tyr	
1315					1320					1325					1330	
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro	Phe	Phe	Asp	Glu	Lys	Glu	
1330					1335					1340					1345	
Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Ser	His	Asn	Ile	Arg	Arg	
1345					1350					1355					1360	
Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly	
1365					1370					1375					1380	
Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys	
1380					1385					1390					1395	
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr	
1395					1400					1405					1410	
Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val	
1410					1415					1420					1425	
Ala	Glu	Leu	Arg	Gln	Leu	Cys	Ser	Ser	Ala	Glu	Val	Asp	Met	Ile	Lys	
1425					1430					1435					1440	
Leu	Gln	Leu	Lys	Leu	Gln	Gly	Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly	
1445					1450					1455					1460	
Pro	Leu	Ala	Tyr	Ala	Arg	Ala	Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg	
1460					1465					1470					1475	
Tyr	Pro	Asp	Asn	Lys	Val	Lys	Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe	
1475					1480					1485					1490	
Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	Val	Asn	Glu	Arg	Leu	Ile	Lys	
1490					1495					1500					1505	
Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	Met	Lys	Ala	Asn	Tyr	Arg	Glu	
1505					1510					1515					1520	
Met	Ala	Lys	Glu	Leu	Ser	Glu	Ile	Met	His	Glu	Gln	Ile	Cys	Pro	Leu	
1525					1530					1535					1540	
Glu	Glu	Lys	Thr	Ser	Val	Leu	Pro	Asn	Ser	Leu	His	Ile	Phe	Asn	Ala	
1540					1545					1550					1555	
Ile	Ser	Gly	Thr	Pro	Thr											

1555
Ser Ser Val Val
1570

1560

1565

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<400> 159
gccggctctg ccattgtgctt actctgagcc acctaacctc ggctgtcttc agtttactca
60
tccgctcacc tgcagaatgg gtgatgctgt cggctacttcg tggcatacag gaaagtgtcc
120
agcatgggtca gcctcagtga gaggtggcca gtggggagtg gtggccactg tacacctggc
180
acagcccaga gatgcatgtg ccaactctgtt gtgtgcttca accaaggggc gctctggcag
240
ggcttgggtg ggacttcccc aagggcattg aaaagttccc agtcaatgag atccatggag
300
accatgggga gtgggggtgca gcccagcct aagaggaccc ccagccctgc cctgtgcccc
360
aggacacacc aggcactgtc ccttgcgcgc tccccagaca acctgtaccc tccaggccac
420
cagttctcgt ccattgacaaa gaaaggagcc ttctaaataa gtgcccgcga gaggtgtcac
480
gcttccctgc cccttcgggg tggacctggg tttcaaagag aagctgccag tgcaacgcgt
540

<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys
1 5 10 15
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
20 25 30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Thr Ser Gln Arg Ala
35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65 70 75 80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
85 90 95
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
100 105 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

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<400> 161
nnacgcgtac gtctttcggc cgaagaagga acgtgggcag gggcctcctt cgctggccgc
60
cgcgcttgcc tcgcagcgac gatgaagggc gacgacagca gcaagatcac ccacaagatc
120
gcccggggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gcgcgcgacg
180
ccgcaggggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag
240
tttgtggaca ttacgtgga tgccgggggc cggacgtcgg atatgacgac gcagctggtc
300
aagacggtgc atgcgtactt tgggtgcgag acgtgcatgc atctgacgtg c
351

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<210> 162
<211> 117
<212> PRT
<213> Homo sapiens

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<400> 162
Xaa Arg Val Arg Leu Ser Ala Glu Glu Gly Thr Trp Ala Gly Ala Ser
1 5 10 15
Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp
20 25 30
Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg
35 40 45
Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met
50 55 60
Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu
65 70 75 80
Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr
85 90 95
Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys
100 105 110
Met His Leu Thr Cys
115

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<210> 163
<211> 360
<212> DNA
<213> Homo sapiens

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<400> 163
gcgtgctcca tcggcacctt gcagatgggc gaattcgcgtg aaaaacgtcgc cggtgccgctc
60
gacacctaca ccttcgctca gcccatcgcc gtatgcgcag gcatcactcc gttcaacttc
120
ccggcgatga ttccactgtg gatgttcccg atggcgattg cctcggtgtaa cactttcgtg
180
ctcaaacctg ccgaacaaga cctctgtctg acgatgctgc tggtagaact ggcgctggaa
240
gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgctg
300

```

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gtcgaccgc cgttgggtacc
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

Ala	Cys	Ser	Ile	Gly	Thr	Leu	Gln	Met	Gly	Glu	Phe	Ala	Glu	Asn	Val
1				5					10				15		
Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25				30			
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
			35				40				45				
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
		50			55					60					
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65					70				75				80		
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
			85					90				95			
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
			100					105				110			
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
			115				120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

gctagcagcc ttcaccctcc tagaggggca ggctcggcga caaggggagg ggggtgccccg
60
tcccagcgag ggacgccccg ggctgggggt gccggctcag cccggggcaa cagcttcacc
120
aagtttgga accgcaacgt cttcatgaag gacaacagct cttcttcacg cacagactcc
180
cgctccccgt cctcctccag gtccccgacg cgccacttcc gcagaagtga ctccactca
240
gactccgaca gctcctactc aggggaatgag tgtcaccctg tgggcccgcg gaaccgcgcc
300
cctaaggggc ggggagggtcg agggggccat atggatcggg gccgaggcag ggcgcagcgt
360
gggaagaggc acgatctggc gcccaaccaag cgagtcgaa agaagatggc ggcgctggag
420
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgctt ccagcacgga
480
cactcccgcc gcctgcgcct cgagccctgt gtgctcgaga tgagcagcct ggagagcagt
540
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag
600
cactacctgc gcctcacctg tgcccccgac ccgtccaccg tgcgccctgt ggcattccct
660

gtggcagggt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaaag agaagcagga
 720
 ctacgcgt
 728

<210> 166
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 166
 Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly
 1 5 10 15
 Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly
 20 25 30
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
 35 40 45
 Met Lys Asp Asn Ser Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
 50 55 60
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
 65 70 75 80
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
 85 90 95
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
 100 105 110
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
 115 120 125
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
 130 135 140
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
 145 150 155 160
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
 165 170 175
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
 180 185 190
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
 195 200 205
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
 210 215 220
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly
 225 230 235 240
 Leu Arg

<210> 167
 <211> 510
 <212> DNA
 <213> Homo sapiens

<400> 167
 nnacgcgtgg aaccagaact caggcccgtg tgaggagtct ggtttggaac acacggggcc
 60
 gcaacacaga attgtcaggt cctgtgccgt gaccaccacc cctcggggcca tgccaggtgc
 120

tggtagagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag
 180
 gtcctcatcg gcgtcctccg gctgggcttc gtgtccgcct acctctcaca gccactgtctc
 240
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgtgtg
 300
 ggctgtcgga tcccgcggca ccagggggccc ggcatgggtg tcctcacatg gctgagcctg
 360
 ctgctgcggc ccgggcaggc caacgtgtgc gacgtgggtc ccagcacggt gtgctctggc
 420
 gtgctgctag ccgcgaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg
 480
 cccacggagc tgctggtcat cgtgggtggc
 510

<210> 168

<211> 128

<212> PRT

<213> Homo sapiens

<400> 168

Gly	Ala	Gly	Gly	Ser	Arg	Gln	Ala	Pro	Ala	Gly	Leu	Thr	Ala	Leu	Arg
1				5					10					15	
Pro	Gln	Val	Leu	Met	Gly	Val	Leu	Arg	Leu	Gly	Phe	Val	Ser	Ala	Tyr
			20					25					30		
Leu	Ser	Gln	Pro	Leu	Leu	Asp	Gly	Phe	Ala	Met	Gly	Ala	Ser	Val	Thr
		35					40				45				
Ile	Leu	Thr	Ser	Gln	Leu	Lys	His	Leu	Leu	Gly	Val	Arg	Ile	Pro	Arg
	50				55					60					
His	Gln	Gly	Pro	Gly	Met	Val	Val	Leu	Thr	Trp	Leu	Ser	Leu	Leu	Arg
65				70					75					80	
Gly	Ala	Gly	Gln	Ala	Asn	Val	Cys	Asp	Val	Val	Thr	Ser	Thr	Val	Cys
			85					90					95		
Leu	Ala	Val	Leu	Leu	Ala	Ala	Lys	Glu	Leu	Ser	Asp	Arg	Tyr	Arg	His
		100					105						110		
Arg	Leu	Arg	Val	Pro	Leu	Pro	Thr	Glu	Leu	Leu	Val	Ile	Val	Val	Ala
		115					120						125		

<210> 169

<211> 537

<212> DNA

<213> Homo sapiens

<400> 169

gaattccacc gcattgctgtg tctggacgta tgtaggctgc ggtagtgtgc gaccgccggt
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 gccttaaagg agagcgggca tcggcggttc agtacgagag ggaagggtgt gcggatactt
 120
 attgtcgggt cggtcatgct catccacacc gttcgatggg tcaattggact ggtcaagcgg
 180
 ggtcacgagg ttcacctggc atcagtccat ccggcggggc gtcactccat tgatccccga
 240
 gttcggatcc acctggcccc acacggcggg aaggcaaaa acgtcgtcaa tgccggctgg
 300

ctgcgatcag tggcggctgg ggtgcaacct gacatcgta acgtccacta tgcgaccggt
 360
 tatggctctgc tcgctcgtct tgcctatatt gacgccccga cgctgctgtc ggtgtgggga
 420
 agtgacgttt acgattcccc ccggggcaaat ccctctatgc gtcacatggt ccgatccaa
 480
 ttggtctcag ctactcggat cgcacgcaca agccactgca tggcgcggtg cagcgcg
 537

<210> 170
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 170
 Cys Ala Thr Ala Gly Ala Leu Lys Glu Ser Gly His Arg Arg Cys Ser
 1 5 10 15
 Thr Arg Gly Glu Gly Val Arg Ile Leu Ile Val Gly Ala Ala Ser Ser
 20 25 30
 Ile His Thr Val Arg Trp Val Asn Gly Leu Val Lys Arg Gly His Glu
 35 40 45
 Val His Leu Ala Ser Val His Pro Ala Gly Arg His Ser Ile Asp Pro
 50 55 60
 Arg Val Arg Ile His Leu Ala Pro His Gly Gly Lys Ala Lys Tyr Val
 65 70 75 80
 Val Asn Ala Gly Trp Leu Arg Ser Val Ala Ala Gly Val Gln Pro Asp
 85 90 95
 Ile Val Asn Val His Tyr Ala Thr Gly Tyr Gly Leu Leu Ala Arg Leu
 100 105 110
 Ala His Ile Asp Ala Pro Thr Leu Leu Ser Val Trp Gly Ser Asp Val
 115 120 125
 Tyr Asp Ser Pro Arg Ala Asn Pro Leu Met Arg His Met Val Arg Ser
 130 135 140
 Asn Leu Val Ser Ala Thr Arg Ile Ala Ser Thr Ser His Cys Met Ala
 145 150 155 160
 Arg Val Thr Arg

<210> 171
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 171
 ctagacaagc tcgcgcgggt gggcttcgac actcttggtc tacagacctt cctaactcgg
 60
 ggggagaagg agtcccgcg atggacgatt cacaagggcg acaccgcccc tgaggctgct
 120
 ggcgtcatcc ataccgactt ccagaagggg ttcacaaagg ccaggtggtg gtccttcggc
 180
 gaccttggtg aatttggcgg cgaaaaggag gccacggctg ctgggaaagt gcggttgagg
 240
 ggcaaggagt acgttatgca ggacggtgac gtagtggaat tccgatttaa cgtgtagctc
 300

tggtttgata cttacttggc ttaaccgcat ctgagatccg tcatatcttt gccgtagcct
 360
 tattggtatg aataacatgc cgtagccaaa g
 391

<210> 172

<211> 98

<212> PRT

<213> Homo sapiens

<400> 172

Leu	Asp	Lys	Leu	Ala	Arg	Val	Gly	Phe	Asp	Thr	Leu	Gly	Leu	Gln	Thr
1				5					10					15	
Phe	Leu	Thr	Ala	Gly	Glu	Lys	Glu	Ser	Arg	Ala	Trp	Thr	Ile	His	Lys
			20					25					30		
Gly	Asp	Thr	Ala	Pro	Glu	Ala	Ala	Gly	Val	Ile	His	Thr	Asp	Phe	Gln
			35				40					45			
Lys	Gly	Phe	Ile	Lys	Ala	Gln	Val	Val	Ser	Phe	Gly	Asp	Leu	Val	Glu
			50			55					60				
Phe	Gly	Gly	Glu	Lys	Glu	Ala	Gln	Ala	Ala	Gly	Lys	Leu	Arg	Leu	Glu
65					70				75					80	
Gly	Lys	Glu	Tyr	Val	Met	Gln	Asp	Gly	Asp	Val	Val	Glu	Phe	Arg	Phe
				85					90					95	

Asn Val

<210> 173

<211> 309

<212> DNA

<213> Homo sapiens

<400> 173

ccatggagtg tcccttgtgc gagcattttg agagctatac caacacccat cctgcaggt
 60
 cccagagccg agccatttct caggagagca ggaaggggagc aggccgaggg gtgctccccg
 120
 ccagccccgg aaccggaggt ctggggagcgc agccgaccag ccctccttgt ctgggcctct
 180
 gtttctctct cgacacaggg aagcagggag gggccgatca gcgacttagg cctgttggct
 240
 gtggtggggc ccctgcggtt tctgggaagc cacggaccct gggatgtacc tgggtttcat
 300
 tcgcagtga
 309

<210> 174

<211> 102

<212> PRT

<213> Homo sapiens

<400> 174

Met	Glu	Cys	Pro	Leu	Cys	Glu	His	Phe	Glu	Ser	Tyr	Thr	Asn	Thr	His
.1				5					10					15	
Pro	Cys	Arg	Ser	Gln	Ser	Arg	Ala	Ile	Ser	Gln	Glu	Ser	Arg	Lys	Gly

tcctctgggga gccatactca tgcctggggca agcggcatat cttggggcatc acctctatca
1140
gtgtttttcac atactggaga atggttcctt ggagcaagct cttcaccaatc ttttagcagtt
1200
cctccatgac cacagcgatg ccctgataac ccaggagctc gcagatagtc ttgaaagtgt
1260
ggagggtccca cgaagtcccg gtagctgccg taaatgctgg agtaggccaa gttcaagcc
1320
ttggatccat gcagatactg aggctgtgca ttaggctgct tatctctttg aaattcctga
1380
gaaaatggta acactgtccg aacaaaccgg ttggtagagc cgttgtagca gtagttgggc
1440
aggaagtcac agttgagctc ccagaagacg tgcagggtga tcctccccta gggcgctgac
1500
acgtttgtgtg ttggcctcccg gaacatggcg tcgaagccgt ccagcgtcag gtaccggctc
1560
agcagcttgtt gggtcacgag gttgatttcc aacaggccat ccagctcaac tatggaggctc
1620
aaatcttcac tttcaaactc tccaatgccg agttctaggg acttatacat ggctgctgag
1680
acgcgctggg tgatcagacg attgaggtct attgatctgc cgaggagctg cacatgcctc
1740
tgcttcagca gcgtctcgta gcggttagac ggcgggaggt ggatcgtggc tcctgatctc
1800
ttgcatctcg atcgtaacgg tttatcaaga agcaaaactc ctgccataac cttataatag
1860
gcaaatatct ggtctgccag cttgtagaca aactgatcaa aacacagggt cacctcagct
1920
tctatctcat cgtacaggaa ctgcttttta aacttggtca gagcatagta ggcgctgtca
1980
ttgtacagat ccaggggagta gagcacgtac tccatcatgg aagggtctctt gggttccagg
2040
atatgggtccg ttagaatcca gggcatcgac atctcaatgg ggaactggat cctcctgcc
2100
atggtcagct ccaggaagaa ctctcggaac cacagctgag aaaggtcaca gcatgctgac
2160
agcgtttcac tgaaatttat caagttagtg tagaagaatg actctcgatg aaagtcctct
2220
atggcgagga caatgggtcc atccaggctg ctctcagggt tcttcttgga gccgcttttg
2280
ctgcaatga gtgattcaag catgggtctc accatgtaca gctgtgtgct ggatggcccc
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2460
tgtaggacgc tgatgaggac attcttcttc ttccgtaccg cctgcgcgag gggctcacgc
2520
agcgtcacct gggcggaagtc ctgcaatgcc gcgtagatgg tgttctctgat ggcctgggtg
2580
aagacgctct ccatcctgcc catgagcacc tgcaggcctt tgatcatggc gatcacctca
2640
acgaaggcaa atttttcttc actgggtgtaa ttgtagcgtg ttggtctctc atattctctc
2700

gcggtgccag gacagtcctt gttgcagaac ttgtctgtgg gatgaaccag cttccaagag
2760
tacacctcca tgacgtgggc gctccacttg gatagaagct gcagaccctg cagggttagg
2820
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2880
acctcactgt tgcgtgtagc agcgagctcg gagatgaagc ggatgtggtc atcccggtac
2940
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3000
cgagatttat tttcctcgta gtgggcctg gctctgatat atcttgccag tcttatttgc
3060
atgtcccaaa atagtggaa caccctggagt tgcttgaagt acttgctgat ttgggataag
3120
tttattcttt tcttggcatc caacttatag atgttactga cactcccatc catcaggtag
3180
agaccaaata ccatgacttt gagaagcatg tgtttctcac tgggcgtcaa atacatcctg
3240
ttctgttagt aatccacaca cagattcaca atatctgccg ggagctcttc gttagccagaa
3300
atcacttcga gctgctgctg cagagactgt gtgactctgt tatgattggc caggaaacatg
3360
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<210> 176

<211> 1393

<212> PRT

<213> Homo sapiens

<400> 176

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Ser	Met	Tyr	Leu	Ala	Met	Pro	Val	Thr	Asn	Ala	Phe	Leu	Ser	Ser	Lys
				35			40				45				
Phe	Val	Ser	Lys	Leu	Ala	Trp	Tyr	Met	Met	Glu	Glu	Gly	Gly	Gly	Ser
				50			55			60					
Met	His	Gly	Cys	Trp	Ser	Gly	Arg	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Thr
65				70					75				80		
Leu	Asp	Arg	Ala	Ser	Ser	Arg	Val	Thr	Cys	Val	Val	Met	Ala	Ala	Val
				85					90				95		
Ser	Val	Phe	Cys	Thr	Gly	Ser	Ala	Ala	Gly	Pro	Gly	Glu	Gly	Pro	Glu
				100				105				110			
Ala	Thr	Ala	Gly	Pro	Arg	Ala	Gly	Ala	Gln	Asp	Ala	Leu	Pro	Arg	Ser

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Ala Ala Pro Pro Val Gln Asn Thr Glu Thr	Ala Ala Met Thr Thr His	
130	135	140
Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp	Leu Leu Glu Glu Leu	
145	150	155
Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro	Pro Pro Ser Ser Ile	
165	170	175
Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu	Asp Arg Asn Ala Phe	
180	185	190
Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr	Val His Ser Ser	
195	200	205
Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr	Ala Val Met Leu Tyr	
210	215	220
Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val	Lys Cys Asn Glu	
225	230	235
Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr	Val Glu Val Leu Glu	
245	250	255
Pro Glu Val Thr Lys Leu Met Asn Phe Met Tyr	Phe Gln Arg Asn Ala	
260	265	270
Ile Glu Arg Phe Cys Gly Glu Val Arg Arg Leu	Cys His Ala Glu Arg	
275	280	285
Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Ile Thr	Leu Gly Lys Phe	
290	295	300
Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys	Asn Met Lys Cys Ser	
305	310	315
Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala	Gln Phe Leu Arg	
325	330	335
Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser	Gln Asn Leu Ser Met	
340	345	350
Phe Leu Ala Asn His Asn Lys Ile Thr Gln Ser	Leu Gln Gln Leu	
355	360	365
Glu Val Ile Ser Gly Tyr Glu Glu Leu Leu Ala	Asp Ile Val Asn Leu	
370	375	380
Cys Val Asp Tyr Tyr Glu Asn Arg Met Tyr Leu Thr	Pro Ser Glu Lys	
385	390	395
His Met Leu Leu Lys Val Met Gly Phe Gly Leu Tyr	Leu Met Asp Gly	
405	410	415
Ser Val Ser Asn Ile Tyr Lys Leu Asp Ala Lys Lys	Arg Ile Asn Leu	
420	425	430
Ser Lys Ile Asp Lys Tyr Phe Lys Gln Leu Gln Val	Val Pro Leu Phe	
435	440	445
Gly Asp Met Gln Ile Glu Leu Ala Arg Tyr Ile Lys	Thr Ser Ala His	
450	455	460
Tyr Glu Glu Asn Lys Ser Arg Trp Thr Cys Thr Ser	Ser Gly Ser Ser	
465	470	475
Pro Gln Tyr Asn Ile Cys Glu Gln Met Ile Gln Ile	Arg Glu Asp His	
485	490	495
Met Arg Phe Ile Ser Glu Leu Ala Arg Tyr Ser	Asn Ser Glu Val Val	
500	505	510
Thr Gly Ser Gly Arg Gln Glu Ala Gln Lys Thr	Asp Ala Glu Tyr Arg	
515	520	525
Lys Leu Phe Asp Leu Ala Leu Gln Gly Leu Gln Leu	Leu Ser Gln Trp	
530	535	540
Ser Ala His Val Met Glu Val Tyr Ser Trp Lys Leu	Val His Pro Thr	

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Asp	Lys	Tyr	Ser	Asn	Lys	Asp	Cys	Pro	Asp	Ser	Ala	Glu	Glu	Tyr
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			580					585					590	Val
Glu	Val	Ile	Ala	Met	Ile	Lys	Gly	Leu	Gln	Val	Leu	Met	Gly	Arg
		595					600					605		Met
Glu	Ser	Val	Phe	Asn	His	Ala	Ile	Arg	His	Thr	Val	Tyr	Ala	Ala
	610				615					620				Leu
Gln	Asp	Phe	Ser	Gln	Val	Thr	Leu	Arg	Glu	Pro	Leu	Arg	Gln	Ala
	625				630				635					Ile
Lys	Lys	Lys	Lys	Asn	Val	Ile	Gln	Ser	Val	Leu	Gln	Ala	Ile	Arg
			645						650					Lys
Thr	Val	Cys	Asp	Trp	Glu	Thr	Gly	His	Glu	Pro	Phe	Asn	Asp	Pro
			660					665					670	Ala
Leu	Arg	Gly	Glu	Lys	Asp	Pro	Lys	Ser	Gly	Phe	Asp	Ile	Lys	Val
	675						680					685		Pro
Arg	Arg	Ala	Val	Gly	Pro	Ser	Ser	Thr	Gln	Leu	Tyr	Met	Val	Arg
	690				695						700			Thr
Met	Leu	Glu	Ser	Leu	Ile	Ala	Asp	Lys	Ser	Gly	Ser	Lys	Lys	Thr
	705				710					715				Leu
Arg	Ser	Ser	Leu	Glu	Gly	Pro	Thr	Ile	Leu	Asp	Ile	Glu	Lys	Phe
			725						730					His
Arg	Glu	Ser	Phe	Phe	Tyr	Thr	His	Leu	Ile	Asn	Phe	Ser	Glu	Thr
			740					745					750	Leu
Gln	Gln	Cys	Cys	Asp	Leu	Ser	Gln	Leu	Trp	Phe	Arg	Glu	Phe	Phe
	755						760					765		Leu
Glu	Leu	Thr	Met	Gly	Arg	Arg	Ile	Gln	Phe	Pro	Ile	Glu	Met	Ser
	770				775					780				Met
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	785				790				795					Met
Met	Glu	Tyr	Val	Leu	Tyr	Ser	Leu	Asp	Leu	Tyr	Asn	Asp	Ser	Ala
			805						810					His
Tyr	Ala	Leu	Thr	Arg	Phe	Asn	Lys	Gln	Phe	Leu	Tyr	Asp	Glu	Ile
		820					825						830	Glu
Ala	Glu	Val	Asn	Leu	Cys	Phe	Asp	Gln	Phe	Val	Tyr	Lys	Leu	Ala
	835						840					845		Asp
Gln	Ile	Phe	Ala	Tyr	Tyr	Lys	Val	Met	Ala	Gly	Ser	Leu	Leu	Leu
	850				855					860				Asp
Lys	Arg	Leu	Arg	Ser	Glu	Cys	Lys	Asn	Gln	Gly	Ala	Thr	Ile	His
	865				870				875					Leu
Pro	Pro	Ser	Asn	Arg	Tyr	Glu	Thr	Leu	Leu	Lys	Gln	Arg	His	Val
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		900					905						910	Val
Ser	Ala	Ala	Met	Tyr	Lys	Ser	Leu	Glu	Leu	Ala	Ile	Gly	Arg	Phe
	915						920					925		Glu
Ser	Glu	Asp	Leu	Thr	Ser	Ile	Val	Glu	Leu	Asp	Gly	Leu	Leu	Glu
	930				935					940				Ile
Asn	Arg	Met	Thr	His	Lys	Leu	Leu	Ser	Arg	Tyr	Leu	Thr	Leu	Asp
	945				950				955					Gly
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			965					970						Tyr
Gly	Arg	Ile	Thr	Leu	His	Val	Phe	Trp	Glu	Leu	Asn	Tyr	Asp	Phe
														Leu

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 1285 1290 1295
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<210> 178
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 178
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 Arg Ile Leu Glu Thr Asp Pro Ala Ala Val Lys Pro Pro Lys Asn
 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
 85 90 95
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
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 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
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<210> 179
 <211> 362
 <212> DNA
 <213> Homo sapiens

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<210> 180

<211> 108

<212> PRT

<213> Homo sapiens

<400> 180

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			20					25					30		
Ser	Pro	Ser	Thr	Ser	Ile	Arg	Met	Leu	Pro	Pro	Thr	Ser	Val	Pro	Ala
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Pro	Tyr	His	Thr	Pro	Thr	Gly	Arg	Ala	Pro	Thr	Phe	Trp	Ile	Arg	Ala
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Ala	Arg	Pro	Asn	Gly	Glu	Phe	Pro	Asp	Ser	Trp	Gly	Cys	Gly	Ile	Phe
65					70				75					80	
His	His	Gln	Pro	Thr	Gly	Asn	His	Leu	Arg	Leu	Phe	Gln	Gly	Leu	Arg
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Asp	Val	Ile	Asp	Arg	Pro	His	Arg	His	Leu	Arg	Arg				
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<210> 181

<211> 297

<212> DNA

<213> Homo sapiens

<400> 181

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 180
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 240
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 297

<210> 182

<211> 99

<212> PRT

<213> Homo sapiens

<400> 182

Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
 1 5 10 15
 Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
 20 25 30
 Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile
 35 40 45
 Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
 50 55 60
 Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
 65 70 75 80
 Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
 85 90 95
 Ala Asn Gln

<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

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 120
 aagcgcctct ctttggcgac cgacgggctc ggccaccagg tctgtctcaa gggctaccag
 180
 gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtgccggc
 240
 gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaaac cgatttcggc
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 351

<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
 1 5 10 15
 Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
 20 25 30
 Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
 35 40 45
 Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
 50 55 60
 Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
 65 70 75 80
 Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

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      85              90              95
Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala
      100              105              110
Asn His Phe Gly Asp
      115

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<210> 185
<211> 396
<212> DNA
<213> Homo sapiens

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<400> 185
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120
gggccacggt ataagcgag caaattagaa agaagagcaa acacagatgt cctctggtgt
180
gtcatgcttc tggtcataat gtgcttaact ggcgagtagt gtcatggaat ctggctgagc
240
aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca
300
ctgttgagcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
360
atttctctct atgtttccat cgaaattgtg aagctt
396

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<210> 186
<211> 132
<212> PRT
<213> Homo sapiens

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<400> 186
Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Arg Gly Cys Thr Ile
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Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
20     25     30
Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
35     40     45
Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
50     55     60
Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
65     70     75     80
Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
85     90     95
Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
100    105    110
Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
115    120    125
Ile Val Lys Leu
130

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<210> 187
<211> 423

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<212> DNA

<213> Homo sapiens

<400> 187

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 120
 gatgagcate gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggtgctcgc
 180
 cgcggagatc gcagtattgc tgacgcggtg gaaactaacg gcacctcac ggcgcggacc
 240
 gacactccgt tgtccgagct ctctgctccg accagcaacg ccagggtgcc gttggccggtt
 300
 gtcgacgagg acttccacct catgggtgtc atctctcggg tgacctgct cgacgcgatg
 360
 tcacgagctc gcgacgaggc aggagagggg tctgtcatgt ccttggagaa caccggaaa
 420
 ctt
 423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5					10				15		
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
			20					25				30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
		35				40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
		50			55				60						
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70				75					80		
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90					95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
			100				105					110			
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
		115			120							125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

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 60

aaatgtttga agatgccggc gtttcgggcc tcaacttggt tcatgcccgt ggttccaccg
 120
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga
 180
 gcaaggtata tcaggctcag aaccaggaaa agcaggggctt taccctcagt ccccatatag
 240
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct
 300
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
 360
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 420
 ctgatttcn
 429

<210> 190

<211> 123

<212> PRT

<213> Homo sapiens

<400> 190

Met	Met	Gly	Ala	Gly	Pro	Leu	Val	Ala	Gly	Leu	Ala	Leu	Gly	Leu	Gly
1				5					10				15		
Glu	Ala	Xaa	Asp	Ala	Leu	Pro	Ser	Ala	Met	Lys	Val	Leu	Ser	Trp	Thr
			20					25				30			
Pro	Leu	Gly	Ala	Pro	Phe	Ala	Val	Ala	Ser	Ala	Val	Tyr	Met	Gly	His
		35				40					45				
Trp	Gly	Lys	Ala	Leu	Leu	Phe	Leu	Val	Leu	Ser	Leu	Ile	Tyr	Leu	Ala
	50				55				60						
Leu	Ser	Trp	Val	Ile	Trp	Thr	Lys	Leu	Leu	Asn	Arg	Ala	Met	Ser	Arg
65				70				75					80		
Ile	Gly	Glu	Ile	Gly	Thr	Thr	Ala	Ser	Lys	Gln	Val	Glu	Ala	Gly	
			85					90				95			
Asn	Ala	Gly	Ile	Phe	Lys	His	Phe	Thr	Ala	Ser	Pro	Arg	Gly	Ala	Ile
		100					105					110			
Ala	Ala	Arg	Thr	Val	His	Met	Leu	Val	Asn	His					
		115					120								

<210> 191

<211> 4845

<212> DNA

<213> Homo sapiens

<400> 191

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 cctccgggctt ctgcctccgg ccaggagttc tggcccgagc aatcggcggc cgatattctg
 120
 tcggggggcg cttcccgagc acggtatctt ctgtatgacg tcaaccccc ggaaggcttc
 180
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
 240
 gaggagtggg tgcttctcct gcctccatgg ggccgcctct atcactggca gagtctcgac
 300

atccaccagg tccggattcc ctggctctgag ttttttgate ttccaagtct caataaaaaac
360
atccccgtca tccagtatga gcagttcatc gcagaatctg gtgggcccctt tattgaccag
420
gttttactgc tgcaaaagta cgcagagggg tggaagaag ggacctggga agagaaggtg
480
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540
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600
ggctcagcct ccatcgtggc gccctctgct ctgagaaaca catcagcccg gtcctgtatg
660
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720
cgtcgcagca tgggtgttgc caggcacctg cgggagggtg gagacagatt caggagcaga
780
catctcaact ccacggacga cgcagacagg atccccctcc aggaggactg gatgaagatg
840
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960
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1020
aaggaatatg aagagctaaa aaagctgtta cccgagatgg tgaggtttga acccacgtgg
1080
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1140
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 4800
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 4845

<210> 192

<211> 428

<212> PRT

<213> Homo sapiens

<400> 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly
 1 5 10 15
 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
 20 25 30
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

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      35              40              45
Tyr Leu Leu Tyr Asp Val Asn Pro Pro Glu Gly Phe Asn Leu Arg Arg
  50              55              60
Asp Val Tyr Ile Arg Ile Ala Ser Leu Leu Lys Thr Leu Leu Lys Thr
  65              70              75              80
Glu Glu Trp Val Leu Val Leu Pro Pro Trp Gly Arg Leu Tyr His Trp
      85              90              95
Gln Ser Pro Asp Ile His Gln Val Arg Ile Pro Trp Ser Glu Phe Phe
      100              105              110
Asp Leu Pro Ser Leu Asn Lys Asn Ile Pro Val Ile Glu Tyr Glu Gln
      115              120              125
Phe Ile Ala Glu Ser Gly Gly Pro Phe Ile Asp Gln Val Tyr Val Leu
      130              135              140
Gln Ser Tyr Ala Glu Gly Trp Lys Glu Gly Thr Trp Glu Glu Lys Val
      145              150              155              160
Asp Glu Arg Pro Cys Ile Asp Gln Leu Leu Tyr Ser Gln Asp Lys His
      165              170              175
Glu Tyr Tyr Arg Gly Trp Phe Trp Gly Tyr Glu Glu Thr Arg Gly Leu
      180              185              190
Asn Val Ser Cys Leu Ser Val Gln Gly Ser Ala Ser Ile Val Ala Pro
      195              200              205
Leu Leu Leu Arg Asn Thr Ser Ala Arg Ser Val Met Leu Asp Arg Ala
      210              215              220
Glu Asn Leu Leu His Asp His Tyr Gly Gly Lys Glu Tyr Trp Asp Thr
      225              230              235              240
Arg Arg Ser Met Val Phe Ala Arg His Leu Arg Glu Val Gly Asp Glu
      245              250              255
Phe Arg Ser Arg His Leu Asn Ser Thr Asp Asp Ala Asp Arg Ile Pro
      260              265              270
Phe Gln Glu Asp Trp Met Lys Met Lys Val Lys Leu Gly Ser Ala Leu
      275              280              285
Gly Gly Pro Tyr Leu Gly Val His Leu Arg Arg Lys Asp Phe Ile Trp
      290              295              300
Gly His Arg Gln Asp Val Pro Ser Leu Glu Gly Ala Val Arg Lys Ile
      305              310              315              320
Arg Ser Leu Met Lys Thr His Arg Leu Asp Lys Val Phe Val Ala Thr
      325              330              335
Asp Ala Val Arg Lys Glu Tyr Glu Glu Leu Lys Lys Leu Leu Pro Glu
      340              345              350
Met Val Arg Phe Glu Pro Thr Trp Glu Glu Leu Glu Leu Tyr Lys Asp
      355              360              365
Gly Gly Val Ala Ile Ile Asp Gln Trp Ile Cys Ala His Ala Arg Cys
      370              375              380
Leu Pro Thr Ser Leu Ser Ala Glu Ser Gly Ser Gly Gly Phe Gln Arg
      385              390              395              400
Phe Phe Cys Pro Lys Tyr Ser Val Ser Glu Gln Met Val Ala Cys Val
      405              410              415
His Ser Gly His Phe His Thr Val Cys Leu Leu Val
      420              425

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<210> 193

<211> 350

<212> DNA

<213> Homo sapiens

<400> 193
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 120
 cgtgccagca tcagcccccga ggaggtcaag ggcgagacca tgttatgttt gggcacgggc
 180
 ccctgggttc cccggggccg cgggtgggggt ttggcccgga tttggcgcgt ttctccagcg
 240
 ccgttaaggg catacgccgc agtttcgagg gctcgtcgcgt ggagaccatc aagcacatcg
 300
 tggcttcggg catggcgtga cgggtggtgcc gcagctgtcc gtgccgcgcg
 350

<210> 194
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 194
 Ala Gly Glu Leu Asp Cys Ala Ile Met Ala Glu Pro Phe Pro Asp Thr
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 Gly Leu Ala Thr Ala Gln Leu Tyr Asp Glu Pro Phe Val Val Ala Leu
 20 25 30
 Arg Ala Ser His Pro Leu Ala Asp Arg Ala Ser Ile Ser Pro Glu Glu
 35 40 45
 Val Lys Gly Glu Thr Met Leu Met Leu Gly Thr Gly Pro Trp Phe Pro
 50 55 60
 Arg Ala Arg Gly Gly Gly Leu Ala Arg Ile Trp Arg Val Ser Pro Ala
 65 70 75 80
 Pro Leu Arg Ala Tyr Ala Ala Val Ser Arg Ala Arg Arg Trp Arg Pro
 85 90 95
 Ser Ser Thr Ser Trp Leu Arg Ala Trp Arg Asp Gly Gly Ala Ala Ala
 100 105 110
 Val Arg Ala Ala
 115

<210> 195
 <211> 495
 <212> DNA
 <213> Homo sapiens

<400> 195
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 gaaatgggtc gcttcgacga aagcgagact ctgcaccgcc ttgcacggg cgtccttgaa
 120
 ccagaacttg gcgacgattt ggccgcccgc ctgctcgatt ctcatcgggt tgctgtcatc
 180
 agcgagggat cgaactggct tgctcgccta cccgtgatcg taggtcgcaa cacggaacag
 240
 ttctgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat
 300

cgcgaatatg cagcaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgctg
 360
 cactgccacg gcgacgcaca cctcggcaac atcgatcatga ttgacggcaa gccggtcctg
 420
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 480
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 495

<210> 196
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 196
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 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
 20 25 30
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
 35 40 45
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
 50 55 60
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
 65 70 75 80
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
 85 90 95
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
 100 105 110
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
 115 120 125
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
 130 135 140
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
 145 150 155 160
 Phe Pro Leu Met Asp
 165

<210> 197
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 197
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 aaagggtatca atccagatga aactgaaggt gaacgtcacg caagcgatga tgagccattc
 120
 tcttcattag cattcaaaat tgcaactgac ccattcgttag gtaacttaac cttcttccgt
 180
 gtgtactcag gtgtaattaa ctctgggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
 360
 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
 402

<210> 198

<211> 134

<212> PRT

<213> Homo sapiens

<400> 198

Gln	Ala	Met	Leu	Asp	Ala	Val	Val	Glu	Tyr	Leu	Pro	Ala	Pro	Thr	Asp
1			5					10					15		
Ile	Pro	Ala	Ile	Lys	Gly	Ile	Asn	Pro	Asp	Glu	Thr	Glu	Gly	Glu	Arg
		20					25					30			
His	Ala	Ser	Asp	Asp	Glu	Pro	Phe	Ser	Ser	Leu	Ala	Phe	Lys	Ile	Ala
		35				40					45				
Thr	Asp	Pro	Phe	Val	Gly	Asn	Leu	Thr	Phe	Phe	Arg	Val	Tyr	Ser	Gly
	50				55				60						
Val	Ile	Asn	Ser	Gly	Asp	Thr	Val	Leu	Asn	Ser	Val	Arg	Gln	Lys	Arg
65				70				75					80		
Glu	Arg	Phe	Gly	Arg	Ile	Val	Gln	Met	His	Ala	Asn	Lys	Arg	Glu	Glu
			85				90						95		
Ile	Lys	Glu	Val	Arg	Ala	Gly	Asp	Ile	Ala	Ala	Ala	Ile	Gly	Leu	Lys
			100				105						110		
Asp	Val	Thr	Thr	Gly	Glu	Pro	Leu	Cys	Ala	Val	Asp	Ala	Pro	Ile	Ile
		115				120					125				
Leu	Glu	Arg	Met	Glu	Phe										
			130												

<210> 199

<211> 507

<212> DNA

<213> Homo sapiens

<400> 199

acgcgtgaag tcgtgcatag atcgggtgtga catagagaag cctccgaccc aagctgcgta
 60
 tatcgacaca agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga
 120
 caatagttaa atccccgaga acccagctat ggaaggggtt ccagatgctc gaaggcctgt
 180
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
 240
 aaagcctgct cctaaagagg atttagatct gatagatcta tcttcagatt caacctcgga
 300
 gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct
 360
 tccctctctc agaatagtcg agagtgcga agaagaggag acgatgaacc aaggcgatga
 420
 cggccctctc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtctc
 480
 cagcctgagc acagctccgc ttgtaca
 507

<210> 200

<211> 153

<212> PRT

<213> Homo sapiens

<400> 200

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Met Glu Gly  Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro
 1              5              10              15
Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
              20              25              30
Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35              40              45
Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50              55              60
Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65              70              75              80
Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85              90              95
Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100             105             110
Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115             120             125
Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130             135             140
His Arg Ser Met His Asp Phe Thr Arg
145             150

```

<210> 201

<211> 527

<212> DNA

<213> Homo sapiens

<400> 201

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gatgtggcta ttatccctgt ttcccagggtg agaaacaggg tcagtgatag agctgggcat
60
tgtgcctgca ggctcaccag ccagtcacct cctcaccaag gatgatgttc tccgtggtag
120
gctggctcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
180
ccttctccat ctctttggct agctgcaagt tctggagctg ctctgtgagg tctgtgatct
240
catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg
300
ccagctgtctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccaattcc
360
gctggtagcc ggctagccgg tcctccagggt ctcggatctg gatgtggtag aactccttca
420
tctccttgcc cagaggcgcc tccacggcca ccaccggctc cttcttgccc cttttcttct
480
tgacttcaag ctcttgctc gccttgcctca cactcttttt gggaggc
527

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<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
 1 5 10 15
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
 20 25 30
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
 35 40 45
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Ala Pro
 50 55 60
 Ser Cys Pro Leu Ser Ser
 65 70

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203
 nggtgcaccgg tggatcatgga caacgcccgc tacgtgggtct acacctcggg atccaccggc
 60
 cgacccaagg gagttgtcgt caccacaccc ggactcgaca gcttcgcact cgaccagcag
 120
 cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac
 180
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgtcccg
 240
 accgacatct acggcgggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
 300
 gcgt
 304

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
 1 5 10 15
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
 20 25 30
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
 35 40 45
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
 50 55 60
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
 65 70 75 80
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
 85 90 95
 His Val Thr His Ala

100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
 nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat
 60
 gcacaattaa atacagtgtt aactttatct tcaccacaat caaaagataa agattttaac
 120
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
 180
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
 240
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta
 300
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
 356

<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1 5 10 15
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
 115

<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcacg
 60
 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcaactgtgtg gtgtgtatgc atgggtgtgtg cactgtgtgca ctgtgtatgc
 240
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
 300
 gtatgcatgg taatgtgcac gtgt
 324

<210> 208

<211> 108

<212> PRT

<213> Homo sapiens

<400> 208

Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209

<211> 168

<212> DNA

<213> Homo sapiens

<400> 209

nnctccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctaccat
 60
 attcaaggtt ccacgactcg cacctgcctt gccaatttta catggagtgg gatacagacc
 120
 gaatgtatgc ctcatgcctg cagacagcca gaaaccccg cacaacgag
 168

<210> 210

<211> 56

<212> PRT

<213> Homo sapiens

<400> 210

Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40
Gln Pro Glu Thr Pro Ala His Ala
50 55

45

<210> 211
<211> 354
<212> DNA
<213> Homo sapiens

<400> 211
tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgttgg aggcaatgtc
60
cagctggcag ctcagaccct tgcacacccat ggaggaagcc tcccaccga cctgcagttc
120
tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct
180
agtgcctcga cagatgaaga catggagacg gaggtgtgca acgaaatcct ggaggacatt
240
ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgtc
300
gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
354

<210> 212
<211> 118
<212> PRT
<213> Homo sapiens

<400> 212
Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
1 5 10 15
Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
20 25 30
Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
35 40 45
Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
50 55 60
Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
65 70 75 80
Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
85 90 95
Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
100 105 110
Xaa Lys Glu Gln Leu Ile
115

<210> 213
<211> 669
<212> DNA
<213> Homo sapiens

<400> 213
attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tgggtgcagtc tattggggaa
60

gttgaacaaa acctggaagg gaaacagggtg tcatcactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccaccctgt agatgggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcgaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta ccccgaggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttggg aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaga gagagagaaa gatgcacatc cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile Ala Gln Ser Gln Ser Val Gln Glu Ser Leu Glu Ser Leu Leu Gln
 1 5 10 15
 Ser Ile Gly Glu Val Glu Gln Asn Leu Glu Gly Lys Gln Val Ser Ser
 20 25 30
 Leu Ser Ser Gly Val Ile Gln Glu Ala Leu Ala Thr Asn Met Lys Leu
 35 40 45
 Lys Gln Asp Ile Ala Arg Gln Lys Ser Ser Leu Glu Ala Thr Arg Glu
 50 55 60
 Met Val Thr Arg Phe Met Glu Thr Ala Asp Ser Thr Thr Ala Ala Val
 65 70 75 80
 Leu Gln Gly Lys Leu Ala Glu Val Ser Gln Arg Phe Glu Gln Leu Cys
 85 90 95
 Leu Gln Gln Gln Glu Lys Glu Ser Ser Leu Lys Lys Leu Leu Pro Gln
 100 105 110
 Ala Glu Met Phe Glu His Leu Ser Gly Lys Leu Gln Gln Phe Met Glu
 115 120 125
 Asn Lys Ser Arg Met Leu Ala Ser Gly Asn Gln Pro Asp Gln Asp Ile
 130 135 140
 Thr His Phe Phe Gln Gln Ile Gln Glu Leu Asn Leu Glu Met Glu Asp
 145 150 155 160
 Gln Gln Glu Asn Leu Asp Thr Leu Glu His Leu Val Thr Glu Leu Ser
 165 170 175
 Ser Cys Gly Phe Ala Leu Asp Leu Cys Gln His Gln Asp Arg Val Gln
 180 185 190
 Asn Leu Arg Lys Asp Phe Thr Glu Leu Gln Lys Thr Val Lys Glu Arg

```

      195              200              205
Glu Lys Asp Ala Ser Ser Cys Gln Glu Gln Leu Asp Glu Phe Arg
      210              215              220

<210> 215
<211> 814
<212> DNA
<213> Homo sapiens

<400> 215
aaatttcgta cccgctccg caccagtacga gcccttgacg atgtgagcct ggctattaag
60
agaggttcca tctcagccgt tatcggggcac tccggagccg gcaaattccac cctggttcgc
120
ctcatcaacg gattagagac tcccacgcgt gcccgcgctct tggtagacgg caccgacgtc
180
tcgcagctct cggacaaagc gatgcgcccg ctacgcgcag acatcgggat gatcttccaa
240
cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
300
gtctattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag ctctcgtcggg
360
ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcggggt
420
ggatattgcc gagcgctagc aactaaacca tggattttgt tggctgacga gtccacctcg
480
gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
540
ctaggggtga cggctcgtct catcaccacg gagatggagg tcgtccgctc gattgcccag
600
caggctctcg tactagcagc tggccatctc gtcgagttcg gaagcgcgcc ccagggtcttc
660
gtcatccac agtcagagac caccacgcgt ttcttgggca cgattatcgg ccagcaccgg
720
agtggggagg aacaggcacg gttgcagtcg gaaaaccacg atgcacgact cgtcgcgctc
780
agttcgggtg ccagtcactc gttcgggtgac gcgt
814

<210> 216
<211> 271
<212> PRT
<213> Homo sapiens

<400> 216
Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
1 5 10 15
Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
20 25 30
Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
35 40 45
Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
50 55 60
Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

```

65		70		75		80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr						
	85			90		95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val						
	100		105		110	
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His						
	115		120		125	
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg						
	130		135		140	
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser						
	145		150		155	160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg						
	165		170		175	
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met						
	180		185		190	
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly						
	195		200		205	
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln						
	210		215		220	
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro						
	225		230		235	240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg						
	245		250		255	
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala						
	260		265		270	

<210> 217

<211> 500

<212> DNA

<213> Homo sapiens

<400> 217

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nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtagagccac
180
ctgttacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggcccttg agctcctgct gatcaggaag tacatccccc gaagatcttt cttcattttc
420
ctgggccatg atgaggagtc atcagggaca ggggctcaga ggaatctcagc cctgctacag
480
tcaaggggcg tccagctagc
500

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<210> 218

<211> 166

<212> PRT

<213> Homo sapiens

<400> 218

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Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
      165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caaggtccgc acgtcccat gtccctcggt ttgcacagtt cttttgccc gcattatggc
120
gaagccgctg agattgcgcc tgatatcaag cgcatcacgg tcaacaaccc cagccccttc
180
acttttttgc gcaccaacag ttatctgata ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgcttg acgaggccca tcacgcggcg ctgctgcgtg ccattgcccg cggccggctc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtgcgcgac ggttttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1             5             10             15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20             25             30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35             40             45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50             55             60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65             70             75             80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85             90             95
Ile Pro Val Ser Thr Arg
      100

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<210> 221

<211> 401

<212> DNA

<213> Homo sapiens

<400> 221

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agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagcccaca ctgctgcagc acacctcgct
120
gcagctctgg ttcctcctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcggct ccagtgaacca cccccccagg gcataccctc ctacagagca
240
ttcccaaaaa aggcctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgctcgtgta accagcatcc aggcctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

```

<210> 222

<211> 124

<212> PRT

<213> Homo sapiens

<400> 222

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Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
      1             5             10             15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20             25             30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35             40             45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50             55             60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65             70             75             80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85             90             95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
 115 120

<210> 223
 <211> 331
 <212> DNA
 <213> Homo sapiens

<400> 223
 tcatgaaatc tgtgggcagt gaccaggag ggtatgggca ggccaacca ggttggtgtg
 60
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
 120
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
 180
 cgtggtgcct ggcagatagt gtctgacccc cnaggacctt cttgctgggc agcccagtc
 240
 aaaagctgtt cccgcttaag ccacccccac cgccttggcc acacctggga catgggtgaa
 300
 gcaagggcac ttcccggggc ttccgtgtcc c
 331

<210> 224
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 224
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
 1 5 10 15
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Val
 20 25 30
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
 35 40 45
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
 50 55 60
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
 65 70 75 80
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
 85 90 95
 Ser Leu Pro Thr Asp Phe Met
 100

<210> 225
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 225
 tgatcacggg cgtgagccac cagcccagca tcccttgctt ttattcgca cctccacctc
 60
 cagaatgacc ctcatccct cctgcacaga cggtgacagc agtaactcct acaaacacca
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
 180
 caaatctctc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
 240
 cctcagccag cgggttccaa accaactccc agcctggcct caccatccca ccgccaaaac
 300
 tttgctcaca ctggcccttc ttcttggaac atgggcctn
 339

<210> 226

<211> 91

<212> PRT

<213> Homo sapiens

<400> 226

Met	Thr	Leu	Ile	Pro	Ser	Cys	Thr	Asp	Gly	Asp	Ser	Ser	Asn	Ser	Tyr
1				5					10				15		
Lys	His	His	Gln	Thr	Asp	Leu	Gln	Glu	Gln	Arg	Asn	Ser	Gln	Ser	Arg
			20					25					30		
Phe	His	Pro	Arg	Arg	Ala	Leu	Lys	Ser	Ser	Arg	Ala	Ala	Cys	Tyr	Gly
			35				40					45			
Gly	Gly	Arg	His	Thr	Leu	Leu	Gly	Ser	Gln	Gly	Leu	Ser	Gln	Pro	Gly
			50			55					60				
Pro	Asn	Gln	Leu	Pro	Ala	Trp	Pro	His	His	Pro	Thr	Ala	Lys	Pro	Leu
65					70				75					80	
Leu	Thr	Leu	Ala	Pro	Leu	Pro	Gly	Thr	Trp	Ala					
			85					90							

<210> 227

<211> 353

<212> DNA

<213> Homo sapiens

<400> 227

gtcgaccctc tcgattgtgg cgaactccat ggctgctgcg ggctcgcta ggctctcgag
 60
 tagctcgacg tcgggttcgc gagggtctgc agcgtggcca tgctgcttct tggatggttc
 120
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcattccggga
 180
 ggccaggccg acaagtgcct cctcctgcca cccgctgagc gacgctgcca tgttagtagta
 240
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgctca ggccgagaga
 300
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgt tctcctgcac ggg
 353

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

1	5	10	15
Leu Thr Ser Glu Asp Ala Val	Leu Asn Met Ala Ala Ser	Leu Ser Gly	
	20	25	30
Trp Gln Glu Ala Ala Leu Val	Gly Leu Ala Ser Gly Met Thr	Pro Glu	
	35	40	45
Gln Val Arg Gln Glu Leu Leu	Glu Ser Pro Glu Glu Leu	Pro Glu Pro	
	50	55	60
Ser Lys Lys Gln His Gly His	Ala Ala Ser Pro Arg Glu	Pro Asp Val	
	65	70	75
Glu Leu Leu Glu Ser Leu Arg	Arg Pro Ala Ala Ala Met	Glu Phe Ala	
	85	90	95
Thr Ile Glu Gly Val Asp			
	100		

<210> 229

<211> 743

<212> DNA

<213> Homo sapiens

<400> 229

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nnggcttaggg acacggcctc ctccccaaca ggcagtgcct gtgcaggctc aggggcatca
60
tcaaaagataa cacagggtg gtcaggggct gctggctgct cctgccccag gactggctcc
120
aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggagg caccaggagg
180
tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
240
agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttag aaagccagcc
300
cagcttgga ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
360
gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaa
420
agagattcac tgggtacctc cagtagtcga gatgtaagcc ttggggactg ggaatttggg
480
aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
540
gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
600
tttcagaaga gagatgtgtc actcggcacc tatggcagcg gggctcgga gccacaggaa
660
caggagttag ggaagagcgc ttggataagg gactacagca gtgggtggcag ctccaggacc
720
cttgacgccc aggacagaag ctt
743

```

<210> 230

<211> 247

<212> PRT

<213> Homo sapiens

<400> 230

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Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

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      1             5             10             15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly
      20
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu
      35
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg
      50
Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln
      65
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val
      85
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val
      100
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser
      115
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu
      130
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly
      145
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln
      165
Gly Gln Asp Leu Gly Lys Arg Asp His Gly Arg Tyr Ser Ser Gln
      180
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu
      195
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly
      210
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Ser Ser Arg Thr
      225
Leu Asp Ala Gln Asp Arg Ser
      245

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<210> 231

<211> 431

<212> DNA

<213> Homo sapiens

<400> 231

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acgcgttgcc caccgagagg ctggcgaggg tgtgcagcac ggcgagtggt ggccaggggtcc
60
cagggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg
120
ccaccaggac gccactcgcc gcctgctgcc agtccagac caggctcctc gtcttggtca
180
tctcgtcgga ggccaggagg atgatggtgc tggctgtgtc cttgtccagc tcactggcgc
240
gactgctcag gacctctcc atggccctca ggaccgctgc tcggtatggg tgtgccagct
300
tgtcatgctg ccgcagatac tcctcgagg caccggagct ctcaccctg ctggagccca
360
tcaccgataa ggacccccctg gtgcaggagc aggtctgcag tgcctgtgct tcctcgggg
420
aggtgcggcc g
431

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<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
 acgcgttcag ggaatgccaga aatctaactg ggtaataaaaa agctgggaga acattccaga
 60
 aaaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt cccagctttc
 120
 gtgctggaat gcacccccat cggaagggt cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaaactc
 240
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc
 300
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tccagttga
 360
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc
 420
 gaaagtcacg cctgcaggct tcctgggcaa gctagtggg tgaagtatgc cacagcaaca
 480
 ggcttctaga gccggtgcc cagctcctac tctgcctctg ccaactcactg actgtgtggt
 540
 cttgagcagg tcacctgtct gacttggtga gagctgacag gcatcacctg ttagaggctt
 600
 acgcgt
 606

<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1 5 10 15
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
 20 25 30
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
 35 40 45
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
 50 55 60
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
 65 70 75 80
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
 85 90 95
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
 100 105

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235
 cgaccgttga ctattctcta caaaccacaa agacaatgat tgatttaact gaatttagaa
 60
 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga
 120
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atggctcaag
 180
 aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
 240
 acattttctca aggagataga ataagtgaaa gaaaattgga ttatttgagc ctcaaaaata
 300
 tgagtgaagc acaatcaaag aatgaatt
 328

<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1 5 10 15
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
 20 25 30
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
 35 40 45
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
 50 55 60
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65	70	75	80
Leu Asp Leu Leu Ser	Leu Lys Asn Met	Ser Glu Ala Gln Ser	Lys Asn
	85	90	95
Glu			

<210> 237

<211> 2059

<212> DNA

<213> Homo sapiens

<400> 237

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ggccataagg gcacgacgca ttcctagccg atgcaccaac acgggcatga agcctgccga
60
gagcacgaag ccggcggtcca tagctacggc ccatcaggtc atgtctgccg tggctccggt
120
gatgtcagac tgcacatgaa atcgggttac gtaccccagg atcatcgcta ccgagtacac
180
cccgaacagc acccgctggg cgccgatcag cgtgaggagg tgccccacca gtggcacttt
240
tcttagatag cggaacccat ccaccacatc ccagtcacc gttctcatcg tccgggaacg
300
atccaccagt ggccggccaa gctcccgcag tgaaaactgc agcccctagg cgaccgagac
360
tgccaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtggtgca caggaatatg
420
gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccttagcgg
480
ccaatcgttg gcatgattga cgatgccgtc aggtagtcgc gcttgctgat ggtgtattcc
540
aaccacagca ccaaggcggt gagcaaaac cggttcaggc tcatcgcgat gagcaacca
600
atgagcaagg ccagggtgga gggcttatcg gcgcaccac ccagaccaa gatcccacgc
660
ccgacccagg tgacggcagc cattcatctg cgtattgtcc gactacacc gtgaggggcg
720
tctctgatct gcagctcatc aagggttacgc gactgcagta cctcaatgca ctcttggtta
780
cccagccca gaacctgcca cagtcacctg agaacaccga cctgcagggt attccaggca
840
gccagaccag gctccttggt gagaagacca ccacagcggc agctttccca gtaccccttt
900
ccctctttgg cacagttgga acctccagtt gataaatgac tgtggactag cgcgcgtttt
960
ttgttttcag agcacacgta aggggtccagc cacagcaggc ccggcgctccc ggtggaaggc
1020
agccctgggc ggaacccagg cgtttaacgg ctactaggc agcccagat ctgggggaagc
1080
agatgagcac gtggggagct ggagtgagct gagcagaagt ttgtgcccc cctgccccca
1140
tcccctccag gccacgtttt agatggccct tgtagttgag ggtcctgggt gtcctcagaa
1200
ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca
1260

```

ccagggcacac gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta
 1320
 gtteccaggagg cccagccttc cccttctccc ccggggcagg gacagtgcgg catattcaga
 1380
 ttcagacctc tttgggctga gccaccttgt gagtgcagtt actgcctttg tgtggccgtg
 1440
 acctctattt gtttgctttt aatttgccaa cctatcgctg ctggcagcac tttttgagca
 1500
 agccgagagc acccattttg gctggggatt cagatcgatg gccttggtcca tgtgtgcctt
 1560
 tctggcttcc ctgatgggtg catgtttcag cgcattgcgc ccagcctttc ccattgtgcca
 1620
 aaccagaagc tccactgccc gtaggctgtc cctgtagccc tgctccctcc ctggaggctg
 1680
 ctcttctgat tctgagagct ggcctagtgg tgcctgaggg ccctttctgc tctctgccc
 1740
 acctgctgag ttgccactcg cagtgttgtc agttcccggtg ttctgagaag aggtcatgcc
 1800
 tgggaggaag ggatcgatc gctgcatcga atcctctctc cgcctgtgtg cccccaggag
 1860
 agtagctgcc tgttgcaact gctccacacc tccccacagc ctccctgcag gtgctgtgtg
 1920
 gccgtgatgt gcagagagca gtgagggagg gttcatgaac cagggtggatc ctctttaaaa
 1980
 aaaaaaaaaa tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa
 2040
 agacttgaaa tgttctaga
 2059

<210> 238

<211> 129

<212> PRT

<213> Homo sapiens

<400> 238

Ala	Glu	Gln	Lys	Phe	Cys	Ala	Arg	Leu	Pro	Pro	Ser	Pro	Pro	Gly	His
1				5				10						15	
Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
			20					25						30	
Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Ser	Phe	Arg
		35					40						45		
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
		50				55						60			
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
		65				70				75				80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
			85					90						95	
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
			100					105					110		
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
			115					120						125	

Phe

<210> 239

<211> 388

<212> DNA

<213> Homo sapiens

<400> 239

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nctctagatca ctctgtagcg catgggttaaa tgctgacaca atagaaaagt gcgaggacat
60
cctcgaatta atgagatgggt ggactggatg agtcaagttc tcgtcgttgc ggcggctgtc
120
ggtcagctgc cctcctcca ctctgcttc tcggcggttac cccataccgt attggccgcg
180
tgttcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag
240
atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgccgcc acgaaacgcc
300
cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgagg atctcagctc tggtaacctat
360
ggtcgtgtat ataaagcaaa ggaacttn
388

```

<210> 240

<211> 104

<212> PRT

<213> Homo sapiens

<400> 240

```

Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
1 5 10 15
Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
20 25 30
Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
35 40 45
Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
50 55 60
Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
65 70 75 80
Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
85 90 95
Arg Val Tyr Lys Ala Lys Glu Leu
100

```

<210> 241

<211> 330

<212> DNA

<213> Homo sapiens

<400> 241

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ncggggggcc gagttgaaag ctgccggcac actggctgtg ctgcttgctt cacttctcgg
60
gatgctgctt ccagggcggy cctgggggaa acatcggcct tcccaggcac ccttagcccg
120
tcccatctgg gggcccttag cacagtcctt gggacccccc atgctgcctt tcaggctgat
180

```

gtggggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt
 240
 gggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcgcca ctggcgccat
 300
 gggaaacggg ttgacttgca caaccagcac
 330

<210> 242

<211> 100

<212> PRT

<213> Homo sapiens

<400> 242

Met	Ala	Pro	Val	Pro	Met	Pro	Leu	Leu	Leu	Ile	Gln	Ser	Thr
1			5				10				15		
Arg	Leu	Ser	Pro	Arg	Glu	Ala	Glu	Met	Val	Ala	His	Gly	Pro
			20				25				30		
Gly	Trp	Ala	Ala	Glu	Phe	Ala	His	Ile	Ser	Leu	Lys	Gly	Ser
			35				40				45		
Gly	Pro	Arg	Asp	Cys	Ala	Lys	Gly	Pro	Gln	Met	Gly	Arg	Ala
			50				55				60		
Ala	Trp	Glu	Gly	Arg	Cys	Phe	Pro	Gln	Ala	Arg	Pro	Gly	Ser
			65				70				75		
Pro	Arg	Ser	Glu	Ala	Ser	Ser	Thr	Ala	Ser	Val	Pro	Ala	Ala
			85								90		
Ser	Ala	Pro	Arg										
			100										

<210> 243

<211> 330

<212> DNA

<213> Homo sapiens

<400> 243

nnacctttctc tccgcgttat taccaaagat gctatgcacg taactgcgga ggaaattctt
 60
 cacacaggcc accccgcccc cactgcgctc gtcgctaata ttcctataa cggtgcggta
 120
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatgggtg
 180
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cgggtgtcccc
 240
 agcgtcaaaag tcaactttta cgggactgtc tcgctgtcgg gagcaattgg acgcaatgtc
 300
 ttctggccgg ctccaatgt tgattctggn
 330

<210> 244

<211> 110

<212> PRT

<213> Homo sapiens

<400> 244

Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

```

      1           5           10           15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
      65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

```

<210> 245

<211> 355

<212> DNA

<213> Homo sapiens

<400> 245

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tctagatcct gaatcaccca cctcctagtt teggattcac ctccgccggc gtcacctgaa
60
aacaatgtcg agcccgaatg gatgatggta gccacaccca tctcggaag gtggaatgca
120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtccccagg catccatctc gagttgacga cgaaaatctt tccagtcacc gccgtagggg
240
ganttgccaa ccacagcatc gaatttgctc agaaggaagt ggctggtggt gagggatttg
300
ccccattcaa tacgcgcac ttccccgaag cgcgctctta ttgcggccaa cgcgt
355

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<210> 246

<211> 101

<212> PRT

<213> Homo sapiens

<400> 246

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Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
      1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
      65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 247
 atggccgcga atgggcacgc tgtcatggtc gtctctcccc gctacgacca gtacaaggac
 60
 gcctgggaca ccagcgctcg gtccgagatc aagatgggag acagggtacga gacggctcagg
 120
 ttctttccact gctacaagcg cggagtggtac cgcgtgttcg ttgaccaccc actgttctcg
 180
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac
 240
 agggacaacc agctgcggtt cagcctgcta tgccaggcag cacttgaagc tccaaggatc
 300
 ctgagcctca acaacaaccc atacttctcc gga
 333

<210> 248
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 248
 Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp
 1 5 10 15
 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met
 20 25 30
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly
 35 40 45
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
 50 55 60
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu
 85 90 95
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
 100 105 110

<210> 249
 <211> 5503
 <212> DNA
 <213> Homo sapiens

<400> 249
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<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

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			20					25					30		
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
		35					40					45			
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
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Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
					70					75				80	
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
				85					90					95	
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
			100					105					110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
			115				120					125			
Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
						135					140				
Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
					150					155					160
Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
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Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
			180					185					190		
Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
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Asn	Gln	Lys	Cys	Thr	Arg	Asn	Asn	His	Arg	Ile	Ser	Ser	Leu	Leu	Cys
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Asp	Pro	Gln	Glu	Gly	Tyr	Leu	Gln	Met	Leu	Gln	Ile	Ser	Asn	Leu	Tyr
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 Ser Thr Lys Pro Trp Asn Gly Gly Arg Ser Met Leu Asp Thr Ile Lys
 275 280 285
 Lys Gly His Ile Thr Gly Leu Thr Gly Val Met Glu Phe Arg Glu Asp
 290 295 300
 Ser Ser Asn Pro Tyr Val Gln Phe Glu Ile Leu Gly Thr Thr Tyr Ser
 305 310 315 320
 Glu Thr Phe Gly Lys Asp Met Arg Lys Leu Ala Thr Trp Asp Ser Glu
 325 330 335
 Lys Gly Leu Asn Gly Ser Leu Gln Glu Arg Pro Met Gly Ser Arg Leu
 340 345 350
 Gln Gly Leu Thr Leu Lys Val Val Thr Val Leu Glu Glu Pro Phe Val
 355 360 365
 Met Val Ala Glu Asn Ile Leu Gly Gln Pro Lys Arg Tyr Lys Gly Phe
 370 375 380
 Ser Ile Asp Val Leu Asp Ala Leu Ala Lys Ala Leu Gly Phe Lys Tyr
 385 390 395 400
 Glu Ile Tyr Gln Ala Pro Asp Gly Arg Tyr Gly His Gln Leu His Asn
 405 410 415
 Thr Ser Trp Asn Gly Met Ile Gly Glu Leu Ile Ser Lys Arg Ala Asp
 420 425 430
 Leu Ala Ile Ser Ala Ile Thr Ile Thr Pro Glu Arg Glu Ser Val Val
 435 440 445
 Asp Phe Ser Lys Arg Tyr Met Asp Tyr Ser Val Gly Ile Leu Ile Lys
 450 455 460
 Lys Pro Glu Glu Lys Ile Ser Ile Phe Ser Leu Phe Ala Pro Phe Asp
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 Phe Ala Val Trp Ala Cys Ile Ala Ala Ala Ile Pro Val Val Gly Val
 485 490 495
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 595 600 605
 Phe Arg Ala Lys Gly Thr Asn Pro Leu Glu Gln Asp Ser Thr Phe Ala
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 Glu Leu Trp Arg Thr Ile Ser Lys Asn Gly Gly Ala Asp Asn Cys Val
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 Ser Ser Pro Ser Glu Gly Ile Arg Lys Ala Lys Lys Gly Asn Tyr Ala
 645 650 655
 Phe Leu Trp Asp Val Ala Val Val Glu Tyr Ala Ala Leu Thr Asp Asp
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 Gly Ile Ala Leu Gln His Gly Ser Pro Tyr Arg Asp Leu Phe Ser Gln

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Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser
                725                730                735
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val
                740                745                750
Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala
                755                760                765
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys
                770                775                780
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser
785                790                795                800
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile
                805                810                815
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu
                820                825                830
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe
                835                840                845
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly
                850                855                860
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro
865                870                875                880
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln
                885                890                895
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly
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<211> 291
<212> DNA
<213> Homo sapiens

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<210> 252
<211> 97
<212> PRT
<213> Homo sapiens

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<400> 252
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      20           25           30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
      35           40           45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
      50           55           60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
      65           70           75           80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
      85           90           95
Arg

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<210> 253
<211> 327
<212> DNA
<213> Homo sapiens

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cccacatgtc gccagtgtat gcgggcacct tgccggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacggtc ggcacgctcc acgagcgcca cgagaagctc gcgcaggac
240
gctcactcgt cgcggtgtcc tccgcggtct ccatcacctg ccctgcgaca tggaacgcc
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<210> 254
<211> 106
<212> PRT
<213> Homo sapiens

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      1           5           10           15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
      20           25           30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
      35           40           45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
      50           55           60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
      65           70           75           80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
      85           90           95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
      100           105

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<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

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 240
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 360
 attagccaac gc
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<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
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 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
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 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
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<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
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<210> 258
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 258
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 20 25 30
 Met Cys Ala Gln Val Leu Ala Glu Arg Phe Gly Leu Gly Gly Ile Phe
 35 40 45
 Phe Gly Leu Pro Thr Met Ala Thr Ser Asn Pro Met Phe Gly Arg Val
 50 55 60
 Arg Glu Trp Leu Asp Ala Val Pro Ala Lys Asp Pro Ser Ser Ile Ser
 65 70 75 80
 Leu Ala His Ser Lys Ala Gly Leu Asn Glu Glu Tyr Gln Gln Leu Met
 85 90 95
 Pro Trp Asn Ala Thr Met Ala Val Tyr Asp Glu Gly Ala Gly Thr Gln
 100 105 110
 Arg Glu Ala Ser Ala Ile Val His Glu Trp Phe Leu Gly Arg Lys Arg
 115 120 125
 Ala Ile Leu Ala Asp His Val Val Gly Thr Ile Asp Gln Ala Leu Phe
 130 135 140
 Thr Gly Leu Lys Ala Lys His Val Val Leu Arg His Leu Gly Leu Ala
 145 150 155 160
 Ser Lys Val Val Ile Ile Asp Glu Val His Ala Ala Asp Val Tyr Met
 165 170 175
 Arg Glu Tyr Leu Lys Val Val Leu Glu Trp Leu Gly Ala Tyr Arg Thr
 180 185 190
 Pro Val Ile Leu Met Ser Ala Thr Leu Pro Pro Ala Gln Arg His Glu
 195 200 205
 Leu Ala Leu Ala Tyr
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<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
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 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg
 180
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 240
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 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
 gctagcccg cgcggttcgt cgtcgatttg ctggcggcag tccctctgat cgtcttcggt
 60
 ctgtggggcg gcatcgtctt cggatcgtcg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtgtgc ctcggtact
 180
 ggacacggtct accttgccag tctcgtcctg gccatcatga tectgccaat tatcactgct
 240
 gttagccgcg acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgccttc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtcgggcac
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcaccctc
 420
 atcctgcaga ccatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtgggtgaga cattcgcgtc gaagattgccc ggtaacttct ccgagggccat tagcgatccc
 540
 accctcgtgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac ctctgtggtc
 600
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accacccctg
 660
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg
 720
 gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcatc ggatcactat
 840
 tccacgcgtc gtgggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccaccacgc tctcgtcggc acccttgaaa ttggccttat tacatcgatt atctcggtag
 960
 cgatcgcctc gatgaccgcg atcttctctag tcgagtacgc ccgcggaaat aagatcgcca
 1020
 aggtcattag ctccgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggccctcat gatcctcatg gttccgacgg tgctcgcgac aaccgaggaa atgctcaagc
 1200
 tt
 1202

<210> 262

<211> 214

<212> PRT

<213> Homo sapiens

<400> 262

Ala Ser Pro Val Ala Phe Val Val Asp Leu Leu Ala Ala Val Pro Ser
 1 5 10 15
 Ile Val Phe Gly Leu Trp Gly Gly Ile Val Phe Gly Ser Ser Gly Ile
 20 25 30
 Ile Asn Gly Tyr Ala Gly Ala Leu Phe Lys Ala Leu Gly Trp Ile Pro
 35 40 45
 Ile Phe Ser Glu Asp Pro Ser Trp Ser Ser Ala Thr Gly Thr Val Tyr
 50 55 60
 Leu Ala Ser Leu Val Leu Ala Ile Met Ile Leu Pro Ile Ile Thr Ala
 65 70 75 80
 Val Ser Arg Asp Val Met Pro Arg Thr Pro His Asp Gln Val Glu Ala
 85 90 95
 Ala Leu Ala Leu Gly Ser Thr Arg Trp Glu Val Ile Lys Leu Ala Val
 100 105 110
 Phe Pro His Ser Arg Ser Gly Ile Ile Ser Gly Ser Met Leu Gly Leu
 115 120 125
 Gly Arg Ala Leu Gly Glu Thr Leu Ala Val Thr Leu Ile Leu Gln Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

<210> 263
<211> 424
<212> DNA
<213> Homo sapiens

```

```

<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatatagac ccatccgccg tgaactttcc
60
gacgtgtgtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacggt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
240
gcttatatgg cctcgccatt cctgccaat ttggacctgg catacccatc ttgcagccca
300
caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

```

```

<210> 264
<211> 99
<212> PRT
<213> Homo sapiens

```

```

<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

```

<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgctccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gcccttcgact cccatcatcg caagctcatc atcactggtg atagccgtga gcaagccctg
 120
 gctcgagctg cccgcgcctt cgacgaaatc gtcatcgacg gcatgccgac ggtcattccc
 180
 tttcaccagg cgggtgttca cgacccggct ttcactgccg ccgacggctg cttcggcgctc
 240
 ttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgctg tcgagggtcaa cggtaaacgc
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Arg Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcac ctagtcaatc caccgatggc gaccttgga aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg cggggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttgc aagctcgcga ttaccgcgac attccgatgc ttgcatcacg tcatggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgcca tcgaggatgc gatgggcatt
 360
 accatcccaa ctgcgtggc atggatacga accctgctcg ctgagttcag cagaatcacc
 420
 tcacacttca catttttgtc atgggtaggc catcaactgtg atgatgccg c
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa Pro Gln Arg Val Phe Ser Ser Thr Arg Lys Ile Met Phe Val Ile
 1 5 10 15
 Gly Ser Met Pro Leu Thr His Pro Ser Gln Ser Thr Asp Gly Asp Pro
 20 25 30
 Gly Lys Lys Tyr Glu Val Thr Trp Leu Asp Leu Gly His Leu His Pro
 35 40 45
 Ser Arg Pro Gly Leu Val Thr Ile Thr Thr Thr Val Asp Asp Asp Val
 50 55 60
 Ile Thr Ser Ser Gln Val Asn Val Gly Asn Leu His Arg Gly Asp Glu
 65 70 75 80
 Lys Leu Phe Glu Ala Arg Asp Tyr Arg Gln Ile Pro Met Leu Ala Ser
 85 90 95
 Arg His Gly Trp Thr Ala Pro Phe Ile Gly Glu Thr Gly Ala Ala His
 100 105 110
 Ala Ile Glu Asp Ala Met Gly Ile Thr Ile Pro Thr Arg Val Ala Trp
 115 120 125
 Ile Arg Thr Leu Leu Ala Glu Phe Ser Arg Ile Thr Ser His Phe Thr
 130 135 140
 Phe Leu Ser Trp Val Gly His His Cys Asp Asp Ala Gly
 145 150 155

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
 60
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccga
 120
 tttgcttatg acaaaactct taaaaaagag ttagaacctt atttacaggt tcttgaacct
 180
 tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa
 300
 ccggcgcttc agtcacacga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tgggtcaaat actacgc
 387

<210> 270

<211> 129

<212> PRT

<213> Homo sapiens

<400> 270

Thr	Arg	Val	Phe	Pro	Glu	Lys	Thr	Asn	Lys	Leu	Glu	Phe	Met	Val
1			5					10					15	
Glu	Val	Ile	Ala	Asp	Met	Thr	Val	Ile	Asn	Pro	Phe	Asp	Phe	Val
			20					25				30		
Glu	Ser	Tyr	Ala	Glu	Asp	Tyr	Pro	Phe	Ala	Tyr	Asp	Lys	Ala	Leu
			35				40				45			
Lys	Glu	Leu	Glu	Pro	Tyr	Leu	Gln	Val	Ser	Glu	Pro	Cys	Ser	Leu
	50				55					60				
Asp	Lys	Trp	Leu	Ser	Gly	Val	Asp	Arg	Glu	Lys	Thr	Pro	Ile	Asn
65				70					75				80	
Phe	Leu	Val	Ala	Ile	Asn	Ser	Arg	Leu	Ala	Gly	Asp	Ile	Gly	Tyr
			85					90				95		
Ile	Arg	Leu	Glu	Pro	Gly	Val	Gln	Ser	Pro	Glu	Glu	Thr	Leu	Thr
			100				105					110		
Met	Lys	Gly	Ser	Cys	Arg	Asp	Thr	Ser	Gly	Leu	Leu	Val	Gln	Ile
		115					120					125		

Arg

<210> 271

<211> 443

<212> DNA

<213> Homo sapiens

<400> 271

gccggcacca acgaaagtc ctctaccgag cgcatggctg attcgctttt gcgtgccttc
 60
 caccgccgag tgggtttggt aaccagccca cacctgcagc gcgttactga gcgcatcggc
 120
 attgatggcc agccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagtctga ggtcttcgtg
 240
 ggcctgtcct atgctgcgtt tgccgacgcc cccgggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattacccgc
 360
 gtgggcacatg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272

<211> 147

<212> PRT

<213> Homo sapiens

<400> 272

Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273

<211> 864

<212> DNA

<213> Homo sapiens

<400> 273

caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctcgctcccc cctgctgtcg
 60
 aagagaagcc aaagccccc cccccacac caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctcg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc
 180
 tgctgcctga gaactggcct ccagccgggtg tectcattcc atggggctcc ctgctgactg
 240
 cattctctga tctgggatga tgtttaccag cccaaaacca gtcattgtct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcc cctcccttcc agtccacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaatgtca
 420
 gcctgtacgg cagagacatg tgggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaac ctactccttg gaaggatttt ttgctttgct tatgaaaagc
 540
 tctgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcac
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatacatat ctttctgatg
 660
 tctattgtat ctcccttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtagtggtg tctatcattg aaagagcatg gactcaaaaca tcagccctga gttcttgagt
 780
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgcccttcac gcgt
 864

<210> 274
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
 1 5 10 15
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
 20 25 30
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
 35 40 45
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
 50 55 60
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
 65 70 75 80
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Gly Phe Gly Phe Ser
 85 90 95
 Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
 100 105 110
 Gln Ser Tyr Phe
 115

<210> 275
 <211> 911
 <212> DNA
 <213> Homo sapiens

<400> 275
 naaatTTaaa ggaacctccc ttctataacy gagagtattt attgcagett tcctttctgt
 60
 ttattttcag gaatgaaagg aattaccag ccttctgctt ttatacctac agctgaaagt
 120
 aattcctttc agcctcaggt gaagactttg ccatctccaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa
 240
 tctgcagcaa aaaagtacaga aagtgtctaca agcaatggag tgactaatct tcctaattga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtccc
 360
 attccggctc agcggactag gcaattggta acttcaccga gtccaatgag ttctctnnga
 420

cggcaaaagt cttccctca atgtacaggt ggtcaactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaaag actccccaga acgttccagc agtcctggtg ggaatcggtc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgtgt ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctcgggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met Lys Gly Ile Thr Gln Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser
 1 5 10 15
 Asn Ser Phe Gln Pro Gln Val Lys Thr Leu Pro Ser Pro Ile Asp Ala
 20 25 30
 Lys Gln Gln Leu Gln Arg Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys
 35 40 45
 Leu Gln Ser Pro Leu Pro Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser
 50 55 60
 Ala Thr Ser Asn Gly Val Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile
 65 70 75 80
 Leu Ser Pro Gln Pro Ile Gly Ile Val Val Ala Ala Val Pro Ser Pro
 85 90 95
 Ile Pro Val Gln Arg Thr Arg Gln Leu Val Thr Ser Pro Ser Pro Met
 100 105 110
 Ser Ser Ser Xaa Arg Gln Ser Ser Ser Pro Gln Cys Thr Gly Gly His
 115 120 125
 Ser Ala His Ala Val Cys Glu Thr Gly Thr Lys Asp Ser Pro Glu Arg
 130 135 140
 Ser Ser Ser Pro Gly Gly Asn Arg Ser Ala Arg His Arg Tyr Pro Gln
 145 150 155 160
 Ile Leu Pro Lys Pro Ala Asn Thr Ser Ala Leu Thr Ile Arg Ser Pro
 165 170 175
 Thr Thr Val Leu Phe Thr Ser Ser Pro Ile Lys Thr Ala Val Val Pro
 180 185 190
 Ala Ser His Met Ser Ser Leu Asn Val Val Lys Met Thr Thr Ile Ser
 195 200 205
 Leu Thr Pro Ser Asn Ser Asn Thr Pro Leu Lys His Ser Ala Ser Val
 210 215 220
 Ser Ser Ala Thr Gly Thr Thr Glu Glu Ser Arg Ser Val Pro Gln Ile


```

225                230                235                240
Lys Asn Gly Ser Val Val Ser Leu Gln Ser Pro Gly Ser Arg Ser Ser
                245                250                255
Ser Ala Gly Gly Thr Ser Ala Val Glu Val Lys Val Glu Pro Glu Thr
                260                265                270
Ser Ser Asp Glu His Pro Val
                275

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<210> 277
<211> 652
<212> DNA
<213> Homo sapiens

```

```

<400> 277
nnaccggtgg ggaactctcgc tgaggtcctt aatggccctt ctctgtgcc ggacggcacc
60
atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggaggtcaaa
120
gagttccagc gcatacgagct gacgattcgc taaccgttcc accacgcaga atggtgttcc
180
ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccagatga attggtcgtg
240
ttgcgtggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaagagttc
300
cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc
360
gcccgtaggg ctgagcagat cgcgcggttg cggcagttag cggtcgagtc gaacctcgac
420
cccgaattcg cgcagaaggt catcacgttc atcgtggccg aggtgggtgcg tcaccacgaa
480
gctattgctg acgattcttg cgacgactct ggagtgccg atacggggga ggcggatgtc
540
cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctgggt caccttcgac
600
gggattccga cgacgactgt gccgggggcg acatccttga cgaccaacgc gt
652

```

```

<210> 278
<211> 115
<212> PRT
<213> Homo sapiens

```

```

<400> 278
Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp
1      5      10      15
Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile
20     25     30
Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Ala
35     40     45
Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala
50     55     60
Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe
65     70     75     80
Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser

```

```

      85              90              95
Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
      100              105              110
Ser Gly Ser
      115

```

```

<210> 279
<211> 348
<212> DNA
<213> Homo sapiens

```

```

<400> 279
cgggagggtca cacaagcatt caaacatag cagatggtaa atgttatgtt atgtgtattt
60
taccacaatc cttaaaaaga aaagaaagaa aggcataatg aacccttagt tacctctcat
120
ccagcttcaa aattgtcagt gcatgggtcaa tctgtgttta tctgcccttc acccaccctt
180
ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
240
ggaagtgtgt gttaatgttg catgtattca taaaacctct aggcatttct agtgcctctc
300
agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
348

```

```

<210> 280
<211> 99
<212> PRT
<213> Homo sapiens

```

```

<400> 280
Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
1      5      10      15
Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
      20      25      30
Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
      35      40      45
Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
      50      55      60
Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
65      70      75      80
Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
      85      90      95
Pro Lys Ile

```

```

<210> 281
<211> 384
<212> DNA
<213> Homo sapiens

```

```

<400> 281
agatctgcgc agatcgataa tggattaaag actcttgacy ctggagtcac cgagatgaac
60

```

aacaagggtg tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg
 120
 aattctcgct taggaantgc cgactcagcg gcagagaaga cgctcgagcg cgttactcag
 180
 acgcgcgtgg gtgccacggc gattaccggc gctgctcaaa atgcatggcg tgattcccaa
 240
 gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
 300
 caaaaacagg ccaggaatct cgtgtcagtg aacggtaccc tgcagaaccc caacggtgat
 360
 tctgtcatta agattcaaca gacc
 384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
1				5					10					15	
Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
			20					25					30		
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
			35					40					45		
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55				60					
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
	65				70					75				80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
				85					90					95	
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
			100					105					110		

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

cgctgagacc aatgtgagac ggccgtcacc aaggcgatgc gcgacaagtc gggttggtagc
 60
 ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
 120
 ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
 180
 tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
 240
 tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgtttctta
 300
 cgcatcaagg aagctcttgca tgaaaaagg gtcattgtgc cttccacgct gcgcttgatc
 360
 cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
 420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgattttctca gaaatctaca aacgtcagaa ctgcattctc ggcatgttaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggg gtatttcgcga agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctgcgtcggt tgtttgcaca accctggggg tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

1	5	10	15
Glu Ile Tyr	Lys Arg Gln Asn Ser	Ile Phe Gly Asp Val Arg Asn Asn	
	20	25	30
Phe Tyr Lys Lys Gly Tyr Arg	Ile Ile Asn Val Ala Asn Gly Val Leu		
	35	40	45
Arg Lys Ile Ser Leu Val Ser	Ala Gly Asn Ala Asp Asn Val Lys Gly		
	50	55	60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe	Glu Leu Val Arg Leu		
65	70	75	80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr	Gly Ile		
	85	90	95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile			
	100	105	

<210> 287

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 287

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nnntaaactgc ccctttgcag tctttattct gggacattag cactgtctgg ttatcttgct
60
tcagttgagg gattcgggac aatagcagtg ctgatggtaa tgttgccgat ttcctgttt
120
gttttgcagg tcacggccag gggctttggg cgcgtgttac agtttgcccta cactgccaa
180
ctgttaactca gcagagaaaa catccgcgag gtcatccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagacc agctcctgaa cagtggaggat
300
ggcctgtttg tgtgccggaa ggatgctgctg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttcagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac ccagatata agaaatacca gcttgcagtg
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtga
720
cgcgccagtg aagagaatga ggaagagagc atcacgctct gcctgtcttg agatgagcct
780
gacgccaaag acagagcggg ggatgtcag atggaccgga aacagcccag ccctgcccc
840
acccccacgg cccagctgg ggcgcctgc ctggagagat ccaggagcgt ggcctcgccc
900
tcctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgccagat
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

```

ggtgacctta aaactgacta caccctcttc acagggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgccccca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctcttc cagcgcttgc
 1200
 gaccaagtga gcacctcggg gcattcttat tctgggggtga gcagtttga caaagacctc
 1260
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgag
 1320
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatcgc gcccaacac
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35				40						45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
	65			70					75					80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85					90						95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105						110	
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115				120						125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
	130				135						140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
	145			150					155					160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
		165						170					175		
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185						190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195				200						205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210				215					220					
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
	225			230					235					240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245					250					255		
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260					265						270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

		275				280				285					
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp															
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr		290				295				300					
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe	305			310			315							320	
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys			325				330						335		
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala		340				345						350			
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser		355				360						365			
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly	370				375					380				400	
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Leu			390						395						
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn		405					410						415		
		420					425								

<210> 289

 $\langle 211 \rangle$ 822

<212> DNA

<213> Homo sapiens

<400> 289

ngcattaccg	ggctgaagac	gggtgtcat	gacctcaacy	atataggcta	ttgttagaac
60	cacgcccggc	cacgcccgcg	aaagcgcaga	cacggcacca	ggaggggtca
120	agcaagtctga	aggcgaaagga	cgagcgcaat	gccgatgaga	tcaggcggga
180	accctgtctt	gcctggcagc	cggggtggag	aacctcgtgg	aggaggtgca
240	tccaagcgtg	aagcatctga	tcgtgccctg	gattttgtgc	agggtgagtt
300	aagagccagg	tcaaagatga	gaaatggtgg	cgcgtcagc	ggatcgcgat
360	gtgctcgtcg	ccggcgctct	cagcattatt	gtgctgcgcg	cgatagtcgg
420	ggcgctaccg	ctcgctcgaa	gcttgagaag	ctgcagcttt	ctcaggcgaa
480	aaagatgcc	agcagcgtag	taaggaagat	gaaaaggcag	ccaagaaaaa
540	ggcaagaaga	acgctaagaa	gtacggcga	ctcgataccg	atgactcgtc
600	cttgccgaga	aaatgctcaa	acaggccgcg	gtgctgcgtg	cacaggcggc
660	tgagaacagt	gccgcctagc	aaacacgggt	cacagcgcaa	aacaggtttg
720	atggtggacc	ggagccaaac	tgtgttacgg	catcatttga	taccgccagc
780	gcgacaatgc	gacgtgggaa	taccagcacc	atgatgacta	gt
822					

<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgcgcg acaagactta cgacggggcgt cgctgcccggg ctgagtgccg ggcccgcctc
 60
 atcaccccc gcacgcctcg ccgcggcggtg gagaccagcg agcgcttggg ccgggtatcgc
 120
 tgggtcgtcg agcgcacett cgectggctc aaccgcttcc ggcgctctgc catccgctac
 180
 gagcggcggtg ctgacatcca cgaagccttc gtgatcctcg gctgcgcctt catctgcctc
 240
 aaccagatca gacgggtttt ttaggtgctg taaagggaga atgggtgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggctgct catctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1             5             10             15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
      20             25             30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
 35             40             45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
 50             55             60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65             70             75             80
Asn Gln Ile Arg Arg Phe Cys
      85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaaatcag tttagtggcg aggcattgaca cggtgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcattgtg ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg cgggcacttg atctgaacag gtttaagggt
240
gcgaagacct tcgatgttcc agtgtgcgtc atagctgggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgattgc ctacgggtgca cgcacaggca agcttgatcc cgcgtgtacc
360
ctcgcggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggttggt gtgtgcaggc tcgcactatt cattctgcgg cggtgcgga gatcaagttt
480
ttctggcctc gtgcataaa ctgtgagttg ccacgggtga gtgattctcg tttctcgatg
540
gtggcggaga cgaccatcg cattggtctg ggcaatgaca aggcgtgtgt gcgcgacttg
600
tcgcgcgaga tctcgtgggc gaagggtctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggtcgggt ggtggcgga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

```

      1             5             10             15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
      20
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
      35             40             45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
      50             55             60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
      65             70             75
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
      85             90             95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
      100            105            110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
      115            120            125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
      130            135            140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
      145            150            155
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
      165            170            175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
      180            185            190

```

<210> 295

<211> 417

<212> DNA

<213> Homo sapiens

<400> 295

```

ttcatatcag gcagtagccg agtccatgcg atcaacaacg tcagcgatc tttcacccat
60
tctggagatgc acctttctcat gggagaaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
300
caggggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcy aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

```

<210> 296

<211> 139

<212> PRT

<213> Homo sapiens

<400> 296

```

Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
1             5             10             15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

      20              25              30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35              40              45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50              55              60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
      65              70              75
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85              90              95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100             105             110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115             120             125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130             135

```

<210> 297

<211> 378

<212> DNA

<213> Homo sapiens

<400> 297

```

tacaccatcg gtgaccagat tgtcgaagct ctgcagggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccagagtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc agggccagat tctcgatttg ctgcgcgtag ccagcgctga aacccatgcg
300
ggcgctcgta tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg cgggacgc
378

```

<210> 298

<211> 126

<212> PRT

<213> Homo sapiens

<400> 298

```

Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
      1              5              10              15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
      20              25              30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
      35              40              45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
      50              55              60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
      65              70              75              80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Arg Val Ala Gln Arg

```

```

      85              90              95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
      100              105              110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
      115              120              125

```

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

```

<400> 299
gtgcacggtt tcgttggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
60
ccagcccaat ggacgtcgat caaacaccac atgctcattg cgcactctca catgctcggt
120
ttcctggaac gtgacgccat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
180
gtgcgcgggtg agctctacca cattgggggtt gagccgggtg ggggtccggtt gtccgatcac
240
gggcccgttgc gtcctagcct gcgcggttacc catccgatct cgggggttcgc tcgagctgac
300
ggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
360
atctcgac
368

```

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

```

<400> 300
Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
1      5      10      15
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
      20      25      30
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
      35      40      45
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
      50      55      60
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
65      70      75      80
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
      85      90      95
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
      100      105      110
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
      115      120

```

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 301
 ggccgggtta ttgccgccc gttgtcggg gaaaccggc agaccttcga gcgcaccggc
 60
 aaccggcgcg actattccgt accgccgcc gaaccgacct tgctcgacag gcttacggac
 120
 gcgggccgga cgggtgatcg aatcggaag attggtgata tctacgcga caaaggcgtg
 180
 tctcaggtgc gtaaggcaat ggcaatatg gccttggtcg atgaaacct cattgccatg
 240
 gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
 300
 gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaggctg
 360
 ccggaagcca tggcgaaatt cgggacgggc gatcttctga tcttgacagc cgatcatggc
 420
 tgcgaccgca ccctcaaggg aaccgaccac acgcgt
 456

<210> 302
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 302
 Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe
 1 5 10 15
 Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro
 20 25 30
 Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile
 35 40 45
 Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg
 50 55 60
 Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met
 65 70 75 80
 Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe
 85 90 95
 Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala
 100 105 110
 Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg
 115 120 125
 Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr
 130 135 140
 Leu Lys Gly Thr Asp His Thr Arg
 145 150

<210> 303
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 303
 nncgtgggca tcgaggagtt cctcgacatg aagtatcagc cgacgcgat tcatcgctcg
 60

tgacagcgggt tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tgttcagtga cagcgagtag gagcagcgcc tgagacgtgt ccgtgagctc
 180
 atggaccgtc aggggtctgtc ggcgatcacc gtcaccgata cggccaacat cttctatctg
 240
 atcgggttaca acgcctggtc gttctacacc cgcagatgc tggctgtgcc gatcgacgga
 300
 gagatgggtcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg
 360
 cccgccgata agatcgctcg ttaccggag agttatgtgc ac
 402

<210> 304

<211> 97

<212> PRT

<213> Homo sapiens

<400> 304

Met	Tyr	Leu	Gly	Ala	Gln	Leu	Phe	Ser	Asp	Ser	Glu	Tyr	Glu	Gln	Arg
1				5					10				15		
Leu	Arg	Arg	Val	Arg	Glu	Leu	Met	Asp	Arg	Gln	Gly	Leu	Ser	Ala	Ile
			20					25				30			
Ile	Val	Thr	Asp	Pro	Ala	Asn	Ile	Phe	Tyr	Leu	Ile	Gly	Tyr	Asn	Ala
			35				40					45			
Trp	Ser	Phe	Tyr	Thr	Pro	Gln	Met	Leu	Phe	Val	Pro	Ile	Asp	Gly	Glu
		50				55				60					
Met	Val	Leu	Tyr	Ala	Arg	Glu	Met	Asp	Arg	Met	Ala	His	Ile	Xaa	Thr
65					70				75				80		
Thr	Ser	Leu	Pro	Ala	Asp	Gln	Ile	Val	Gly	Tyr	Pro	Glu	Ser	Tyr	Val
				85					90				95		

His

<210> 305

<211> 375

<212> DNA

<213> Homo sapiens

<400> 305

nnacgcgtcg gttccgcacc gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgctgtcct ggcgaatatg ggcgatcagc cggtagacgtt cgggtagctc gctcacctcg
 120
 gccgccattt cggatgcgac acgcgcgcct gcgcgtctcg cctccagcaa ctctcgagac
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccc
 240
 tcgcatcgcg tcggaatcga catgcagcac cctcctgcc ggatcgatgg cgtaatacgt
 300
 gcgacgggtac acggcgcggt ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
 360
 acgtcacatc atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagtctctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 gggttaggaag gctattctct ttggccactc tcattcctaag acctattttg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgacac
 180
 tttgatgtct cttcttctca cccactcacc ccaccctggg ggttggggga aaaagtggc
 240
 tcaaagctgc ggttcagagt tccttgtaaa caaggctcct cctcactgt cctcaccctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaaccac
 360
 gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagtctg ggggaagcct cacttgagg ggagctggg cagtggcagc tccttggaa
 480
 tggctcagcc tetggacatc accccaccca accagagccc tggctcttgc tggatgtcca
 540
 cagatgagt cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgat ccctgtgcat atggtcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggctc cgagccgac
 180
 tcgctgcata ccccaatggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgct aacttcaccc tgttgaggga gcagctgcac
 300
 gatgtcctcg atacctgtgc cgagcgagag gccggtgtcg tgctgatcgc attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcgggcaaag tctacggtgt tactcgggag
 420
 cgcacccgcc ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu


```

                20                25                30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35                40                45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50                55                60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
65      70                75                80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85                90                95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100               105               110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115               120               125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130               135               140

```

<210> 311
 <211> 358
 <212> DNA
 <213> Homo sapiens

```

<400> 311
acgcgtatcg aaaatatccc tccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtggtggt cattggctct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
cggatgctgt gggaagccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccgccgag gccgcgcggc tgcttagctg cagcgctcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

```

<210> 312
 <211> 116
 <212> PRT
 <213> Homo sapiens

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<400> 312
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```

```

                100                105                110
Leu Val Lys Arg
                115

<210> 313
<211> 347
<212> DNA
<213> Homo sapiens

<400> 313
ncaactgaaa gcattgagat gagcgacgtg ctgtcccctt tccacccac caaggccaac
60
acccttggtg gcgaaccgcg caccatccgc acctgaacg cgcacatcat tgcgctgacc
120
agtggcaaa ggcggctggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
180
cgctgggac tgcgctgtgt ggtactggac gccgacctgg gcttgccaa cttggacgtg
240
gtgctgaacc tctaccccaa ggtgacgctg cagcatgtgt tcaccgcaa ggcctcgctg
300
caagacgcgg tggtcacggc ccccgggcgc ttccatgtgc tgctagc
347

<210> 314
<211> 115
<212> PRT
<213> Homo sapiens

<400> 314
Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
1 5 10 15
Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
20 25 30
Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
35 40 45
Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu
50 55 60
Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
65 70 75 80
Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
85 90 95
Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
100 105 110
Val Leu Leu
115

<210> 315
<211> 544
<212> DNA
<213> Homo sapiens

<400> 315
nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc
60

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gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctcgtccc ggggccatcc
 120
 aacaccttgc tgctcagcgc cegtttccat ttcgggtcgc tgcggggcgc gcccttcate
 180
 ctgcttgagg cggtgggcta ctgcctatcc atttcggcat ggggctgggt attggcgcg
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtcgggggc cggttaacttc
 360
 cgccatgggc ccttgcacct gttcgtggca accctgtcga accccaaggc gctgatcttc
 420
 gccagcgtga tctttcccg caaggcgctc ctgcacttct ggaacaacta cagcatctcg
 480
 ctgctggcct tcttggttgt gctggcgccc atcgggatgc tttgggtcgg gctggggggc
 540
 ggta
 544

<210> 316
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 316
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
 1 5 10 15
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
 20 25 30
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
 35 40 45
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
 50 55 60
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
 65 70 75 80
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
 85 90 95
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
 100 105 110
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
 115 120 125
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
 130 135 140
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
 145 150 155

<210> 317
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 317
 nggtcagcct ctcgccagc caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagaggttt gtccactgag agaagcacat tggaaagggg ggcgtgggccc tgggactgtg
 120
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgnnggtg
 180
 ggggtgtggg taacatgccg tgcatttttg ggggttgcca tgagtggcac accatggggg
 240
 tggcatgtgg ggcattgtat catgtggtgt tggcgagca aactcagctc ttacctggct
 300
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1			5					10						15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
		20				25						30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35				40					45				
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50				55					60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65				70					75					80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	

Leu Leu

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtacccct cccggcagtc ctattctcga gctgagcggg cacagtggcc
 60
 cagttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
 120
 agggcatgat atgtacagga ggcgacgatg ctcaagtgcg cgtatatgat ctgactagct
 180
 caactcttcg aacagcatct gctcaaggac ggcgtctctg aaacagtcca tataaacaaa
 240
 gccattcacc gggaatagac ggatggcgtg tcggcgacga agtgccgggtg ctcgcttata
 300
 cggccccgtc tatggccaac aatgctagct ggctcggcat gcctgcgcga tcaaaacgca
 360
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagtgag tggactgagt
 420
 atacgtccn
 429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 ngtgcacgac gtgctcgcca agtccctcgg gtcctctaata gcgatcaacg tgggtcacgc
 60
 caccgtcgat gcgttgacgc agctcgagga gccgaagag gtcgcccgtc gccgcggcaa
 120
 gtccgttgag gagatcgccc cagcagccat gctgcgtgag cgcaaggagg cgcacgaggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc
 240
 acccagatca agtctggcat cgctaccaag ccaaatcacc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga caccgtcacc aaggaggacc gcccgagatt ccgcggcatg
 360
 gtccggacgc ttgcgcacct cgctcaccat gaagaggtgg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgctc ctggtgcccc caaggccaag acccgcggtg gtcgtggtga
 480
 gggttccaag ggtaagaccg ctggtcgcgg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

      1           5           10           15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
      20           25           30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
      35           40           45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
      50           55           60

```

<210> 323

<211> 468

<212> DNA

<213> Homo sapiens

<400> 323

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ntccggagccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaaat
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtag caccctgggt
180
tgccctcagt aaatgagggc acatattcgg acttgtcaga agtacctaga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca tttaataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

```

<210> 324

<211> 156

<212> PRT

<213> Homo sapiens

<400> 324

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Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
      1           5           10           15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
      20           25           30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
      35           40           45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
      50           55           60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
      65           70           75           80
Pro Leu Gln Glu Leu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
      85           90           95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
      100          105          110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
      115          120          125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

```

130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccctgctg gggagatggc
 60
 actggagccc ctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccaggaa tcccactcc cgcagatgac ttgcccaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcaccactt ggttcaactgt gtgcttcagg
 300
 gtccccagg tttagggtgct tcatgccctg ctgggaacga gacacgctcc tgccctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtgtt ctttccattt ggtctgtcag gtgaaaaact
 60

ccggctgggg gaaaagcgtc cggtggttg ttggtaaaga gggcgctga tgggctctgg
 120
 ggaatggagg atggcgacc ggctgtgggt ggactgtgga aacgggggt ggcagtgcc
 180
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
 240
 agctcggtat gggctcagag cgacccacga aaataccagg ggccaagtaa aatgaacca
 300
 ccctttaaca gtgcacaaag cgctggcaca cgggccacgt ctggtgacgc aggctgcccc
 360
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
 420
 cgccccgtgc cactctggc cagccggagt tttcaccta cagaccaata ggaagaaca
 480
 cgggcccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgcc
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40				45				
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50				55					60					
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65				70					75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85					90					95		
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
		100					105					110			
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
	115					120					125				

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
 60
 gctcttcagt cttttctgct cactgagcag tgttttctcg atacccttgg tatectgcaa
 120
 gcagcctcgt tatgactcct aactccattg cctccatgg cccctgggag ctctctctct
 180
 ctttctctcc aggtagtaga gcaatgcttc tggtctcttg tgcacagaag gggttccac
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atactcctgcc ccacctcttt
 300
 ctggtagcac acagcaacct tgcatagtat ctggtatcat taccttccca atcaacaggg
 360
 cttgatttct tataggactt ttctctcag atttacattg cttcttt
 407

<210> 330

<211> 113

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ile	Pro	Ala	Thr	Met	Gln	Gly	Cys	Cys	Val	Leu	Pro	Glu	Glu	Gly
1				5					10					15	
Gly	Ala	Gly	Tyr	Lys	Gly	Asn	Asn	Tyr	Val	Ser	Arg	Ser	Pro	Ala	Leu
			20					25					30		
Ser	Cys	Gly	Lys	Pro	Phe	Cys	Ala	Gln	Glu	Ala	Arg	Ser	Ser	Ala	Leu
		35					40					45			
Leu	Pro	Gly	Glu	Lys	Glu	Arg	Glu	Ser	Ala	Gln	Gly	Pro	Trp	Arg	Ala
		50				55					60				
Met	Glu	Leu	Gly	Val	Ile	Thr	Arg	Leu	Leu	Ala	Gly	Tyr	Gln	Gly	Tyr
65					70					75				80	
Gln	Glu	Asn	Thr	Ala	Gln	Trp	Ser	Arg	Lys	Thr	Glu	Glu	Leu	Gln	Ala
			85						90					95	
Leu	Phe	Pro	His	Gly	Phe	Leu	Glu	Gly	Ile	Pro	Gly	Glu	Gly	Thr	Leu
			100					105						110	

Arg

<210> 331

<211> 523

<212> DNA

<213> Homo sapiens

<400> 331

tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccg cgccacttct gctgaggcca tggagtcgat cggagccagg
 120
 tacgacggat cggccggggtt ggccggaagt cagctcggcg tcgagtgtcc cgtgacaagg
 180
 ttcgacgcag cggtgaact cttcgtcgaa ttgttgaaca ccacagaccc ggttgaagag
 240
 gacatcgccc gtcagatcga cgccggcgca gcctccctgg ccagaccagg ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggtcgctc
 360
 ctgcccacga tcggtaccct ctcgtcgggt gaaaagctca acgcccgcag cgcacgagaa
 420
 ttctgggccc cgcactggac gatctccgat gccgtgctgg tgggtgccgg agagggagtc
 480
 gaggacctcg acttgtaaat attcaaggag tggacgacca gct
 523

<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgaggca tgacgggtgaa ggtgcccaacc
 60
 gatccccatc accgccccggg agttccattg aagtctcgca aggcacgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccca
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccaccacc cggtggcaag
 240
 gaacggggccc gcaactacga tgcgggtggcc cagctcgtcg cgcagcgagt cgcgcgggtca
 300
 cacggccgga tcaactccaa acggctgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

```

Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1             5             10             15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
      20             25             30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
      35             40             45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
      50             55             60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
      65             70             75             80
Gly Tyr Glu Gly Ser Ala Arg Asn
      85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

```

gtgcacgcct tgctggggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtagctttt
60
ggcagggggag ggcattcgcg gctcatcctg cagcggttgg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgctttt
180
tccatcnggc accagggggtt cagccatctc ggggaactgc gcgccccagc cgtgtccgggt
240
gtgctgctgg acctggggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgttttc atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

```

<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

```

Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1             5             10             15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
      20             25             30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
      35             40             45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
      50             55             60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
      65             70             75             80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
      85             90             95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

```

100      105      110
Thr Thr Pro Met His Gly
115

<210> 337
<211> 447
<212> DNA
<213> Homo sapiens

<400> 337
cagcctctct cgcaccgcgc cgggtgtgaag cacgggcatg ccggtgtgca agtggcacca
60
cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa
120
ccgctcatct ctgtgcccac agctcccccgc cttccatgtg acccagaaaat ggaaccacgc
180
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc tctgtgcaa
240
acaggcgcca tcattgtcagc cgggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
300
cacgtccaac ttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
360
gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg
420
tttctgtact gtttttacag ccaattg
447

<210> 338
<211> 111
<212> PRT
<213> Homo sapiens

<400> 338
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
1      5      10      15
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
20      25      30
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
35      40      45
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
50      55      60
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
65      70      75      80
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
85      90      95
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Ala
100      105      110

<210> 339
<211> 588
<212> DNA
<213> Homo sapiens

<400> 339

```

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgctca
 60
 gatcggttat cctgcagttg ccattcatca gacaaatcca gtggaaccca atggaagaca
 120
 ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta
 180
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
 240
 tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
 300
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatccctg acaagaata
 360
 ttcgatcatc tgcccccagg aagaacgcag cacctggtga gtgctgcccc ctacctggaa
 420
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcac ggtgccgacc gcacgcgctg
 480
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
 540
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
 588

<210> 340

<211> 123

<212> PRT

<213> Homo sapiens

<400> 340

Met	Glu	Asp	Thr	Asp	Leu	Gln	Ala	Leu	Met	Ala	Arg	Leu	Glu	Leu	Leu
1				5					10					15	
Ile	Asp	Arg	Val	Glu	Gln	Leu	Lys	Ser	Gln	Asn	Gly	Leu	Leu	Leu	Ala
			20					25					30		
Gln	Glu	Lys	Thr	Trp	Ala	Arg	Xaa	Arg	Ala	His	Leu	Ile	Glu	Lys	Asn
			35				40					45			
Glu	Ile	Ala	Arg	Arg	Lys	Val	Glu	Ser	Met	Ile	Ser	Arg	Leu	Lys	Ala
			50			55				60					
Leu	Glu	Gln	Asp	Tyr	Glu	Leu	Ser	Asn	Ser	Val	Thr	Cys	Arg	Ser	Ser
			65		70				75				80		
Thr	Lys	Asn	Ile	Arg	Ser	Ser	Ala	Pro	Arg	Lys	Asn	Ala	Ala	Pro	Gly
			85					90					95		
Glu	Cys	Cys	Pro	Leu	Pro	Gly	Arg	Pro	Lys	Gly	Val	Lys	Ser	Ala	Ala
			100					105					110		
Ala	Ala	Lys	Ser	Ser	Val	Pro	Thr	Ala	Ser	Pro					
			115					120							

<210> 341

<211> 401

<212> DNA

<213> Homo sapiens

<400> 341

ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtagacc ctcggccttt
 60
 gcaatgaacg acacgcgcgac agttgcgacc gcgcgcagcc tgatcctgcg tggctctctt
 120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctg ccttctctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgtag atgctgggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctgttgccga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgcgggg
 360
 ctgggggtga acctggcggt tgccgcagcg tgaggacgcg t
 401

<210> 342
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 342
 Xaa Arg Ala Ala Tyr Leu Leu Tyr Leu Ala Tyr Ala Thr Trp Arg Asp
 1 5 10 15
 Arg Ser Ala Phe Ala Met Asn Asp Thr Pro Thr Val Ala Thr Ala Arg
 20 25 30
 Ser Leu Ile Leu Arg Gly Phe Leu Leu Asn Ile Leu Asn Pro Lys Leu
 35 40 45
 Thr Ile Phe Phe Leu Ala Phe Leu Pro Gln Phe Val Thr Pro Gly Gly
 50 55 60
 Thr Ala Pro Ala Leu Gln Met Leu Val Leu Ser Gly Val Phe Met Ala
 65 70 75 80
 Met Thr Leu Ala Val Phe Val Leu Tyr Gly Leu Leu Ala Asn Val Phe
 85 90 95
 Arg Arg Ala Val Val Glu Ser Pro Arg Val Gln Asn Trp Leu Arg Arg
 100 105 110
 Ser Phe Ala Thr Ala Phe Ala Gly Leu Gly Leu Asn Leu Ala Phe Ala
 115 120 125
 Gln Arg
 130

<210> 343
 <211> 389
 <212> DNA
 <213> Homo sapiens

<400> 343
 gtgttcgcga actacatggc gtccctgcgc ttcagcgtgg tcgagtcggc gcgcacgcga
 60
 ggggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg
 120
 gcggcgcttg cgacctgca gttcctgtgg gtgtggaacg acctgtctcat cgccaagctc
 180
 ttccctacca acgacaaccc caccgtgatc gtcaagctcc aacagcttcc cnnngggccc
 240
 aaggccccag gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctaccatg
 300
 atcgtcttct tcgtgtccca gaacttctgt gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg ccctctaaagg catggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatctc cagttgtgtac aacagtacac gctgtagaaa tgaaacctgc taaagggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctcgtagtgg tgcttacggt
240
actctacggt tacgtagtgg tgaatgcgt aaaatccctg ctgagtgtgc tgcaacaatc
300
ggtgaagtgg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

                20                25                30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
                35                40                45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
                50                55                60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65                70                75                80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
                85                90                95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
100                105                110
Leu Gly Lys Ala Gly Ala Thr Arg
115                120

```

<210> 347

<211> 565

<212> DNA

<213> Homo sapiens

<400> 347

```

accggtgatg ccaaagggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgcgc tcatacatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgaccctcg tcccggccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggctggatc gacgcctacc cgcctcgcac atcgaggagg aagggatcac ccacgaggaa
300
aagctggccg cctggcccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcagg tcaagccgtc
420
gtcggatcgc agaacagtgt ctgcccgctc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgagggtc gggaggattg ctgctacccc agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

<210> 348

<211> 188

<212> PRT

<213> Homo sapiens

<400> 348

```

Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1                5                10                15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
                20                25                30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
35                40                45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```



```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65      70      75      80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85      90      95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100      105      110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115      120      125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130      135      140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
      145      150      155      160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165      170      175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180      185

```

<210> 349

<211> 339

<212> DNA

<213> Homo sapiens

<400> 349

```

ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggt cggctaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgtttcag gctcatccca gtttgccgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg ccccgagacc gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

```

<210> 350

<211> 113

<212> PRT

<213> Homo sapiens

<400> 350

```

Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1      5      10      15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20      25      30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35      40      45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50      55      60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65      70      75      80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

85 90 95
 Ala Leu Ala Gly Phe Arg Glu Pro Gln Arg Thr Leu Glu Leu Phe Asp
 100 105 110
 Ala

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgcccc gtgccgagac ccggggccttc aggagccggc ccggggagag aagagtgcgg
 60
 cggcggacgg agaaaacaac tccaaagttg gcgaaaggca ccgccctac tccggggctg
 120
 ccgcgcctc ccgcgccca gccctggcat ccagagtacg ggtcgagccc gnggcatgg
 180
 agccccctg gggaggcggc accaggagc ctggggcccg gggctccgcc gcgaccccat
 240
 cgggtagacc acagaagctc cgggacctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccn ntcctcctc tctcctctg aggcgctctg gcccatccag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 352
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
 1 5 10 15
 Arg Arg Val Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
 20 25 30
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro
 35 40 45
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
 50 55 60
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
 65 70 75 80
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
 85 90 95
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Trp Arg Arg
 100 105 110
 Ser Gly Pro Ser Arg Pro
 115

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
 60
 attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt
 120
 gaacccattt cagctgttgt cagccacac gccctcatgc tgttgctggt gaagcctcaa
 180
 tttgaggttg gttgcaaggc tttgggagcc catggcggtg tcacggagcc gccctgcgc
 240
 ttgcaggcca tcgcggtgtg catggcagca gcggtagatt tgggttggcg tatgcgtgac
 300
 gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa
 360
 cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctacttggt tcttgtgaac
 420
 gacacgagcc ctctgagata cgttgctcgc gtacccatg ccacgcggga cgacgctttt
 480
 gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttccg
 540
 gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
 600
 gagtgcgcc acgagggcga ggtggtcgc gtctttggcg gcgacggcac gatcttcga
 660
 gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgtc
 720
 ggttttcttg ctgagctgga gcgctccgat atggcgatc tagtgaacaa ggtgtgttcg
 780
 cgcgactaca ccggtgagga tcgcctcgtg cttaaaacca ccgtcacga gcattccgga
 840
 caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaggcgc agccggcg
 900
 cgcgatgctg acgttctggc gtctgtcgac gagttgcgg tgcaacgctg gagttgcgac
 960
 gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgggccc
 1020
 gtcagtggc ccgatctcga ccgatgctc atggtgccgt tgagcgctca cgctctcttt
 1080
 gctcgaccgc tggatcatgag cccagctgct cgagtggacc ttgacatcca gccagacggt
 1140
 tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
 1200
 agaatcaccg tcgtccgcca tcccagcgtg ctgcgcattg ctgctctggc cgcgcagccc
 1260
 ttcacatcgc gtctggtcaa gaagtgtgag ctcccggtca gcgggtggcg tcagggtcgt
 1320
 gaccgtcacc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
 1380
 tcacgatga gacggtctc gaaccctcat ccgcgctgac ggcagtcacc ggcgagaccg
 1440
 gcgccggaaa gaccatggtg gtcaccggt
 1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

```

Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1          5          10          15
Val Val Val Val Thr His Ala Thr Arg Asp Ala Phe Asp Ala Ala
 20          25          30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
 35          40          45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50          55          60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
 65          70          75          80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
 85          90          95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
100          105          110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
115          120          125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
130          135          140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145          150          155          160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
165          170          175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
180          185          190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
195          200          205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
210          215          220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225          230          235          240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
245          250          255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
260          265          270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
275          280          285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
290          295          300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Thr Ser
305          310          315

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<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

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nggattccac ctcttggaaat ggaaaccac ataccagttc tcttctcga tttgaatgag
60
gatgacctca gtgccaatga gcagcttggt ggcccccatg catccggcgt gaactccatc
120

```

ctgcccaagg agcatggcag ccagtttttc tacctgccca tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca ctggaatggg
 240
 gtcacaccac agaataaaag gatttaccta attgtgaaaa ccacagtcca actcagccac
 300
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaacagg
 360
 agttttcacgc agagtttgaa gaggagaata tccttgaaaa atatatttta ttctgtgggt
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagtgaa aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356

<211> 186

<212> PRT

<213> Homo sapiens

<400> 356

Xaa	Ile	Pro	Pro	Gly	Met	Glu	Thr	His	Ile	Pro	Val	Leu	Phe	Leu
1			5					10					15	
Asp	Leu	Asn	Ala	Asp	Leu	Ser	Ala	Asn	Glu	Gln	Leu	Val	Gly	Pro
		20					25				30			
His	Ala	Ser	Gly	Val	Asn	Ser	Ile	Leu	Pro	Lys	Glu	His	Gly	Gln
		35					40				45			
Phe	Phe	Tyr	Leu	Pro	Ile	Ile	Lys	His	Ser	Asp	Asp	Glu	Val	Ser
	50				55				60					
Thr	Ala	Ser	Trp	Asp	Ser	Ser	Val	His	Asp	Ser	Val	His	Leu	Asn
65				70					75				80	
Val	Thr	Pro	Gln	Asn	Glu	Arg	Ile	Tyr	Leu	Ile	Val	Lys	Thr	Thr
			85				90						95	
Gln	Leu	Ser	His	Pro	Ala	Ala	Met	Glu	Leu	Val	Leu	Arg	Lys	Arg
			100				105					110		
Ala	Ala	Asn	Ile	Tyr	Asn	Lys	Gln	Ser	Phe	Thr	Gln	Ser	Leu	Lys
		115				120					125			
Arg	Ile	Ser	Leu	Lys	Asn	Ile	Phe	Tyr	Ser	Cys	Gly	Val	Thr	Tyr
	130			135						140				
Ile	Val	Ser	Asn	Ile	Pro	Lys	Ala	Thr	Glu	Glu	Ile	Glu	Asp	Arg
145			150						155				160	
Thr	Leu	Ala	Leu	Leu	Ala	Ala	Arg	Ser	Glu	Asn	Glu	Gly	Thr	Ser
			165						170				175	
Gly	Lys	Thr	Tyr	Ile	Glu	Lys	Tyr	Thr	Arg					
			180					185						

<210> 357

<211> 323

<212> DNA

<213> Homo sapiens

<400> 357

acgcgtgcgt gtgttgtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
 60
 gtacgatcag gctgaaggct gatcaggcac aaggctcttg gggagagccc tggttccagc
 120
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagactgc acccgctggg
 180
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggtctga cagagtggat
 240
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
 300
 gtcaccatgg gtcagcgagg atn
 323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5				10					15		
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
		20					25					30			
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35				40					45				
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50				55					60					
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65				70				75					80		
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
			85					90					95		
His	Thr	Thr	His	Ala	Arg										
			100												

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgcgc ggtgatggcc gaccttcgcg aatcgggcgc aatcagagcag
 60
 gatcgggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgcgc
 120
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggtcgtgc
 180
 aagctgaagt tcttcggcga gtacaccctg ttcgacaacc tggcccccaa ctcggttggt
 240
 tcgttcgaat aacggatgat tccgg
 265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10           15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
          20           25           30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
          35           40           45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
          50           55           60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65           70           75           80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggaccacctg gctacaaatc tgtcctgagg atcagcctca cccaccggac catccctctc
120
aacctcatga aggtgcacct catggttagcg gtggagggcc gcctcttcag gaagtgggtc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttgtt tccgtgggtt atgaatatga atcctgccca
300
gatctaattc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaacat catgccctca acattcaaag tggcatcctg
420
cacaagggga atgngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10           15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
          20           25           30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
          35           40           45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
          50           55           60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65              70              75              80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
      85              90              95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
      100             105             110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
      115             120             125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
      130             135             140
Gly Glu Asn Gln Phe Val Ser
145              150

```

<210> 363

<211> 502

<212> DNA

<213> Homo sapiens

<400> 363

```

gggtacacaaa aagtttgcca cagtattcac actccagggtc tccataaacc ttccagatcc
60
gctcacacaa gctgggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaa
120
cggtgatgcc tgaccggtgc tcaggggcag ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg tttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgtttctgc ccttccccta
300
gggggctctg ggcgccatgg ctttctctgat ctgaccagc actctggggc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt ttccaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364

<211> 136

<212> PRT

<213> Homo sapiens

<400> 364

```

Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1      5      10      15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
      20      25      30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
      35      40      45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
      50      55      60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65      70      75      80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```



```

      85              90              95
Ala Phe Met Lys Val Leu Asn Ser Leu Gln Lys Lys Gln Met Asn Thr
      100              105              110
Ser Leu Cys Glu Arg Ile Trp Lys Val Tyr Gly Asp Leu Glu Cys Glu
      115              120              125
Tyr Cys Gly Lys Leu Phe Trp Tyr
      130              135

```

<210> 365
 <211> 333
 <212> DNA
 <213> Homo sapiens

```

<400> 365
atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
60
ccactgatcg ttgggattct atttgggggtt gagaccctct ctggagtctc tgctgggtgcc
120
cttgtctctg gtgttcagat tgccatttct gcatccaaca ctgggtggtgc ctgggacaac
180
gccagaagat acattgaggc tggagtttca gagcatgccca ggacccttgg cccaaaaggt
240
tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
300
tctggccctt ccctcaacat cctcatcaag ctt
333

```

<210> 366
 <211> 111
 <212> PRT
 <213> Homo sapiens

```

<400> 366
Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu
1      5      10      15
Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr
20     25     30
Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala
35     40     45
Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr
50     55     60
Ile Glu Ala Gly Val Ser Glu His Ala Arg Thr Leu Gly Pro Lys Gly
65     70     75     80
Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro
85     90     95
Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu
100    105    110

```

<210> 367
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 367

gcgttcgtcg cactaccg cgccggcgga acccttgacg agctactcga agcatggaca
60
tggcagcagc tcggtgtaca cagcaaaccc gtgngccttg tacgactcga cnncttctgg
120
gcaccgctga ccgcgctact caaccacatg accatcgaaa gtttcattcg ccttgaggagc
180
cgccgctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
240
accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
300
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
360
cngttcaggt ggcccgaat g
381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1				5					10				15		
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
			20					25					30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
			35				40					45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50					55					60				
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70					75				80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
					85										

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatat cgcacacaca ccgctcccct ctgcgcgaat tcgcagacaa
60
acttgcgagc gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
120
gtacgcgagt tctcggacat caacgcgaac gtcgggcaag atactgtcaa cgccatctac
180
acattctacg agcagcaagc gaccagtctt cttcgccagc tgaacgacct cccaccggaa
240
gagcttcccg acgtcatcga ggaactcttc cgctgtcca ctgatgtcct tctttaccat
300
ttccagcaag ctt
313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacgggtc acgtcatcct ggcgattcca cagggtggtga cgtcatggat cggccctcatc
 60
 tgcgatcgcca ttggcacggg ctttatcaag ccgaacctct ccacgggtgt aggaggctctt
 120
 tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggetaccac
 240
 gtagggttca ttgccgtgc tatcgggtatg gctctgggtc tgatcgccct cttccacgggt
 300
 cgttccaaac tgcgtgagct cgccttcgac atcccaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgctccgcgg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

```

<210> 373

<211> 475

<212> DNA

<213> Homo sapiens

<400> 373

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acatgttgga aaaattgcct ccactctcgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcactgtgcct
120
gctctctctc ggttctctaa tcctttggcc aaacatttcc cccacaaccc tccactccag
180
ttggctgggc actgcctctc agaaagaagt cccaggctcc tgcagcccc agagcgctcg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggaccctac
300
accctaccct gtaccaccac atcccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaaggtcca atccactcag ttcttaaatg aaaaacagtt
420
gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcggtg tgcac
475

```

<210> 374

<211> 109

<212> PRT

<213> Homo sapiens

<400> 374

```

Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1              5              10              15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20              25              30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35              40              45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50              55              60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65              70              75              80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85              90              95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100              105

```

<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcgtt ttttcacat ggcgcaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct cttcatagc ggcagtgggt gcgaagctgg gctgcccgca gcgcactatg
 240
 ggcaacggcg agctgctgta ccagcgtttc catctatttc atgcgcgcag tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 cgcgtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
 60
 aggcgtggaac gagggtgtgt gtgttcgggt tggactcagg gaactgccgc agacgcccag
 120
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcagggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttgggttcggg caagggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cgggtgaactt
 300
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagtgtt ggaccggctg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttatt tgtaaataat aaattcatta tttctagttg gttagggtact
 60
 atgggctgtg gttaccagg tgctatggca gctaaaattg cttattccaaa ccgtcaagca
 120
 gtacgtatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaaa
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tgggtggtaaa ggctatgttg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatggctcaa gatgttccaa caatcgtt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

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naccggtcat aggcgggccc agtggaagac cacgccaaca cagttgggtg agatcccgct
60
tgaggggcaag gtccctgcgcg tcccgcgaaa tctgggtcaag gcctaccact ctggggtgat
120
cgacgtcgcg gactgaaccc tgggagcctg ggcgggtccag catgactgct caggctcatt
180
acccaaaacgc gtgcgtcccc taggggtgtc gtcgatgagca agccccgaagt gacctgccc
240
gattccgccc ccgacgacct cgctcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgacactac gtcggcggtgg ccttaagcaa tggctcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccaggtg
420
atccccgagt gggatgaagg tgtccaagg atgaaggctc gtggacgacg caaactcgtc
480
atccccacc accttgctta cggtcgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgtggtct tcgtctcga ccttgctaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
      50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
      65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

```

nggagcaaca cctgggtcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
 60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
 120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctccccgctt
 180
accagctggg ctctatctac agagagagca atggcttccc ttccttgaa ggaagtctca
 240
ccctcacaag gacacttgat ccgctgcaaa gcagaaaagtg tgcgggaccct ttgggaaggg
 300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
 352

```

<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```



```

      50              55              60
Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser
65              70              75              80
Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile
      85              90

```

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

```

<400> 385
g c g g g c g c c a c g a a a t g c g c c t t c a c c g g a c g c c a g g t t g a t c g a g c c g c c a
60
g c a c c t c g g g c a a t g t c c t g g g c c t g a c t g g c a c a c g c a a t c a a a g c g a g c a c a a c a c a
120
c a a a a a c g c a t c a t g a g g c a g a c g c c a g g g a a g t g a c a g a a g c g c a g c a g g c g c g c g g c
180
g a t t g g a a a t a t c g g t g a g g c t a a t g g t c a c a g c g c t t g c a g g t t g t a t t c g g t g g c c a
240
a t t c g c g g a a c g a c a g c a c c g c c a g t t c c a g t c g c c g c g c a g c a c c a g g c g a c g c a a g c
300
t g c g g c g c a a c t c c g g g t g c a c c a a c a a c a c g c a c t g t t c a
342

```

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 386
Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
1      5      10      15
Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
      20      25      30
Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
      35      40      45
Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
      50      55      60
Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
65      70      75      80
Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
      85      90      95
Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
      100      105

```

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

```

<400> 387
a c g c g t g a c g c g c c g g c a t c g g a a g c g t t g a c t g c a g a g a g a c c g c g c a c g t g g c t g t g
60

```

ggacgtgctg gcacgtctga catgggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgcgtgat ctgcgccatg cgcggcagca agcgcctgat
 180
 gctgttcggt cagagctgct cgaagcgcag caagcatgtg cctcgtgccca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1				5					10				15		
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
		20					25					30			
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
		35				40					45				
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
		50			55					60					
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65				70			75						80		
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
			85				90						95		
Pro	Arg	Ala	Arg	Ser	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg
		100					105						110		
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtccact gtcatgacgc gaagctcgcc gtgcagtcgg tccacgtccg
 60
 ggccctccac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggaacgag
 120
 gtatttcggt tggagacgct tgggggtcaat tacggccagg tgcgcgccgt cgatgccctg
 180
 acgaccaccg tagagcgcg caccatcacc tgccctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtgggcgat ccaaggggca acaaagtctc caggaggggg actggtcaac
 300
 cagcagggtt cttgggctga cccccgcaaa gccgacgccg cgaccgctcg acgaatggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg cgcgtctgtg aggcgcctat cacggtgaca ctctcggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcacgcctntg ttcagcgact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggcgc ggatcattgt cgagcccatc
240
ttgcaaggag cgggaggcat ttggccgttg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg
360
actggcaaac ttttcgcatg cgagtgggcc gatatcggtc ctgacatcat ggtggttggg
420
aaatccatga ctggcggata cctgacccag tcgggc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

```

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1             5             10             15
Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
      20             25             30
Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Gly Arg Arg Gly
      35             40             45
Asp Val Val Gln Arg Gly Arg
      50             55

```

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

```

naccgcttgc tcgctattgg ttgctactcg gcctacgaag gtatctacac catgatgact
60
gagcggggacc ggtacccggc ttcccgattt ccgacggtgt gcatcccgcc ttctatcgac
120
aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
180
gaggcgatgg acaagattaa ggagtcgggt atcgcgtcca gacgctgctt cgctcgctgag
240
acgatggggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgctgag
300
cggatctata ccaacgagga cggtatctcc ctggacgac tagccaacga cgtccattgg
360
ttgcgggagt c
371

```

<210> 394

<211> 123

<212> PRT

<213> Homo sapiens

<400> 394

```

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1             5             10             15
Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
      20             25             30
Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
      35             40             45
Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
      50             55             60
Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
      65             70             75             80
Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
      85             90             95
Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
      100            105            110
Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
      115            120

```

<210> 395

<211> 351

<212> DNA

<213> Homo sapiens

<400> 395

gaattctagtg tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
60
gcgacaggtg gtcttgtgca tggtagaaaag gcagtcacaag cctatgtctc tgaacctgtc
120
tctcatttct gttttctact ttacgattta tggttatctca tactcccat gttgcctgtt
180
ctccagtttt tttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag
240
ggcagaattg tgtccaacag ctcttaaatg cagcgagaa actgtgatgt taaaaacatc
300
ttgttatccg gccccaaaac atgttgtcct tggtaactct tactggtttg t
351

<210> 396

<211> 90

<212> PRT

<213> Homo sapiens

<400> 396

Met	Val	Glu	Arg	Gln	Ser	Lys	Pro	Met	Ser	Leu	Lys	Pro	Ala	Leu	Ile
1				5					10					15	
Ser	Val	Phe	Tyr	Phe	Thr	Ile	Tyr	Val	Ile	Ser	Tyr	Ser	Pro	Cys	Cys
			20					25					30		
Leu	Phe	Ser	Ser	Phe	Phe	Thr	Cys	Val	Ile	Ser	Ile	Leu	Leu	Phe	Leu
			35				40					45			
Leu	Asn	Phe	Cys	Leu	Arg	Ala	Glu	Leu	Cys	Pro	Thr	Ala	Leu	Lys	Cys
	50				55					60					
Ser	Ala	Glu	Thr	Val	Met	Leu	Lys	Thr	Ser	Cys	Tyr	Pro	Ala	Pro	Lys
65					70				75					80	
His	Val	Val	Leu	Gly	Asn	Ser	Tyr	Trp	Phe						
			85					90							

<210> 397

<211> 483

<212> DNA

<213> Homo sapiens

<400> 397

gccgtcatta aagagatcac ccctctcctc caacctggtg atgtcctcgt cgacggtggt
60
aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
120
tatgttggtta ctggcatctc cggtggggga gtcggggccc tgagggtccc atcaattatg
180
cctggcgggg ttaaggaate ttacgaaate atcggaccgg tcttagaaaa aatctccgcc
240
cacgtcgacg gtgaacctcg ctgcgcatgg atgggtactg acggcgccgg acattctcgtc
300

aagatgggtcc ataatggcat cgagtaagcc gatatgcagt tcattggcga ggccgccccttc
 360
 ctttttgcgn tgcccgccgg tttgaccaat gctgagggcg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaaag
 480
 gat
 483

<210> 398

<211> 161

<212> PRT

<213> Homo sapiens

<400> 398

Ala	Val	Ile	Lys	Glu	Ile	Thr	Pro	Leu	Leu	Gln	Pro	Gly	Asp	Val	Leu
1			5						10				15		
Val	Asp	Gly	Gly	Asn	Ala	Tyr	Phe	Gly	Asp	Thr	Arg	Arg	Arg	Glu	Glu
			20				25					30			
Glu	Ile	Arg	Pro	Thr	Gly	Ile	His	Tyr	Val	Gly	Thr	Gly	Ile	Ser	Gly
		35				40				45					
Gly	Gly	Val	Gly	Ala	Leu	Arg	Val	Pro	Ser	Ile	Met	Pro	Gly	Gly	Val
	50				55					60					
Lys	Glu	Ser	Tyr	Glu	Ile	Ile	Gly	Pro	Val	Leu	Glu	Lys	Ile	Ser	Ala
65				70					75				80		
His	Val	Asp	Gly	Glu	Pro	Cys	Cys	Ala	Trp	Met	Gly	Thr	Asp	Gly	Ala
			85						90				95		
Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp	Met
		100						105					110		
Gln	Phe	Ile	Gly	Glu	Ala	Pro	Phe	Leu	Phe	Ala	Xaa	Pro	Ala	Gly	Leu
		115					120					125			
Thr	Asn	Ala	Glu	Ala	Ala	Asp	Ala	Phe	Glu	Ser	Trp	Asn	His	Gly	Asp
	130					135					140				
Leu	Asn	Ser	Tyr	Leu	Val	Glu	Ile	Thr	Ser	Arg	Val	Leu	Arg	Ala	Lys
145				150					155					160	

Asp

<210> 399

<211> 314

<212> DNA

<213> Homo sapiens

<400> 399

nngggaatga agaccaccca gcccttcctt tcctcaaate ttctccaggc ttctgtgcag
 60
 ggctcatcca cccatccact cattcaccca tctatccate cactcatcca cccatccagt
 120
 cattcaactca ttgtgccate cactcatgta cccatccact cattcgccca ttatccatc
 180
 cactcaacca tccactcacc caccatcca nctcatcacc cgtccagtca cccatctacc
 240
 caccatgta tccatccact catccaccca tccactcacc tgtccatcca cttatccacc
 300

catctactca ccca
314

<210> 400
<211> 104
<212> PRT
<213> Homo sapiens

<400> 400
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
1 5 10 15
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
20 25 30
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
35 40 45
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
50 55 60
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
65 70 75 80
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
85 90 95
His Leu Ser Thr His Leu Leu Thr
100

<210> 401
<211> 2165
<212> DNA
<213> Homo sapiens

<400> 401
gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgtatca ggtagtttta
60
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggtattgt ttaatgggtg
120
caaaatgaaa gatctattga agtttacta tacattgcatt tgattgaacc ttggagagtt
180
ttatgaaaa gaggggcac ccttgccatc tgtttgccag tcttctctgc cccttccctt
240
gaaatgectg cctctttttt gccacagatt tttctctgacc atccgaactc agatgggggc
300
ctctaagtgc ttcttgagata ttccacaatc ccttcacaag gccacagtcg gaagtgaatt
360
atctggagggt gcctggggcat ctgtgttgga agggagtgaa gactcaccag ccagtcagtt
420
tgtggggtac agttgtccca caaaaatcag gcatgttcac ctccctctg gggccctaca
480
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct ggggaagtgg aaagggcagc
660
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaaggtcccc atatgaactt
720

cctacagggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga
780
aaaatttcctc ttgtcatcac aagcgagtg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggcccgagt tacacaggct cccggaatac agacctggga agataggga ggagagggga
960
agcttgtggc cttttgatcc gcccccgaa tggccacgt gcgctgtctt gctgccttca
1020
tctcctgtct agaggccttc tccttcccag agacctcctt ggatgggtct aaggagagaca
1080
ctgccccggc ctttttcctt gcaatcaca ggtccaaatc ctccaggctg cgcttgatcg
1140
gcccgcggc cccaatgttc tacgggtcca ttttcgggtg caggattggg tggaccatgc
1200
cttccatctt cctgaaatc tccagtctca catggtgagg ttttctgat cttgaaagcg
1260
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttggggg
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgccttg ctctcctggg
1380
gccctgtggt ggaatgagcc agggccagga ccttgccggt aggtttgtgc gggttcttgg
1440
gaaggctcag atctgtaggc tgatcatccg taggggcttc tgctgccgc gacttttgt
1500
cttgagggtg cagggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag
1560
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattg gatgtctgtt
1620
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgagg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc cctttctctc aagagttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaagggg ttaagtgat
1800
gcttgagaga gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggtt tgctttgaa actctggagc tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac
1980
tggaacacaa gtcaccccta gcaatcagtt tctttttgct gatcaaggg ggtggggagc
2040
cataagggtg gctgctggag aggctggccc cactcacttg ggacaaaagc ttttcttgg
2100
ccagtgggga catcatgcct ggggtgcccc tagagtagag caggggcggt taattaagtc
2160
catgg
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1 5 10 15
 Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Arg Gly Ser Leu Trp
 20 25 30
 Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
 35 40 45
 Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
 50 55 60
 Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
 65 70 75 80
 Pro Asn Pro Pro Gly Cys Ala
 85

<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaacgggtc
 60
 gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccga actcgtccag
 120
 ccttcgcccc cgctgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
 180
 cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
 240
 cagccccgaca tggctgtctt ggtggacgtc ggccacgaag ccggccacct cgccttatac
 300
 catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcgg cgaattcat
 360
 gctatgatc
 369

<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1 5 10 15
 Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
 20 25 30
 Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
 35 40 45
 Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
 50 55 60
 Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
 65 70 75 80
 Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

      85              90              95
Leu Ala Leu Tyr His Leu Trp Gln Ala Phe Tyr His Arg Pro Thr Leu
      100              105              110
Gly Gly Ala Cys Gly Glu Ile His Ala Met Ile
      115              120

```

<210> 405

<211> 840

<212> DNA

<213> Homo sapiens

<400> 405

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gaattccgc gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgttc
60
gactcgcctt ggaccacgag ggcctgtctg gagacagtgg tggaggagag cgacccaag
120
ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgacctg cagtggaggac
180
gtggaggcca ccgtgcccac gctgcagcgg accaagtcac ggatcgagca ggggtatcgtg
240
gaccgctcag agacggggcgt gctggacaag aaggaggggg agcaagccaa ggcgctgttt
300
gagaaggtga agaagtccg gacccatgtg gagggagggg acattgtgta ccgctctac
360
atgcgcgaga ccatcatcaa ggtgatcaag ttcacctca tcattctgta caccgtctac
420
tacgtgcaca acatcaagtt cgacgtggac tgcacctggg acattgagag cctgacgggc
480
taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
540
tacatcagcc tagtcatctt ctacggcctc atctgcattg atacactgtg gtggatgcta
600
cggcgctccc tcaagaagta ctctgttgag tcgatccgtg aggagagcag ctacagcgac
660
atccccgacg tcaagaacga cttcgccttc atgctgcacc tcattgacca atacgaccgg
720
ctctactcca agcgcttcgc cgtcttcctg tcggagggtga gtgagaacaa gctgcggcag
780
ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
840

```

<210> 406

<211> 91

<212> PRT

<213> Homo sapiens

<400> 406

```

Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
  1             5             10             15
Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
      20             25             30
Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
      35             40             45
Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

```

```

      50              55              60
Ser  Glu  Asn  Lys  Leu  Arg  Gln  Leu  Asn  Leu  Asn  Asn  Glu  Trp  Thr  Leu
65              70              75              80
Asp  Lys  Leu  Arg  Tyr  Gly  Glu  Lys  Thr  Thr  Arg
      85              90

```

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

```

<400> 407
g c c t a t t g t a   c c a g c t c t c c   a g g g c t g g g g   a c t t g c t a g a   g c a g g g t t c c   c a g t g c c c c c
60
a g g c t c t a c t   t t g c t c t g c c   t g g t c t c a g g   g t g t a g g g g a   t g g a g a g c t g   g a c t t c c a g c
120
c t g c t t c t t g   g c t g t c t a g g   g g c c a g g g g c   t c g g g a c a c a   g a g c t c c t g g   a g g c c g a g c a
180
c a a g c c c t t g g   g c a g a g g t g a   g g c a g a g c t c   t g a c t g t t t c   a t t c g a c t a c   g t t g c c a a g g
240
a g a t g c t c g c   t c g g a g t g g t   t g c t c t g g c t   c t g g g a t t c c   a a a c c a a g c t   g c c t t c t c t g
300
a t g t g g c c c t   a g t g c t c t g g   g c g g a t g t a c   c t t g g c t c t g   c c t g g a c c c t   c t c t c t c t t c
360
c a g g c c c t c g   t c c c a c c a g g   a t g a t g c c t a   t c c a g a g c t c   a t t g t c c t c t   c c c a c t t c c t
420
c c c c g a g c t t   c c c a t t c c g t   g t c t c t c t g g   a g g g c c c a t c   a t c a t c c t g g   t g g a g g t g t t
480
g c a c t g a g g a   c c a c a g c a g c   c c t c g c a t t c   c c a c g g g c a a   a g g g g t a t g t   g t a g g
535

```

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

```

<400> 408
Met  Leu  Ala  Arg  Ser  Gly  Cys  Ser  Gly  Ser  Gly  Ile  Pro  Asn  Gln  Ala
1              5              10              15
Ala  Phe  Ser  Asp  Val  Ala  Leu  Val  Leu  Trp  Ala  Asp  Val  Pro  Trp  Leu
      20              25              30
Cys  Leu  Asp  Pro  Leu  Ser  Leu  Pro  Gly  Leu  Cys  Pro  Thr  Arg  Met  Met
      35              40              45
Pro  Ile  Gln  Ser  Ser  Leu  Ser  Ser  Pro  Thr  Ser  Ser  Pro  Ser  Phe  Pro
      50              55              60
Phe  Arg  Val  Ser  Leu  Glu  Gly  Pro  Ser  Ser  Ser  Trp  Trp  Arg  Cys  Cys
65              70              75              80
Thr  Glu  Asp  His  Ser  Ser  Pro  Arg  Ile  Pro  Thr  Gly  Lys  Gly  Val  Cys
      85              90              95
Val

```

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg
 60
 ggacttcgca ttacgactaa tatttctctt gccacaact tcaatatgga tgaattttct
 120
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
 180
 agaaaaattga ccgaaattgc tggctcttcag caaggggagt atcaggtgtc agatgcgact
 240
 gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt
 300
 gcagggaattt ccttttttgt tggagggact ggtgttatga acatcatgct ggttcgggtg
 360
 acggagcgtg cgcggt
 375

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1			5					10			15				
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20				25						30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
			35				40				45				
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
			50			55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr
			65			70				75				80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
			100				105						110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
			115				120					125			

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

ccacatactt caccctcttc accccctcca cctactccac cacctggcag tcgccatcga
 60
 ggatggggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
 120
 gcacgcggtc gggggccctt gagctcgaag gcgcggcgca tcgggcagtg ctccgcggcc
 180

tggtcgcagg gcacgtcgta ctggtgcgag acgcggaagc acttgtggcc gatgtaggcg
 240
 cgatcggtcg tccccaaactg gcgctgatag gccgtgtaca caacacaaac tgttgactc
 300
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc
 360
 ctgctggtag cgcgtggggg ggatggggca tagcgtcggg gaggagggtg
 409

<210> 412

<211> 119

<212> PRT

<213> Homo sapiens

<400> 412

Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413

<211> 357

<212> DNA

<213> Homo sapiens

<400> 413

ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggt agggactcca
 60
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccg cccacatcca gctggacccc ctgtcataca gcagccaaca
 180
 acacccatgt ttgtagctcc ccccccaaag acccagcggc ttcttcactc agaggcctac
 240
 ctgaaatata ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
 300
 ctggcagctc ggagacgga cgtccatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414

<211> 119

<212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
      65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
      100          105          110
Glu Gln Glu Ser Arg Leu Pro
      115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

```

tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatatga atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccggtccattg tcagaattca agggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcgggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
      35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

```

65          70          75          80
Gln Ala Pro Asn Leu Ala Ile Arg Leu Ile Val Ser Asn Pro Pro Glu
          85          90          95
Gly Gln Pro Ile Ser Arg
          100

```

<210> 417

<211> 483

<212> DNA

<213> Homo sapiens

<400> 417

```

gaattcctcg ccgtctctga ggtgggagag gacacctttg tgcgctccac cgagggagag
60
tacgcggcca acgtcgaggc cgtgggtgacc ccagcaccgg cggagaaaga tattgagggc
120
cagccagaag cacaggaaca tgacaccccg ggtacagaga ccattgagaa gctggctcgaa
180
tgggcccagg gcgcaggcat tactgtaaac ccccgcggtg ttgtttatta taccctcaag
240
tgcatgatga tcaagctcca ccacccggcc gcggagagcg aagagcgcgga gtccgagttg
300
gcggcgggtt tcattccctgg cgatcgagag ctggatgaaa agcgccttga ggccgcactc
360
gagccggtgg agttttagtt ggcaggggat aaggactttg cagacaaatga ctctctagtc
420
aagggtctatg ttggcccgcg cgctttgaac gccaatggca tcaaggtctt ggccgatcca
480
cgc
483

```

<210> 418

<211> 161

<212> PRT

<213> Homo sapiens

<400> 418

```

Glu Phe Leu Ala Val Ser Glu Val Gly Glu Asp Thr Phe Val Arg Ser
1          5          10          15
Thr Glu Gly Asp Tyr Ala Ala Asn Val Glu Ala Val Val Thr Pro Ala
20          25          30
Pro Ala Glu Lys Asp Ile Glu Gly Gln Pro Glu Ala Gln Glu His Asp
35          40          45
Thr Pro Gly Thr Glu Thr Ile Glu Lys Leu Val Glu Trp Ala Gln Gly
50          55          60
Ala Gly Ile Thr Val Asn Pro Arg Val Val Cys Tyr Tyr Thr Leu Lys
65          70          75          80
Cys Met Met Ile Lys Leu His His Pro Ala Ala Glu Ser Glu Glu Arg
85          90          95
Glu Ser Glu Leu Ala Ala Val Leu Ile Pro Gly Asp Arg Glu Leu Asp
100          105          110
Glu Lys Arg Leu Glu Ala Ala Leu Glu Pro Val Glu Phe Glu Leu Ala
115          120          125
Gly Asp Lys Asp Phe Ala Asp Asn Asp Phe Leu Val Lys Gly Tyr Val

```

130	135	140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro		
145	150	155
Arg		160

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
 atttcacccc agggaaaacca gtaaggacca atgattaagc ccaagggttg gtaccgagtt
 60
 cggatccata agtaccggcc gccccagggtg ctggaatttg gggtcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtggggtg ggctgagctc
 180
 aagccccctg ctacatactt tagtagtaac gactccccgat ctgcattccaa cacatttacc
 240
 gaactttctag taagcgcccc ccgctgcaag cgaaagcact cccctgccaa gaaacagatc
 300
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga aggggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgtttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 ttccagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc ataccggtatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 ttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggctctcat
 660
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaatttttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg


```

      50              55              60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65              70              75              80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
      85              90              95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
      100              105

```

<210> 421
 <211> 406
 <212> DNA
 <213> Homo sapiens

```

<400> 421
ggatccacca tgatggagcc caccacacca tcctcagtc acctgctgca gcttctccat
60
aaccacaac aggtcaatct tgtctcccta aacacaccat gtgtctctcat gctgccatgg
120
tttgcctggg gccctctcta cctcctctgc tttctggaga acccttgca ctcctccaag
180
ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcgtgga
240
ttcatgaaga ttggttctact gtcagccctt gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

```

<210> 422
 <211> 104
 <212> PRT
 <213> Homo sapiens

```

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1      5      10      15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
      20      25      30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
      35      40      45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
      50      55      60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65      70      75      80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
      85      90      95
Gly Thr Lys Ser Tyr Gln Cys Leu
      100

```

<210> 423
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 423
 ngccacccta cgctcgcct gcaatggcaa cttcagatcc cgggtggcac cgtagtctta
 60
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agaggagaaa
 120
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg
 180
 ccgggcgcce cagccacacc gcgttctctg gccctcgcaa atggctccct gttggtgccc
 240
 ctcttgagt ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc
 300
 aactctactg caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aaccgcagcg acaggccccc acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtctctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggcacacaag tgaggagag
 540
 gagggccgaag accagatcct cgcggaccgc gcggaggagc agcgtgtgtg caacggggac
 600
 ccctctcggt acgtttctaa ccacgcgt
 628

<210> 424

<211> 209

<212> PRT

<213> Homo sapiens

<400> 424

Xaa	His	Pro	Thr	Pro	Arg	Leu	Gln	Trp	Gln	Leu	Gln	Ile	Pro	Gly	Gly
1				5				10						15	
Thr	Val	Val	Leu	Glu	Pro	Pro	Val	Leu	Ser	Gly	Glu	Asp	Asp	Gly	Val
			20					25					30		
Gly	Ala	Glu	Glu	Gly	Glu	Gly	Glu	Gly	Asp	Gly	Asp	Leu	Leu	Thr	Gln
		35				40						45			
Thr	Gln	Ala	Gln	Thr	Pro	Thr	Pro	Ala	Pro	Ala	Trp	Pro	Ala	Pro	Pro
		50				55					60				
Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	Val	Pro
		65			70					75				80	
Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	His	Asn
			85						90					95	
Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	Ala	Thr
			100					105						110	
Gly	Pro	Pro	Lys	His	Ala	Pro	Gly	Ala	Gly	Gly	Glu	Pro	Asp	Gly	Gln
			115				120						125		
Ala	Pro	Thr	Ser	Glu	Arg	Lys	Ser	Thr	Ala	Lys	Gly	Arg	Gly	Asn	Ser
			130			135					140				
Val	Leu	Pro	Ser	Lys	Pro	Glu	Gly	Lys	Ile	Lys	Gly	Gln	Gly	Leu	Ala
				150						155				160	
Lys	Val	Ser	Ile	Leu	Gly	Glu	Thr	Glu	Thr	Glu	Pro	Glu	Glu	Asp	Thr
				165				170						175	
Ser	Glu	Gly	Glu	Glu	Ala	Glu	Asp	Gln	Ile	Leu	Ala	Asp	Pro	Ala	Glu

145

150

155

<210> 427

<211> 546

<212> DNA

<213> Homo sapiens

<400> 427

ctagcggtag tagaaggtat gcagtttgat cgcggctact tgtctcogta tttcatcaac
 60
 aatcaagaaa caatgaatgc agagctagaa aacccattta ttcttcttgt tgataagaaa
 120
 atttctaata tccgtgactt gctaccaatt ttggaaggtg ttgctaaagc atcgcgcccc
 180
 ttgttgatca ttgcggaaga cgttgaaggc gaagcggttg caaccttggt tgtaaacact
 240
 atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
 300
 gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
 360
 attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcggt tacattgaca
 420
 aaagaaaagta caacgattgt tgatggtgag ggtgtgtgac ctaataattac tggtcgtggt
 480
 gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
 540
 gaacgc
 546

<210> 428

<211> 182

<212> PRT

<213> Homo sapiens

<400> 428

Leu	Ala	Val	Val	Glu	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	
1			5					10				15			
Tyr	Phe	Ile	Asn	Asn	Gln	Glu	Thr	Met	Asn	Ala	Glu	Leu	Glu	Asn	Pro
			20					25				30			
Phe	Ile	Leu	Leu	Val	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Asp	Leu	Leu
			35				40					45			
Pro	Ile	Leu	Glu	Gly	Val	Ala	Lys	Ala	Ser	Arg	Pro	Leu	Leu	Ile	Ile
			50				55				60				
Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr
65				70					75					80	
Met	Arg	Gly	Ile	Val	Lys	Val	Ala	Ala	Ala	Lys	Ala	Pro	Gly	Phe	Gly
				85					90					95	
Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Val	Leu	Thr	Gly	Ser
			100					105					110		
Thr	Val	Ile	Ser	Glu	Glu	Ile	Gly	Ile	Lys	Leu	Glu	Glu	Ala	Thr	Ile
			115				120					125			
Glu	Gln	Leu	Gly	Thr	Ala	Lys	Arg	Val	Thr	Leu	Thr	Lys	Glu	Ser	Thr
			130				135					140			
Thr	Ile	Val	Asp	Gly	Ala	Gly	Val	Ala	Ala	Asn	Ile	Thr	Gly	Arg	Val

```

145              150              155              160
Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
              165              170              175
Glu Lys Leu Gln Glu Arg
              180

```

```

<210> 429
<211> 425
<212> DNA
<213> Homo sapiens

```

```

<400> 429
gctagcagcc cttacaggag acgggctaataataatgcag cagtggctcc gacaacttgc
60
ccgttgccagc cggctacgga tccatttgct tttagtagac aggcgcgtcca aagtacacca
120
ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt
180
tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcaggggacc
240
ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
300
tgcatggaca cttcagcac ctctggggc tgagatgaac aggagtgcag aggtcgggtcc
360
cagttcagag cctgaagttc agactctgcc atatcttct cactacattc caggagtgga
420
tcctg
425

```

```

<210> 430
<211> 130
<212> PRT
<213> Homo sapiens

```

```

<400> 430
Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
1      5      10      15
His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
20     25     30
Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
35     40     45
Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
50     55     60
Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
65     70     75     80
Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
85     90     95
Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
100    105    110
Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
115    120    125
Asp Pro
130

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<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 ctagccatcc accagcgtag acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag
 120
 cctnaccogt gcccggactg cgagcggcgc ttctctcct cctctcgctt ggtcagtcac
 180
 cggcgtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tcttttgtag
 60
 ctcatggagg agcgtggcgc gtagtcggag gccgccgcgc tcatgccgct gctgtccggg
 120
 accgaccgag gcgcgtggga cactgttggt tgctgctacc tcgagcggca ccaagggaat
 180
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggt gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcagatg cctcgacacg ctgtacatgg ccgcacatca gcccggaagg
 420
 gctctgacat actacatgcy cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtag
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcagggaatgc
 540

gcccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac
 600
 tcgattccca tccagcgcgc catgggcgag ctgca
 635

<210> 434
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 434
 Xaa Pro Ala Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu
 1 5 10 15
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala
 20 25 30
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr
 35 40 45
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro
 50 55 60
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu
 65 70 75 80
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr
 85 90 95
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala
 100 105 110
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu
 115 120 125
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr
 130 135 140
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr
 145 150 155 160
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu
 165 170 175
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met
 180 185 190
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met
 195 200 205
 Ala Gln Leu
 210

<210> 435
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 435
 nncgtacgtt cgcgtatttt ccgcgccccg gaagctatcg ataataaagt tcaaccgctg
 60
 atccagcgtt agcaatggcg ggcacaggaa gggctacttag gcatgcagaa agaaaagctt
 120
 tccgctctga tggatggtga atcgttcgac agcgagctgt tgagttctct gtcgaagat
 180
 cgaacgcttc aacaaagctg gcagggtat cacctgatac gtgacacact gcgaggtgat
 240

gtcgggcaag tgatgcattc cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 ccgccccgcg tgggtccctc cgccgttcag gaattctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgtccc tgggcgagcc agattacgca aatcggtatg
 420
 gcggcctcgc tgcgctggc ggtgatcgtc ggctgcagc agtacaacca gccttctcgc
 480
 ccatcgaacg cgt
 493

<210> 436
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Ser Phe Asp
 1 5 10 15
 Ser Glu Leu Leu Ser Ser Leu Ser Gln Asp Arg Thr Leu Gln Gln Ser
 20 25 30
 Trp Gln Gly Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
 35 40 45
 Gln Val Met His Leu Asp Ile Ala Asp Arg Val Ala Ala Ala Leu Glu
 50 55 60
 Lys Glu Pro Ala Arg Leu Val Pro Ser Ala Val Gln Glu Ser Gln Pro
 65 70 75 80
 Gln Pro His Thr Trp Gln Lys Met Pro Phe Trp Asp Lys Val Arg Pro
 85 90 95
 Trp Ala Ser Gln Ile Thr Gln Ile Gly Met Ala Ala Cys Val Ser Leu
 100 105 110
 Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ser Ala Pro Ser
 115 120 125
 Asn Ala
 130

<210> 437
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 437
 ntggtaaccg gtgtccctga tatggaccct gctgtgttag agcgtaaatt atttatttta
 60
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttat
 120
 attaatacat tctcatacaa aacaatcggt tataaaagtc agttaaccac tgaacaagtg
 180
 ccacaatatt tcttagatgt acaaaatcca agtatggtaa cggcatttagc gcttgttcac
 240
 tcacgtttct caacaaatc atttcctcgt tggcggttag cacaaccatt ccgttatcatc
 300
 gctcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt ttctactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tctgcagca gctgcaccag
 60
 ctteccaggg gccggctgga cctggccacg caaagcctga cgggtggagac ctgcagggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggctctgag tgactgcatg
 180
 ctacgcgagg aagggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcgggggc ctggc
 395

<210> 440

<211> 128

<212> PRT

<213> Homo sapiens

<400> 440

```

Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1             5             10             15
Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
      20             25             30
Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
      35             40             45
Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
      50             55             60
Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
      65             70             75             80
Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
      85             90             95
Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
      100            105            110
Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
      115            120            125

```

<210> 441

<211> 364

<212> DNA

<213> Homo sapiens

<400> 441

```

gccagctact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagcccg
60
ggcggcgagtg tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
120
gacgggttga acttcgcctt ccacgctcca caggacgggc gggggcttggc cgcgctctac
180
ggcgggtccga aaggcttga gaacaagctc gatgcctttt tcgcgacgcc ggaacacgcg
240
gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggt ccggatgggc
300
caattgggca tgtccaacga gccctcgac catattccct acatctacaa ctatgccggc
360
gcgc
364

```

<210> 442

<211> 121

<212> PRT

<213> Homo sapiens

<400> 442

```

Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1             5             10             15
Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
      20             25             30
Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
  50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
  65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100              105              110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115              120

```

<210> 443

<211> 430

<212> DNA

<213> Homo sapiens

<400> 443

```

accgggttacg gctcagtgc acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
  60
ctcatgggtgc tggcaatccc ctctcgcaag atcctctcga cgacctgtc catcggatcg
  120
ggcggttcctcg cgcgctcttc cgcccctggc atgggtcatcg gcggagccac tggcgcggca
  180
ctgtggcgccc tcctcgaggg gctgccaggt atcccatcct caccgatgag ttctgtcatt
  240
gtcggcatga tcgcctgctt cggtgcgggt gcccatgccc cactcggcgt gctgctcatg
  300
gttggcgaga tgaccgaaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
  360
gctggccgag ttgtcgggga caettcgatc tacacctctc agctcaagga tcgcctggag
  420
ggcgacgcgt
  430

```

<210> 444

<211> 143

<212> PRT

<213> Homo sapiens

<400> 444

```

Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
  1              5              10              15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
      20              25              30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
      35              40              45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
      50              55              60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
  65              70              75              80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
      85              90              95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

```

          100              105              110
Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr
      115              120              125
Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala
      130              135              140

```

```

<210> 445
<211> 360
<212> DNA
<213> Homo sapiens

```

```

<400> 445
ccatggggcct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
60
tcttgcttta ttgctcacc tgtccagggt tccctctgtt tgtgaggagg ctgctgccac
120
cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtgggagg acctttcctt
180
agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat cccttctctc
240
tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
300
caagtgggaa caagccatga aggagctgca ccccgaaaag tctgagggtg ggacacgcgt
360

```

```

<210> 446
<211> 101
<212> PRT
<213> Homo sapiens

```

```

<400> 446
Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
 1          5          10          15
Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
      20          25          30
Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
      35          40          45
Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
      50          55          60
Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
      65          70          75          80
Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
      85          90          95
Gly Leu Pro Arg Gly
      100

```

```

<210> 447
<211> 487
<212> DNA
<213> Homo sapiens

```

```

<400> 447
acgcgtgaag ggggaaattg ctctgcccac ctgaggatta atcattaccc tggaaccctt
60

```

cccaaggcca tcaaggaaca cgcacccctt accagacett ccagctgctg ggggctctcc
 120
 gagtgaggct gaggtcatgg agaaggggaat ggggggcccc catggccagc tggacctgat
 180
 cactgctccc cactcagcc acagccctca gggccctgtg ccagtcacaga agccattca
 240
 gggacacett tggccaatgt tctgtttcat ctgagaggca accttcccca gtgcccacac
 300
 catagcgttt tcccccaaac accctcagga aggaggggacc actacctgtg cagggggggg
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccattcacc cccattgcct
 420
 ttctctcta ctccacctg gccagcttcc ctcaagtccc ctctgcctc agtgccctt
 480
 cacgcgt
 487

<210> 448

<211> 117

<212> PRT

<213> Homo sapiens

<400> 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1				5					10					15	
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
			20					25					30		
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
		35					40					45			
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
	50					55					60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65				70					75					80	
Ala	Ser	Tyr	Gly	Glu	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser
			85						90				95		
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100					105						110	
Cys	Pro	Phe	Thr	Arg											
			115												

<210> 449

<211> 353

<212> DNA

<213> Homo sapiens

<400> 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
 60
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaa
 120
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaagat cgaggccctg
 180
 gagcatgaga gccaggcct gcagctggag aaccggactc tgaggaaagt tctggacacc
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
 300
 gagaacctgg agctgcgcag gctgttgag accatgcgga gacgacaacg cgt
 353

<210> 450

<211> 117

<212> PRT

<213> Homo sapiens

<400> 450

Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu
 1 5 10 15
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
 20 25 30
 Leu Gln Arg Leu Gln Glu Glu Asn Arg Gly Arg Leu Ala Arg Lys Val Thr
 35 40 45
 Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
 50 55 60
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
 65 70 75 80
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
 85 90 95
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
 100 105 110
 Arg Arg Arg Gln Arg
 115

<210> 451

<211> 444

<212> DNA

<213> Homo sapiens

<400> 451

gtgatgcggc tgactaagcc tactttatcc accaatatcc cagtaacatg tgaagagaaa
 60
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cggttaatgg
 120
 gcagaagttt taatgttggg agaaatgctg accttaccac agaatttttg gaatatattt
 180
 ttgggagaga ccttttcag ttatatcagc gttcataatg atagcaatca agttgtaaaa
 240
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaatct ttcagcctcc
 300
 aatgctgcag tggctgaact taaaccggat tggtgtattg atgatgtcat acatcatgaa
 360
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
 420
 gaaaaaatgt atttcagaaa attt
 444

<210> 452

<211> 148

<212> PRT

<213> Homo sapiens

<400> 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
  1              5              10              15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20              25              30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35              40              45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50              55              60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
      65              70              75              80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85              90              95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100              105              110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115              120              125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130              135              140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

```

gctagctctg accccacctt tgccaagtgg cactagggtg gccaatgggg actagggttg
  60
tataattgga aaatacagtc tccctctgtt tccaagaaa gcccagatg acctgggggt
  120
tgaaaggcac tcccgctggg tgcttctctg gagcaggttg ggggcagcgg ggcggcgggg
  180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactgggt
  240
gcgttttggg atgggctggc ctgcgcgggt gtcgtttcag agcacacaga agagaccctg
  300
ccacaggagg agtgggagga gaagctgttg atgttctctg gagacacctt ggccatcatt
  360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
  1              5              10              15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

	20		25		30
Gln	Ala	Ser	Pro	Ser	Gln
	35		40		45
Leu	Pro	Trp	Ser	Trp	Gly
	50		55		60
Leu	Pro	Pro	Thr	Cys	Ser
	65		70		75
Ala	Pro	Gly	His	Leu	Gly
		85		90	
Phe	Gln	Leu	Tyr	Asn	Pro
	100		105		

<210> 455

<211> 602

<212> DNA

<213> Homo sapiens

<400> 455

cctaggcaaa gcatgcccac cctacacctcc cttaccctta ccccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgtggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcc ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcagggt gggaagcaga gatctcgctc tcttggagct
420
ggagctgggt ggtggggctc cttcctgggt ctgcgaggc tcattgggga ggtggcagcg
480
accctctcag gagcctctgt cgccctgact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

<210> 456

<211> 100

<212> PRT

<213> Homo sapiens

<400> 456

Met	Pro	Thr	Leu	Pro	Pro	Leu	Thr	Leu	Thr	Leu	His	Phe	Pro	Leu	Ser
	1		5				10				15				
Thr	His	His	His	Arg	Cys	Tyr	Cys	Met	Cys	Leu	Leu	Thr	Leu	Thr	Ala
		20					25					30			
His	His	Pro	His	Trp	Asn	Val	Arg	Thr	Thr	Lys	Ala	Gly	Leu	Leu	Ala
	35				40					45					
Ala	Leu	Ala	Thr	Ala	Gly	Ser	Pro	Glu	Leu	Cys	Arg	Val	Leu	Gly	Thr


```

      50              55              60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65              70              75              80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
      85              90              95
Leu Ala Thr Tyr
      100

```

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

```

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gcccccgacc
60
agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
120
tcccttctg ctggccgcaa cagccagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcattcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcagggtg gggtatccgc ccggcgggcgg
300
gagcaccggg acgccggggc gccg
324

```

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 458
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
1      5      10      15
Arg Pro Glu Val Arg Glu Leu Phe Leu Phe Cys Thr Cys Pro Gly
20      25      30
Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
35      40      45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
50      55      60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65      70      75      80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
85      90      95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
100      105

```

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctcgcg ggaggcgcg cgcgagagtgc
60
gggtgtcgaa caccagactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
120
ctggggttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccggtggtt
180
tatgctgcgg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaggg
240
agaggctca cccgacagct gggcatcgga ttacgaagc ccacgacgaa tcttctctgc
300
ctcctcaag ccgatcatcg gcatgccagg tttgtggtg aatgcttcga tcaacacact
360
aggatcggtg gggccacca catacaccga gcggcaatcg agcggatacg acctc
415

<210> 460

<211> 105

<212> PRT

<213> Homo sapiens

<400> 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1				5					10					15	
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
		20						25					30		
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
		35				40						45			
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
	50				55						60				
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
	65				70				75					80	
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
			85						90					95	
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
			100					105							

<210> 461

<211> 357

<212> DNA

<213> Homo sapiens

<400> 461

acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggtcacaac
60
cggtgcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca
120
gtcctctaga ccagctcaga gagtcccggt gtcggtaccg tcgagactca gtacacaact
180
gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact
240
gtcgtttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt
300
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtggtgcga tgcgaggaat cgcctcgat cctggtgcgt
 120
 accggagagt ccatctgagc ccttcttgtg gcggtgatgc cgggatatcc gtagaattag
 180
 cggtcggacg agccatccgg gtgatcgagg cagcggtagg ttgtcgagga aagtcggggc
 240
 tccatagagc aggggtggtgg gtaacgcccc ccgggggtga ccgcggggaa agtgccacag
 300
 agaacagact gccggtttcg agccggtagg ggtgaaacgg tggagtaagt gccaccgcg
 360
 tcatcggtga cggtgacggc atggcaaac ccacctggag caaggccaag aagaccgtga
 420
 ggctcgcgagc gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1             5             10             15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115             120             125

```

<210> 465

<211> 438

<212> DNA

<213> Homo sapiens

<400> 465

```

gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaatc tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgct agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcgttat cattacgggt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaa cggtggggat tagcgattct
300
catggcactt tagaagtgg caaggtagct gattttgtct gctgggatgt ggaagcccc
360
gggtgaacttt gttattggtt aggagagcag ttagtaaac aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466

<211> 143

<212> PRT

<213> Homo sapiens

<400> 466

```

Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
      1             5             10             15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro
      55             60

```

```

65              70              75              80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
      85              90              95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
      100             105             110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
      115             120             125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
      130             135             140

```

<210> 467

<211> 460

<212> DNA

<213> Homo sapiens

<400> 467

```

ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccca gcggttaagc
60
tgcatccctg caccttcttc tcccaccgct tcaaagccac agtgaggaaac ttcggagctt
120
ctgcagtgga agatggcggt ggaggaatgg atgccctggc tagaagagggc ggaatatctg
180
ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctccctaccgg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
360
ttcctccagg cttgctgtc acccggggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

```

<210> 468

<211> 118

<212> PRT

<213> Homo sapiens

<400> 468

```

Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
  1              5              10             15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
      20             25             30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
      35             40             45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
      50             55             60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65              70              75              80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
      85              90              95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
      100             105             110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469

<211> 381

<212> DNA

<213> Homo sapiens

<400> 469

cttgtgcaca cgttattttt ccaatacaaa tagtttaaaa agtaaactcc aaatacctat
 60
 aagccccctc aaagcacctt ccaaatatga accttggtta tgcccaagggt ccagaggggt
 120
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact
 180
 ccctgggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
 240
 tgacccaaaa tccattcggc cctgggatact ggagaggcag aggcctctgc tgatgagaag
 300
 ccctgagttc ctggctagct gtggttaacc acaaaaaatg cgggggggtga tgattttcga
 360
 agtccatcgg caaagaaaga c
 381

<210> 470

<211> 110

<212> PRT

<213> Homo sapiens

<400> 470

Met	Asp	Phe	Glu	Asn	His	His	Pro	Pro	His	Phe	Leu	Trp	Leu	Thr	Thr
1				5					10					15	
Ala	Ser	Gln	Glu	Leu	Arg	Ala	Ser	His	Gln	Arg	Pro	Leu	Pro	Leu	
			20					25				30			
Gln	Tyr	Pro	Gly	Pro	Asn	Gly	Phe	Trp	Val	Lys	Ala	Ser	Leu	Pro	Gln
		35				40					45				
Pro	Gly	Gly	Pro	Gly	Phe	Met	Glu	Tyr	Arg	Leu	Glu	Ser	Arg	Glu	Ser
		50			55					60					
Ala	Trp	Gly	Pro	Arg	Gln	Leu	Ser	His	Ala	Pro	Gly	Ser	Trp	Ala	Phe
65					70				75					80	
Leu	Gly	Asp	Pro	Ser	Gly	Pro	Trp	Ala	Leu	Thr	Arg	Phe	Ile	Phe	Gly
				85				90				95			
Arg	Cys	Phe	Glu	Gly	Ala	Tyr	Arg	Tyr	Leu	Glu	Phe	Thr	Phe		
			100				105						110		

<210> 471

<211> 378

<212> DNA

<213> Homo sapiens

<400> 471

accggtgact acctcgagca ctggattgac atgggtaaaa agggcgggcga ccgcatgccca
 60
 gaggtcttcc tggttaactg gttccgcccgc ggcgacgatg gccgcttctc gtggccgngg
 120

cttggcgaaa acttcccggt cctanagtgg atcatcgacc gcattgaagg caacgtagag
 180
 gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
 240
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgcgttg acccgaagga atgggaaggc
 300
 gatatgcaag acaacgccga gtacctgaac ttctctgggt cccgcgtgcc cgagggaagt
 360
 tggaaccagt tccgcgcc
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5					10					15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
			20					25					30		
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
			35				40					45			
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
		50				55					60				
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65				70						75				80	
Asp	Phe	Asp	Val	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Pro	Lys
			85				90					95			
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
			100				105					110			
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
			115				120					125			

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaagg acccatccca tgccacctgt cctagaaat gtttccctt
 60
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
 120
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctccacc
 180
 ctgcttccat ttccctctcc agggaacagg tgtacctccc ctctccctg tcctcctcag
 240
 atgccccagg ggctctctac ttcatctctg ccgaccctgc caggagtggc ctcaggggta
 300
 gaggttccta gttggagaat ttgcttgac gaaggtgaa
 339

<210> 474

<211> 97

<212> PRT

<213> Homo sapiens

<400> 474

```

Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1           5           10           15
Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
      20           25           30
Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
      35           40           45
Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Cys Pro Pro Gln
      50           55           60
Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65           70           75           80
Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
      85           90           95
Glu

```

<210> 475

<211> 345

<212> DNA

<213> Homo sapiens

<400> 475

```

acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc
 60
agcgccctgcc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtcccacagc cataatcccc
 180
aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa
 240
ggtaaaatat ctccagatcc gggctctctg ggcgactcgc tatgtggggg tccctgaagc
 300
ctttgatgga tcttgtaga agtgggttgt tcatcttggg gtttt
 345

```

<210> 476

<211> 111

<212> PRT

<213> Homo sapiens

<400> 476

```

Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1           5           10           15
His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
      20           25           30
Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
      35           40           45
Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
      50           55           60
Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

```



```

65              70              75              80
Pro Ala Trp Arg Arg Gly Leu Ser Gly Arg Arg Trp Gly Ala Pro Ser
              85              90              95
Lys Ala Trp Lys Glu Ala Gln Ser Leu Glu Gly Thr Leu His Ala
              100              105              110

```

<210> 477

<211> 422

<212> DNA

<213> Homo sapiens

<400> 477

```

acgcgtggcc gagccagcgt gctcaaggaa atgggtcaacg gcactcttat taacggctgg
60
gactctcccc aggtggaacg ggcactggac ctgtgcatgg cgtgcaaaagg gtgcgccccga
120
gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaataatc
180
cgtcaccgtc tccgccctcg ctcccacctg acgatggggc tgctgccccat gtgggaacgt
240
ttgctcaate ggaccccagg agcggcgtcg ctggctaacg cagtgtcttc gatgccggtc
300
ttgcacagtc ttgctagatg gacagccggg gtggatcagc gtcgtcccct cccccattc
360
cagccctcgg ccagattggc cagtcgcgag gccgccccgg ttaaggagat tgtggcggat
420
cc
422

```

<210> 478

<211> 140

<212> PRT

<213> Homo sapiens

<400> 478

```

Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
1              5              10              15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
              20              25              30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
              35              40              45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
50              55              60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65              70              75              80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
              85              90              95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
100              105              110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
115              120              125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
130              135              140

```

<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
 cgcggtggcca ttggccgggc gctggtgctg caccgcgac tgggtattgc cgatgagccg
 60
 atctcgccgt tggacatgac catccagaag cagattcttg agctgttcga ggccttgacg
 120
 gcgcagtacg gctttgcttg cctgttcacg tcccacgacc tggcagcggg ggaacgcacg
 180
 gcccaccggg tggcggtgat gagcgagggc aggggtgggtg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgacgca ccctacacc cgcaagctgc tggccgcgcg cagccccttg
 300
 gagaaacttg aaaacgggtg ctaccgcacg cgccaggggc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg
 60
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc
 120
 cctgcctcgc cggcttgccg tggcttcctc agtggttagga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgccctgtct cccagcaggg cccacaanca
 240
 cccagtcag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
 300
 gcctttctc ctgcaggacc aggaaccgc tgccctgtcc ctgccccagg aaacctcag
 360
 taaatcccc gtcatttgag ttccccctca gcgccagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgcy t
 441

<210> 482

<211> 120

<212> PRT

<213> Homo sapiens

<400> 482

Lys	Leu	Leu	Thr	Val	Ala	Phe	Ser	Leu	Leu	Asn	Met	Ser	Ser	Ile	Ser
1				5					10					15	
Pro	Thr	Tyr	Trp	Ala	Lys	Ser	Cys	Leu	Cys	Phe	Gly	Thr	Ser	Ser	Lys
			20					25					30		
Thr	Thr	Pro	Leu	Asp	Gly	Ala	Phe	Pro	Ala	Leu	Pro	Ala	Cys	Ala	Gly
		35				40					45				
Phe	Leu	Ser	Val	Arg	Ile	Thr	Ile	Thr	Leu	His	His	Glu	Ser	Arg	Arg
	50				55					60					
Pro	Ser	Pro	Cys	Asp	Cys	Cys	Pro	Cys	Ser	Gln	Gln	Gly	Pro	Gln	Xaa
65				70					75					80	
Pro	Ser	Pro	Gly	Pro	Gly	Ser	Arg	Trp	Val	Ala	Asp	Ala	Gln	Glu	Trp
			85						90					95	
Gly	Ser	Gly	Ser	Ala	Ser	Ser	Pro	Ala	Gly	Pro	Gly	Asn	Arg	Cys	Pro
			100					105					110		
Val	Pro	Ala	Pro	Gly	Asn	Pro	Gln								
			115				120								

<210> 483

<211> 330

<212> DNA

<213> Homo sapiens

<400> 483

acgcgttcac tccctgatgg ccacgcacga gctaacggag ggatggggcg aaggggaaggc
 60
 caagggttgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
 180
 agcgtctgcc cagccacaga tccctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctggggcc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1 5 10 15
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
 20 25 30
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
 35 40 45
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
 50 55 60
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
 65 70 75 80
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
 85 90 95

<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
 60
 gccacagtctc gcgatcgccg cattcgcccg gccggaatcg agaaggaatg cgtggacgta
 120
 cggggggatgc caaaggaatc ttgtcgaggg cttcgcgccg ctcgacgtgg atcacctgta
 180
 cccgacggagc gtgggggaagc cgtcccgcaa gctcacggga ctcgcgcaca tcgatgtgcg
 240
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctcgcgcgac gcctcagcgg
 300
 tgggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtgcgc gttatgtcgg
 360
 cattccatt cctcggg
 377

<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1 5 10 15
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
 20 25 30
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
 35 40 45
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
 50 55 60
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

```

65              70              75              80
Pro Arg Ser Pro Gln Arg Trp Phe Pro Thr Ser Ala Gly Thr Trp Arg
      85              90              95
Arg Val Ala Trp Arg Ser Pro Leu Cys Arg His Ser His Ser Ser
      100              105              110

```

<210> 487
 <211> 459
 <212> DNA
 <213> Homo sapiens

```

<400> 487
nnacgcggttaa gatcgattgt ggatcagcac cgatgctggt cccccgacg ttgttgttgg
60
cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttgggtg ttccactga ggtaaagaat
120
agtgagtttc gtgtggctgt gacgccggcg ggtgttcattg cggttgggttg tcgtgggtcat
180
gaggtgttgg ttcaggctgg tgcgtggtgt gggttcgggta ttccggattc ggatttttgtg
240
ggtgctgggtg cgccgggttgt ggggtgatgtg gaggcgggtg ggggtgatgc tgatttgggtg
300
ttgaaggtga aggagcctgt tgcggaggag tatgggagggt tgcataagggt tttgggtcttc
360
tttactgtatc ttcatattggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacgggtggag ttggccgat
459

```

<210> 488
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 488
Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
1      5      10      15
Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
20      25      30
Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
35      40      45
Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
50      55      60
Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
65      70      75      80
Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
85      90      95
Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
100      105      110
Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
115      120

```

<210> 489
 <211> 542

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgtactgag tgcgggtggtg gatggcgacg acagtggcaa gccgctgctc
 60
 aaccagcacg gttgctacaa agtgcgcttt ccatttaccg cgcgtcaaaa gcccgacact
 120
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac
 180
 ttcccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggctgctg accaaactcg gaaaccccg gcatggtcgt tgagcgtaac
 300
 gccaccacga gcgccttctc cacggccgga gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct ggggtgcgct ggcggaaca cegttcttcac actgggcaat
 420
 ggcaaaagtcg ccggcgcgca actgcgcacc aacgccccat atgcaattga catcgctctc
 480
 gctcaaacac gaagtgcggc gcgtgtactc attgtcgatg ggcaccgggg acccgcgagg
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly
1				5					10				15		
Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe
			20					25					30		
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg
			35				40				45				
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu
		50				55					60				
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg
65					70					75				80	
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val
			85					90						95	
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His
			100					105					110		
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly
		115					120					125			
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala
		130				135					140				
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe
145					150					155				160	
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg
				165				170						175	
Gly	Pro	Gly	Gly												

180

<210> 491

<211> 825

<212> DNA

<213> Homo sapiens

<400> 491

nacgcgtcga ggcgacggtc ggcgcgctca tggcgactgt tctcgagggc acatgggaac
 60
 gcatcgggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tggggcgccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggaggggtca atcgaattgg
 240
 tcgacgtgtc ggtcgggtgac gaagagcgca gagtgcagct caccatgaag ggagcatgcc
 300
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg
 360
 natcgcgca gccgggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaaagccac tcgtagacgc attcctcctc ggcatccaat
 480
 tcctccgggg ccgcccggag gacttcgtcg gcagtaacct ggtgatgat cctagcctg
 540
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgctg catcacaggg
 600
 ttcattggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
 660
 tcttcccagc gcgcccgcgac atcctcggcg tcatggtcga catggaattg cgcgtcagct
 720
 gagtgcgtgt cacgataggg gctggggcagg atcaatcgac gcacctcgct gtccctctgg
 780
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
 825

<210> 492

<211> 58

<212> PRT

<213> Homo sapiens

<400> 492

Met Asn Gly Trp Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493

<211> 863

<212> DNA

<213> Homo sapiens

<400> 493

nacgcgttcc aacctcgta aaacggctat cgcaggaaat gacccaact ggggtcgcat
 60
 cctcgcggcg atcggatgtg ttcttgagaa tatagctccc ttccgatccc accagggtga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgtcgatatg agggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata ggcggtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggg ttccagggcg cactgtcgtc
 420
 gtgaaatatg gcggcaacgc gatgggtgat ccggtctgc agcaggcctt cgccgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacgggtg tggccctcag
 540
 atcaatgccca tgcttgctga atccgctacc ccggtggagt tccgtaattg tttgcccgtg
 600
 acatctccgg aggtcatgga ggttgctcgg atggtgctcg tcgggcaggg gggccgtcag
 660
 ctcgtaaac gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
 720
 ggcctttttt cggcccgaa gtccgggga attgttgatg gcgagcaaat agacatgggt
 780
 ttatggggag acatcggtga cgtcaacatc gatctcgta tctctatgct tgatcgggtg
 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala
 1 5 10 15
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg
 20 25 30
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val
 35 40 45
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala
 50 55 60
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile
 65 70 75 80
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly
 85 90 95
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu


```

          100              105              110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115              120              125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130              135              140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
      145              150              155              160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165              170              175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180              185

```

<210> 495

<211> 514

<212> DNA

<213> Homo sapiens

<400> 495

```

gcgcgcgaca ccggtgcccc gattagcgtg ccagtggttg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tccccgggcc ttcgatgacc ttgagcccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cgccaagatt
240
ggcctctttg gcgcgcgttg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcggtt ttcgccggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcataacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccggggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtaactg ctgtgggacc ttgg
514

```

<210> 496

<211> 171

<212> PRT

<213> Homo sapiens

<400> 496

```

Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1          5          10          15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20          25          30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35          40          45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50          55          60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
      65          70          75          80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```



```

      35              40              45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
 50              55              60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
 65              70              75              80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85              90              95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100              105              110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115              120              125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130              135              140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
      145              150              155              160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165              170              175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180              185              190

```

<210> 499

<211> 444

<212> DNA

<213> Homo sapiens

<400> 499

```

acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
 60
ctgccttctg cctgaccctc tggcttctca agcagctctat acgtgagaag ccctttcttc
 120
aagtgaagaac ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
 180
tcctcaactg gggggttga ggaggttact tcactttctca aaacctcaat ttccttatct
 240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaaatgc ctggcacagt
 300
agggcagtta ccgtcatgga gaacagaaaag gccccgagct atcctggatg tggtgagaat
 360
gggtccctgga tcctgcctgc tcggcctttt cattctcttc ttacacctaca ggctccacca
 420
aagggcctct gaaaaacacag ggtg
 444

```

<210> 500

<211> 105

<212> PRT

<213> Homo sapiens

<400> 500

```

Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
 1              5              10              15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20              25              30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

35	40	45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe		
50	55	60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu		
65	70	75
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr		
85	90	95
Gln Leu Asn Thr Ala His Pro Ser Arg		
100	105	

<210> 501

<211> 800

<212> DNA

<213> Homo sapiens

<400> 501

```

agatctgac cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
ggtagctcctt attcaatgag aggcctgagg tgagaccgc catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gacctgttac tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccggtca aagctgagga gtttgtgggtg
300
ctttctcagg aaccttctgt caggaaacc attgcacca aaattgcaag accttcata
360
gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcatggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgcgctact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcaactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttccag ggaagtggga agcttttagct
780
atcttgcttc agaaactgaa
800

```

<210> 502

<211> 103

<212> PRT

<213> Homo sapiens

<400> 502

```

Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
1          5          10          15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

                20                25                30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
   35                40                45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
   50                55                60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
   65                70                75                80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
   85                90                95
Ala Leu Asn Tyr Leu Glu Ser
   100

```

<210> 503

<211> 538

<212> DNA

<213> Homo sapiens

<400> 503

```

nnacgcgttg tcgtctctcc gatcattgat tttgttgtat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc atttgtgaaat ttcataaggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttcagact attggaaggg gaaggtcccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaaagcga aactgggtcat cgggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgtg
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaac caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggccct tcacgcgt
538

```

<210> 504

<211> 179

<212> PRT

<213> Homo sapiens

<400> 504

```

Xaa Arg Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
 1                5                10                15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
 20                25                30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
 35                40                45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
 50                55                60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
 65                70                75                80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```


	100		105		110									
Val	Ile	Ala	Arg	Leu	Ser	Asp	Leu	Gly	Trp	Gly	Gly	Ala	Leu	Arg
	115		120		125									

<210> 507

<211> 499

<212> DNA

<213> Homo sapiens

<400> 507

gcccggcggtgt tcaacctcat ggtgtggggc ttcattaccg acgtcatcga tgcccaggag
 60
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgc aaa
 120
 cttgcccagg ccattgcccg tggaatcgcc ggagccatgc tgacgatgat cggctaccag
 180
 tctctctccc aaggtggtgc cgttcagtcg ggtccgctcg tcaatcacct gtacacgctc
 240
 gccaccgcga tcccgaagat ctgctgcctc ggcgctgccc tgctcatgct gggctaccgc
 300
 ctcaccgcgc acaagggtgt gcgcaacgcc gacgagttgg ctcgtcgcca cgcagtacag
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
 420
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc
 480
 cgtcacattt gtgacgctg
 499

<210> 508

<211> 125

<212> PRT

<213> Homo sapiens

<400> 508

Ala	Gly	Val	Phe	Asn	Leu	Met	Val	Trp	Ala	Phe	Ile	Thr	Asp	Val	Ile
1			5					10					15		
Asp	Ala	Gln	Glu	Val	Met	Ser	Gly	Glu	Arg	Glu	Asp	Gly	Val	Ile	Tyr
		20					25				30				
Gly	Val	Asn	Ser	Phe	Ala	Arg	Lys	Leu	Ala	Gln	Ala	Ile	Ala	Gly	Gly
		35				40				45					
Ile	Gly	Gly	Ala	Met	Leu	Thr	Met	Ile	Gly	Tyr	Gln	Ser	Ser	Ser	Gln
	50				55				60						
Gly	Gly	Ala	Val	Gln	Ser	Glu	Ser	Val	Val	Asn	His	Leu	Tyr	Thr	Leu
	65			70				75						80	
Ala	Thr	Ala	Ile	Pro	Thr	Ile	Cys	Cys	Leu	Gly	Ala	Ala	Leu	Leu	Met
			85					90					95		
Leu	Gly	Tyr	Pro	Leu	Thr	Arg	Asp	Lys	Val	Val	Ala	Asn	Ala	Asp	Glu
	100					105					110				
Leu	Ala	Arg	Arg	His	Ala	Val	Gln	Ala	Glu	Gln	Asn	Ser			
	115					120					125				

<210> 509

<211> 360

<212> DNA

<213> Homo sapiens

<400> 509

ttggccatgg atttggtctcg caagttcagt cccaaagatg tcacgctcta tctaattggac
 60
 ttccgggacca atggtgtggc accactaggc caattaccac aggtggcgga caccttgctt
 120
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
 180
 cgtaagaagc tcttgtccga ctacgggtgtt ggtacactag agctctaccg tcaggctagc
 240
 ggcagcaag agccggccat cgtcatcctg ctggacagtt atgagtcctat gaaggaagag
 300
 gcctatgaag cggagctctt cagcgtcttg gtgcggatct cccgggaagg tctcagcatc
 360

<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

Leu	Ala	Met	Asp	Leu	Ala	Arg	Lys	Phe	Ser	Pro	Lys	Asp	Val	Thr	Leu
1				5					10				15		
Tyr	Leu	Met	Asp	Phe	Gly	Thr	Asn	Gly	Val	Ala	Pro	Leu	Gly	Gln	Leu
			20					25					30		
Pro	Gln	Val	Ala	Asp	Thr	Leu	Leu	Leu	Asp	His	Thr	Glu	Lys	Ile	Ala
		35					40					45			
Lys	Phe	Val	Arg	Ile	Met	Glu	Arg	Glu	Leu	Asn	Arg	Arg	Lys	Lys	Leu
	50				55					60					
Leu	Ser	Asp	Tyr	Gly	Val	Gly	Thr	Leu	Glu	Leu	Tyr	Arg	Gln	Ala	Ser
65				70					75				80		
Gly	Gln	Gln	Glu	Pro	Ala	Ile	Val	Ile	Leu	Leu	Asp	Ser	Tyr	Glu	Ser
			85					90					95		
Met	Lys	Glu	Glu	Ala	Tyr	Glu	Ala	Glu	Leu	Phe	Thr	Leu	Leu	Val	Arg
			100					105					110		
Ile	Ser	Arg	Glu	Gly	Leu	Ser	Ile								
			115				120								

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

ntcgcgaacc gcgctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc
 60
 actgcgttcg gcgatgccgg catcgccagc atcgggcgca agatgcagga cgatctcgac
 120
 gacgggatgg actggctggg caaggagggc atcgctcgaca agggccgggt gtgcatcgtc
 180
 ggggcctcct atggcggcta tgccgcgatg tggggcgcca tccgcaatcc cgaacgctat
 240

cgctgcgcgg cgagcctggc ggggggttgcc gattaaggcc atgctcaaat ataaccggcg
 300
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 c
 361

<210> 512
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 512
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 1 5 10 15
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
 65 70 75 80
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
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 120
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatgggtgt cttcttatgt ggggtgaaat gcactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcgccg
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 360
 gacacgcgt
 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

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      1             5             10             15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20             25             30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35             40             45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50             55             60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65             70             75             80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85             90             95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100             105             110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115             120

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<210> 515
<211> 387
<212> DNA
<213> Homo sapiens

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<400> 515
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120
tccttcaagc tcttcgtggt ctacaagggc gtcttctctc cggacgacgg gcagatcctg
180
cgggcggttc agaagggcgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
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360
gccgacctga cgggtgcgcc gttgtac
387

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<210> 516
<211> 129
<212> PRT
<213> Homo sapiens

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<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
      1             5             10             15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
      20             25             30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
      35             40             45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
      50             55             60
Lys Gly Ala Asp Asn Gly Ala Met Met Met His Ala Glu Asn Gly
      65             70             75             80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```

```

      85              90              95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu
      100              105              110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
      115              120              125
Tyr

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<210> 517
 <211> 377
 <212> DNA
 <213> Homo sapiens

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<400> 517
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agaccccttc gggccaacag tggggagggg ctgccgtctg agccactgtt ccgacagggg
120
attcgcgagt tccgggggag ctgggggactg agctgcgggc ctctctgggt ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt
240
ccctgagctt cccaggaga aggggggcca atttgagct tgcttttcac ctgagatgag
300
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360
aggaagggga ggggccc
377

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<210> 518
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 518
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
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Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
20      25      30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
35      40      45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
50      55      60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65      70      75      80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
85      90      95
Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
100      105      110
Pro Thr Ser Pro Ser Arg
115

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<210> 519
 <211> 311

<212> DNA

<213> Homo sapiens

<400> 519

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 120
 aagaaattga taatttttcta ggaaacatg acttaccaaa attaactcta gaaaagaatc
 180
 gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgccca aacctggaat
 240
 tcatgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc
 300
 cagaacttaa g
 311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
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Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20					25					30		
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
			35				40					45			
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50					55					60				
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65					70					75				80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85						90						

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

<400> 521

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 120
 accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc
 180
 ctgtgtaccg gccgtaccgg cgtgcgcccc gtgggtggtag aaacttatgc caaggcgctc
 240
 aacgccggca tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg
 300
 gccccgctgg ctcaactgcgc cctagcgctg ttgggtgagg gtgaggtacg cn
 352

<210> 522
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 522
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 Ala Arg Arg His Ile Pro Glu Glu Met Arg Ala Gln Leu Gln Leu Ser
 20 25 30
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu Glu
 35 40 45
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
 50 55 60
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
 65 70 75 80
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
 85 90 95
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly
 100 105 110
 Glu Gly Glu Val Arg
 115

<210> 523
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 523
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 tcagagccac caagctgcgg caccatctaa ggagaacatg tcccctggag gtctctgtag
 120
 aagctcctgg ttgagaagc cctgaagctg ggtggcatca atgtccagcc tctgtctgagc
 180
 atatctgttg aaaatgcttt gttgggagcc atgttctgaa gggcttccct tcattctgag
 240
 gttgaaatgg ctgctcaggt gcctgtcact gtctggcatt ttcaggaaga ttcggagcaa
 300
 gaactccgct gattttctcc gtgtctgtgc aaccacaaca tagttcccag ggctcagatg
 360
 gtaagtcagtg gtgaagttgc ggcggaattt attatttttag ctttgagacag tgtttctgaa
 420
 cgaggaaaaa aacacgggtg gaaattttctc ccggaaccgc tgtgagccag ccagaatcac
 480
 ttggaaatcg agtggaatt ttgcatcttc tgettcca aa tttgatgggtg tgacagcaac
 540
 tgtgacgcac acgacaacat tgggtgccttc cattggctct tgcacagaga agttgaattg
 600
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 693

<210> 524

<211> 193

<212> PRT

<213> Homo sapiens

<400> 524

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Asn Phe Ser Val Gln Glu Pro Met Glu Gly Thr Asn Val Val Val Cys
          20           25           30
Val Thr Val Ala Val Thr Pro Ser Asn Leu Lys Ala Glu Asp Ala Lys
          35           40           45
Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg
          50           55           60
Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln
          65           70           75           80
Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu
          85           90           95
Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala
          100          105          110
Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His
          115          120          125
Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His
          130          135          140
Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp
          145          150          155          160
Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr
          165          170          175
Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp
          180          185          190
Leu

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<210> 525

<211> 1101

<212> DNA

<213> Homo sapiens

<400> 525

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120
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180
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240
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300
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360
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420

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aggtggaaaa gaaacttggg ctttctcaag gcggttagaca cgaaccgagc aagcgtcggc
 480
 caagactctc ttgagccag aagcttcaca gacctgctgc tggatgatgg gcaggacaa
 540
 aacactcaga tcgaggagga tacagaccac aattactata tatctcgaat atatgggtcca
 600
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 660
 aagattcatg gaattattgtc caatactcat cggcaagctg caagagttaa tctgtccttc
 720
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 780
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 840
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 900
 gcacttgtag tccagtggga ccatgtacat ctccaggata attataacct gggaagcttc
 960
 acattccagg caaccctgct catggatgga cgaatcatct ttggatacaa agaaattcct
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 1080
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<210> 526

<211> 290

<212> PRT

<213> Homo sapiens

<400> 526

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Leu	Cys	His	Phe	Thr	Asp	Gln	Phe	Gln	Phe	Ala	Asp	Gly	Lys	Pro	
			20			25						30			
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe	Pro
		35				40					45				
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His	Arg
	50					55					60				
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg	Ala
	65				70				75					80	
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu	Leu
			85					90						95	
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr	Asp	
		100				105						110			
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala	Ser
		115				120						125			
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val	Lys
		130				135					140				
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val	Asn
	145				150					155				160	
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile	Thr
			165					170						175	
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg	Met

```

      180              185              190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro
      195              200              205
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala
      210              215              220
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
      225              230              235
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
      245              250              255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
      260              265              270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His
      275              280              285
Arg Ile
      290

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<210> 527

<211> 5343

<212> DNA

<213> Homo sapiens

<400> 527

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120
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180
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420
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480
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660
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780
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900
aaacttggtg agcagggtcc gcagatcctc agtgtccaga gagtctacat tcagacaagg
960

```


gaagagaagc gtattaacct gaccattggt agcagagcct atttgetgcc caacacatcc
1020
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1080
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3360
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3900
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4140
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<210> 528

<211> 886

<212> PRT

<213> Homo sapiens

<400> 528

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Glu Ala Asn Ser Leu	Gly Val Thr Trp His	Lys Met Arg Gln Met Trp			
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Asn Asn Lys Asn Asp	Leu Tyr Leu Asp Asp	Asp His Ile Ser Asn Gln			
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Pro Phe Leu Arg Ala	Leu Leu Gly His Cys	Ser Asn Ser Ala Gly Ser			
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<210> 529

<211> 4566

<212> DNA

<213> Homo sapiens

<400> 529

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<210> 530

<211> 802

<212> PRT

<213> Homo sapiens

<400> 530

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Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro Glu Gly Cys
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Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly Ala Arg Gly Asp
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Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
65           70           75           80
Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
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Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
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Ile Pro Gly Lys Val Gln Phe Phe Ser Ser Glu Gly Ser Asp Thr Ser
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Val Pro Ile Pro Val Val Pro Leu Arg Gly Val Asp Asp Ser Tyr Pro
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Pro Gln Lys Lys Ser Phe Met Met Leu Lys Tyr Met His Asp His Tyr
145          150          155          160
Leu Asp Lys Tyr Glu Trp Phe Met Arg Ala Asp Asp Val Tyr Ile
          165          170          175
Lys Gly Asp Arg Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu
          180          185          190
Pro Leu Phe Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly
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Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
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225          230          235          240
Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly
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Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala Ile Thr Leu His
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Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu His Ser Tyr Met Leu
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Asp Leu Gln Leu Gly Ile Pro Pro Ser Phe Met Arg Phe Gln Pro Arg
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Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
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Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
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Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg
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Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys
          500                      505                      510
Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu
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Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe
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Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile
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Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe
          595                      600                      605
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Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe
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Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe
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Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys
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Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp
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Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val
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Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
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Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg
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Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
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Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
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Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
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<210> 531

<211> 321

<212> DNA

<213> Homo sapiens

<400> 531

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<211> 96

<212> PRT

<213> Homo sapiens

<400> 532

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			20					25				30			
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
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Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
	50				55					60					
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
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<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

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      65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
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<211> 404

<212> DNA

<213> Homo sapiens

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240
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300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
360
cgggcgctgt tcgaatcgtc catcgacaac ctgctcgaac cggt
404

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<210> 538

<211> 118

<212> PRT

<213> Homo sapiens

<400> 538

```

Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
      1              5              10              15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
      20              25              30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
      35              40              45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
      50              55              60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
      65              70              75              80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
      85              90              95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
      100              105              110
Asp Asn Leu Leu Glu Arg

```

115

<210> 539

<211> 534

<212> DNA

<213> Homo sapiens

<400> 539

```

nnacgcgtga aaaagaagaa aatgaaggaa agcgaggctg acagcgaggt gaagcatcaa
60
ccaattttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc
120
ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct
180
gatggggcaa cagtgcagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
240
attagtccag aactggctga aagcacggta atagccaaag tcaatgggtga actgtgggac
300
ctggaccgcc cattggaagg ggactcttct cttagagctgc ttacatttga taatgaggaa
360
gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgtgtgaaac
420
tacattatat aagaggccac atattgaatt cacgaatgtt gagttttttg ggggtttctta
480
agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa
534

```

<210> 540

<211> 143

<212> PRT

<213> Homo sapiens

<400> 540

```

Xaa Arg Val Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu
1           5           10           15
Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu
20          25          30
Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys
35          40          45
Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
50          55          60
Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
65          70          75          80
Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
85          90          95
Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
100         105         110
Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
115         120         125
Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
130         135         140

```

<210> 541

<211> 551

<212> DNA

<213> Homo sapiens

<400> 541

```

ggtaccgagc tgcgcgtgtg gtatgcggcc ttctatgcc agaagatgga caagcccatg
60
ctgaagcagg ccggtcttgg cgtccacgct gcaggcacc cagaaaaacg cgcctccgtg
120
gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttctc ggagctgcag
180
ctcctcaatg gtaaggagga cgtgtgggga gcccagttg taaaactcct gtgtcgattt
240
ctctctgact tacgctgtca cctgtctgcy gctgtcgggg gtgtccaga ctttgccttg
300
tctgccccat tgcccccaa ttagtctgcc agaaccaagg ctttctcagg gtttaaagct
360
tctgggcagt ccgcttccc acccccagacc cctgcaggcc tcaactctca ctcctcctgg
420
ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
480
caggagccag ccgtggcatg tgttgtgcac tcttgctttt gttgtctcta cttgacagcc
540
ccctcacgcy t
551

```

<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

```

Met Asp Lys Pro Met Leu Lys Gln Ala Gly Ser Gly Val His Ala Ala
1      5      10      15
Gly Thr Pro Glu Asn Ser Ala Pro Val Glu Ser Glu Pro Ser Gln Trp
20      25      30
Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn
35      40      45
Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg
50      55      60
Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val
65      70      75      80
Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg
85      90      95
Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro
100     105     110
Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser
115     120     125
Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg
130     135     140
Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys
145     150     155     160
Leu Tyr Leu Thr Ala Pro Ser Arg
165

```

<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
 nnaaaagccgg acatgaatac cgcgattgct ggcaaaactg tcttgaccat cattctggcc
 60
 ggggggcaaa gcagcgcctt ggcgccgatg acgcgatcagg tggccaaacc agccgtgccc
 120
 ttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg
 180
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
 240
 gggcgctcct gggatctgga cgcacccgcg ggtggcctga aggtcatgcc gcccttttcc
 300
 ggccctgccc atgaggacgg tggcttttcc gaaggcaacg cacacgcgt
 349

<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr
 1 5 10 15
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
 100 105 110
 Asn Ala His Ala
 115

<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca
 60
 caagaaattg ttggtgtcat cacagggttct gcaatgccgg gtggttcagc aaaccgtatc
 120
 ccaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaacaa
 180

atgtataacg aactcaaaac agtgggattta actattcaaa atgctggcgg tgtacgcgca
 240
 gatattttac cggggaatgt aacctttaac gatgcttata cttctctacc ttctgggaat
 300
 acggtatata cctataaaat ggaaggttca ttagtgaaac aagtgcctga agatgcaatg
 360
 ctatttgctt tgggtccccc cccccccccc
 390

<210> 546
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 546
 His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys
 1 5 10 15
 Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met
 20 25 30
 Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro
 35 40 45
 Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu
 50 55 60
 Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Val Arg Ala
 65 70 75 80
 Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu
 85 90 95
 Pro Phe Gly Asn Thr Leu Tyr Thr Lys Met Glu Ser Ser Leu Val
 100 105 110
 Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro
 115 120 125
 Pro Pro
 130

<210> 547
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 547
 aagcttggtt ttctgatttt tattcaaatc tctatcatgg atgaagcatg cagtttcaga
 60
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcat
 120
 gaagcctcca acatatatttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
 180
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
 240
 tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcaactaaact cnnnnccnn
 300
 nnccnn
 306

<210> 548

<211> 90

<212> PRT

<213> Homo sapiens

<400> 548

```

Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
 1             5             10             15
Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
          20             25             30
Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
      35             40             45
Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
 50             55             60
Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
65             70             75             80
Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa
          85             90

```

<210> 549

<211> 780

<212> DNA

<213> Homo sapiens

<400> 549

```

nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat
60
gttttaatac tacacatatt gtctgtaagt atgaagagaa aggcataatca gaaatatctc
120
aattcagcga ttgaaatgt ttactttctg ttattgaaa attttgtgtc tttttcacca
180
tggtattttt ttctctctgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
240
gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt
300
tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
360
aagatttcta aggatgcagg gatgcccatc cagggccagg catgcttctg caaatatgca
420
cagggggcag acagcgtaga gcccatgttc cggcattcca agaacacata tctgggcta
480
cagcttatta tcgtcatcct gccggggaag acaccagtgt atcggaagt gaaacgtgta
540
ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaa
600
tctctcaaaa ctctgtcaaa cttgtgccta aagataaatg ttaactcgg agggatcaat
660
aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
720
gccgatgtca ctcattccac tgctggtgat ggaaagaagc cttctattgc tgctgttgta
780

```

<210> 550

<211> 192

<212> PRT

<213> Homo sapiens

<400> 550

```

Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1             5             10             15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
      20             25             30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
      35             40             45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
      50             55             60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
      65             70             75             80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
      85             90             95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
      100            105            110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
      115            120            125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
      130            135            140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
      145            150            155            160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
      165            170            175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
      180            185            190

```

<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

```

nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
120
gaaccgtctc cgtcgtcaat cgcaccgggc ccgcgggccc cgacgactgc agtaccaccg
180
actagttcgt cgtcggggccg ctgaccgatg cgcccatcgg cgggctcacc tggctggcgc
240
tagcggggggc ttcatgtgac ccataaccaca gcgtccgcta aattgccnc c
291

```

<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

```

Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1             5             10             15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

```

                20                25                30
Pro Thr Asn Ser Ala Pro Ser Glu Pro Ser Ser Ser Ile Ala
   35                40                45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
   50                55                60
Ser Gly Arg
65

```

<210> 553
 <211> 471
 <212> DNA
 <213> Homo sapiens

```

<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattgggtgca tatcatttca ctacaattaa acctcaactta
120
gggtgtgttt ccacaaaaga tcaacgtagt ttgtttatgg cagatttacc aggtttaatt
180
gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatattgagc gggtctgaag gtagagaacc tattgaagat
300
tataaaagta ttaatcaaga attagctgcy tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggattttacct gaatcacaag ataattttaa cttgttttaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcy t
471

```

<210> 554
 <211> 157
 <212> PRT
 <213> Homo sapiens

```

<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
 1          5          10          15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
 20          25          30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
 35          40          45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
 50          55          60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
 65          70          75          80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
 85          90          95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
100          105          110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
115          120          125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

```

```

      130              135              140
Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg
145              150              155

```

<210> 555
 <211> 300
 <212> DNA
 <213> Homo sapiens

```

<400> 555
tctagagatt gagaacaatt atggatacag aaatgggtga ttccgtcaaa tatattcgag
60
attcggaaatc atgtgaggct cgcgtgctgg agatcttagc cagaagggcg tccatgatgg
120
tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
180
ttaataaagt acctagaatt gtctgcctgc ttctccggct tagtggtgttc gtcgctgcgg
240
caatagggtgc ccgtgcggta tggggcggcg cttccggtaa tcccgatctt gttcacggt
300

```

<210> 556
 <211> 93
 <212> PRT
 <213> Homo sapiens

```

<400> 556
Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
1      5      10      15
Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
20      25      30
Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
35      40      45
Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
50      55      60
Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
65      70      75      80
Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
85      90

```

<210> 557
 <211> 678
 <212> DNA
 <213> Homo sapiens

```

<400> 557
atcttccccg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
60
gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcagggtctac
120
gtgttccccg ctacccacta tgtcgccggc ccggaacgta tggagcgggc catagcgctcc
180
atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag
240

```

gccccacggt tacgtatgcg tactacctac gatatacgaga tgatgcagca ggtcggtgcc
 300
 tgttgtggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccg ctcagccccg
 360
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atccccagtg
 420
 accgtcccg agattggcgg gatgtatgag ggggacatga gccgcaacgc gacattggta
 480
 gaacatggtt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
 540
 acccagcgga tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa
 600
 cgagctcacg gcgtcgctga acaaatcatt cgcccgacag gtctggtgga tccggagatt
 660
 atcgtcaagc ctacgcgt
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile	Phe	Pro	Val	Tyr	Glu	Glu	Asn	Ala	Leu	Arg	Val	Glu	Phe	Phe	Gly
1				5					10					15	
Asp	Glu	Ile	Glu	Ala	Leu	Thr	Thr	Met	His	Pro	Leu	Thr	Gly	Glu	Val
			20					25					30		
Ile	Ser	Glu	Asp	Glu	Gln	Val	Tyr	Val	Phe	Pro	Ala	Thr	His	Tyr	Val
		35					40					45			
Ala	Gly	Pro	Glu	Arg	Met	Glu	Arg	Ala	Ile	Ala	Ser	Ile	Gln	Gln	Glu
		50			55				60						
Leu	Glu	Glu	Arg	Leu	Ala	Val	Leu	Glu	Arg	Asp	Gly	Lys	Leu	Leu	Glu
65				70					75				80		
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Thr	Tyr	Asp	Ile	Glu	Met	Met	Gln
			85					90					95		
Gln	Val	Gly	Ala	Cys	Ala	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
			100				105						110		
Gly	Arg	Ala	Pro	Gly	Ser	Ala	Pro	Asn	Cys	Leu	Leu	Asp	Tyr	Phe	Pro
		115				120						125			
Glu	Asp	Phe	Val	Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
		130			135						140				
Ile	Gly	Gly	Met	Tyr	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Thr	Leu	Val
145				150					155					160	
Glu	His	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Lys
			165					170					175		
Phe	Asp	Glu	Phe	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Val	Tyr	Leu	Ser	Ala
			180				185						190		
Thr	Pro	Gly	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	His	Gly	Val	Val	Glu	Gln
		195				200						205			
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Glu	Ile	Ile	Val	Lys	Pro
210					215						220				
Thr	Arg														
225															

<210> 559
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 559
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa
 60
 tggaatgcag tcagagggaa ggaactgccn gcttaaaagt tcctatgctg cgctttccag
 120
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
 180
 tatggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
 240
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta
 300
 ggggtcaaaaa cattcagtct gggaccatat ctaga
 335

<210> 560
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 560
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1 5 10 15
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
 20 25 30
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
 35 40 45
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
 50 55 60
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
 65 70 75 80
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
 85 90

<210> 561
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 561
 ngcgcgcccc ctctctccgat ggcgcgagg atccagccca agcctctgac ccgcaagccg
 60
 atcctgctgc agcggatgga ggggtccag gaggtggtga atatggccgt gatcgtgccc
 120
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttctgttttg gttaaagaga
 180
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttaa tattgtcaga
 240
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat
 300

gatacctgttt gtccctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
 360
 ctggcactgc tctgagagtg ggcagcgctt gggaggttat cggaccagtg ctgtggcctc
 420
 aggcctgcaa tttgatgttg aaacccggca tgtgtttatc ggtgaccact caggcca
 477

<210> 562
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 562
 Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu
 1 5 10 15
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val
 20 25 30
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val
 35 40 45
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln
 50 55 60
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro
 65 70

<210> 563
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 563
 ccatggcaga cagggagctg agcggcctgc ggacccaggt gcaccagagc atggtgcccc
 60
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccceaaga
 120
 aaaggaaggg aaaaggcctc aaccttgccc agggctggaa cccacaggag gccagggtac
 180
 ggggcagacg gatggcagca gcactgcctg agagtgggg gagctccca ggggcagcaa
 240
 gtggcgggca gagggcttgg ccactgcac tggtttctgt gaccacagtt ggccctgccc
 300
 ctcccactgc gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
 360
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
 403

<210> 564
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 564
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser
 1 5 10 15
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

20							25				30				
Thr	Gly	Asn	Ala	His	Pro	Lys	Lys	Arg	Lys	Gly	Lys	Gly	Leu	Asn	Leu
35							40				45				
Gly	Gln	Gly	Trp	Asn	Pro	Gln	Glu	Ala	Arg	Val	Arg	Gly	Arg	Arg	Met
50							55				60				
Ala	Ala	Ala	Leu	Pro	Glu	Ser	Trp	Gly	Ser	Ser	His	Gly	Ala	Ala	Ser
65							70				75				
Gly	Gly	Gln	Arg	Val	Trp	Pro	Ser	Ala	Leu	Val	Ser	Val	Thr	Thr	Val
85							90				95				
Gly	Leu	Pro	Ala	Pro	Pro	Leu	His	His							
100							105								

<210> 565

<211> 311

<212> DNA

<213> Homo sapiens

<400> 565

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nctcttccat ggagcagccc catcttcact ctccacctgg ggccaggcct tccacagcag
60 ccaccaccaca ggcaccacag agaggctgcg cggaggacac aggagagagg gagccacgg
120 gcaagatctc caccgctttt ccagctccc tgggtcagcc ccacgggacc tctctctctc
180 ttctccacat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240 gcttggcgcg cacagacctg gacaatgtcc cagttagggc tggaggtgct agaagggcac
300 agggggcccc n
311

```

<210> 566

<211> 101

<212> PRT

<213> Homo sapiens

<400> 566

[illegible]

<210> 567

<211> 929

<212> DNA

<213> Homo sapiens

<400> 567

atcacatcgg tcgctgaacc ccgacgagcc tcacctgtc gaaatattca tccttgagat
 60
 cagcccaagt gccgtcgacc tctacctcgg tgagggctgc gggcggtgac caacagccga
 120
 cctcgtcttc ggctccactc atggcggaac gttccgtgc cagtcggggg atcgtcgggg
 180
 catgggggat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgccgacgca
 240
 cggatcagat gccgcagtaa tagagggctc gcatgaattc gaccggacaa tccagttgga
 300
 ggacgtccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
 360
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacagtcg gtgagcggac
 420
 gctcccgatc cccgcccga gcatgggatg cgggctgtgc atgtctcatg aggaacagag
 480
 tgtgcatgga tccatcgttg cacttcgcgg tcgccgcggt tctacgatgt tggcatgcg
 540
 ttgacggatt tgggcattga tgaggcgct acctaccgcc ggaacgtccc tgaacccgat
 600
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg
 660
 acggcggtgc ctttcgataa cgtcaggct ctgatagata cctgggattt gtcgtgggtg
 720
 gggtatcaca actctcgggt gagcgggtga ttacatgccc cagccgctgt gaacggccca
 780
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
 840
 gtcttcgctg ctgctggcta tgcacatata gtcgtcgatc cactgggtca ggggtggggc
 900
 caccacaacct tgacggaaaa ctgtccgga
 929

<210> 568

<211> 71

<212> PRT

<213> Homo sapiens

<400> 568

Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro
 1 5 10 15
 Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu
 20 25 30
 Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp
 35 40 45
 Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr
 50 55 60
 His Asn Ser Arg Val Ser Gly
 65 70

<210> 569
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 569
 ncgcaaacct caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
 60
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac
 120
 ctgctcgatta cttaatgggtc gaaggaacgg aacttgtgta ttcaaacatg gaagaactac
 180
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac
 240
 tcaaggaaca accaacagcc gttgctctct tctcggatgt tgataaacgg ccagagatta
 300
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcgggtactt
 360
 cccatgtcta n
 371

<210> 570
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 570
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1 5 10 15
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
 20 25 30
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
 35 40 45
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
 50 55 60
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
 65 70 75 80
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
 85 90 95
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
 100 105 110

<210> 571
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 571
 nacgcgtatc ttcgctgggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca
 60
 ccgggccttg acggggccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc
 120
 gtteccacct ccttcgccga cctcggcgctc cgagaagata tctgccaggc gctggaaggg
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tccccattgc cgtcgagggc
 240
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgctt cggcattacc
 300
 atcttgacgc gcatcaccct gcccggtgac gaagggtggg aagaactcac caccaaaggc
 360
 aagcccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg
 407

<210> 572

<211> 100

<212> PRT

<213> Homo sapiens

<400> 572

Leu	Thr	Glu	Thr	Thr	Val	Ser	Val	Pro	Thr	Ser	Phe	Ala	Asp	Leu	Gly
1				5					10					15	
Val	Arg	Glu	Asp	Ile	Cys	Gln	Ala	Leu	Glu	Gly	Val	Gly	Ile	Val	Ser
		20						25					30		
Pro	Phe	Pro	Ile	Gln	Ala	Met	Ser	Ile	Pro	Ile	Ala	Val	Glu	Gly	Thr
		35					40					45			
Asp	Leu	Ile	Gly	Gln	Ala	Arg	Thr	Gly	Thr	Gly	Lys	Thr	Leu	Ala	Phe
	50				55				60						
Gly	Ile	Thr	Ile	Leu	Gln	Arg	Ile	Thr	Leu	Pro	Gly	Asp	Glu	Gly	Trp
65				70				75					80		
Glu	Glu	Leu	Thr	Thr	Lys	Gly	Lys	Pro	Pro	Ser	Thr	Arg	Asp	Val	Pro
			85					90						95	
Leu	Pro	Gly	Ser												
			100												

<210> 573

<211> 393

<212> DNA

<213> Homo sapiens

<400> 573

acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
 60
 actacagaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
 120
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
 180
 ccaccgcga ggcagccgag gactttggcc gccgactggc tcacaccac cgagccgggg
 240
 cctcacacct gggggctgca cctgacgggt ttgttccga cgatgggtat atcgccgtg
 300
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc
 360
 gcatcgaacc atatatggac agtctcgacg ctg
 393

<210> 574

<211> 124

<212> PRT

<213> Homo sapiens

<400> 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Arg Pro Asp Gly Ala Gly
      20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
      35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
      50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
      65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
      85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
      100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
      115          120

```

<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

```

nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt ggggtagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct ggggttatgag gatggatcag aacttcagg gcctcagggg
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggcct tagagatggg tcaggaggcc tccaaggaat gggatcagca
360
gatgggcccgt gt
372

```

<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
      20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
      35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

<210> 577

<211> 432

<212> DNA

<213> Homo sapiens

<400> 577

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nagcgcgaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggtat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagttc caaaaccggt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtat accgcgaggt acgccaccta caagattccc tcaacgcgcg catgaccgcc
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtac tggccctgct ggactacatc
360
gacgaccgtc cagacggttt tcggatcatc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578

<211> 118

<212> PRT

<213> Homo sapiens

<400> 578

```

Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
      65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 579
 ggcccaaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc
 60
 ctgctcccag ggatcaccac cttaccacgc ggccacctg ccccccggt ccccgcggcg
 120
 cccggcccct ggctgcgcag acccctcttc agcctgaagc tgtccgacac agaggacgct
 180
 ttctctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtgtt cgtgcaggcg
 240
 gccttgggcc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccc
 300
 tcctcacgcc cgccccggg
 320

<210> 580
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
 1 5 10 15
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro
 20 25 30
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
 35 40 45
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
 50 55 60
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu
 65 70 75 80
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro
 85 90 95

<210> 581
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 581
 nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc
 60
 cagctcgcca tgggcttcaa gacgccagta cgcattgcaca gcgtcgacc caagaccgcg
 120
 gaagcccgcg aggtgcattt ccgcccgctc ctgttcaact atgccaagac cagcgtggag
 180
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgccggaa
 240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca
 300
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
 360
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
 419

<210> 582

<211> 139

<212> PRT

<213> Homo sapiens

<400> 582

Xaa	Asp	Gly	Asn	His	Ser	Leu	Trp	Lys	Glu	Leu	Asn	Gly	Gln	Leu	Asp
1			5					10					15		
Val	Gln	Phe	Phe	His	Val	Gly	Met	Gly	Phe	Lys	Thr	Pro	Val	Arg	Met
		20					25						30		
His	Ser	Val	Asp	Pro	Lys	Thr	Arg	Glu	Ala	Arg	Glu	Val	His	Phe	Arg
		35				40					45				
Pro	Ser	Leu	Phe	Asn	Tyr	Ala	Lys	Thr	Thr	Val	Asp	Thr	Lys	Gln	Leu
	50				55					60					
Thr	Gly	Asp	Leu	Gly	Phe	Ser	Gly	Phe	Lys	Leu	Phe	Lys	Ala	Pro	Glu
	65			70					75				80		
Leu	Asp	Arg	His	Asp	Val	Leu	Ser	Phe	Leu	Gly	Ala	Ser	Tyr	Phe	Arg
		85						90					95		
Ala	Val	Asp	Ala	Thr	Arg	Gln	Tyr	Gly	Leu	Ser	Ala	Arg	Gly	Leu	Ala
		100						105					110		
Ile	Asp	Thr	Tyr	Ala	Lys	Lys	Arg	Glu	Glu	Phe	Pro	Asp	Phe	Thr	Gln
		115				120						125			
Phe	Trp	Phe	Glu	Thr	Pro	Ser	Lys	Asp	Pro	Arg					
	130					135									

<210> 583

<211> 407

<212> DNA

<213> Homo sapiens

<400> 583

cttttgatca atgctgatgg cacgaagcta tcgaaaaagt cgggtgatgt ccgcgtagct
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 gattatatgg agcaggggatg ggagccggag acgctggtga acctagtgc cctcagggc
 120
 tatagctatg cgaatttggga gcatgctgat catgatgtca agacgatgaa cgaactcatc
 180
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt
 240
 gtgtttttga acaagcatca ctgacaaaat aagctggcgc tcgccacgac gtgtgagcag
 300
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
 360
 tcagatgatt atatcctgcg cgtcgtgaaca ctgggacccc aacgcgt
 407

<210> 584

<211> 135

<212> PRT

<213> Homo sapiens

<400> 584

```

Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
 1             5             10             15
Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
      20             25             30
Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
      35             40             45
Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
      50             55             60
Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
      65             70             75             80
Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
      85             90             95
Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
      100            105            110
Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
      115            120            125
Val Thr Leu Gly Pro Gln Arg
      130            135

```

<210> 585

<211> 502

<212> DNA

<213> Homo sapiens

<400> 585

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nnacgcgtcc tcgctggata tgaggctgtg aagaggggaac gctgcgtcat tgatctggac
60
gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt
120
cgggctcggt accgacattt cgttgtcgac gaataccagg acgtttctcc gctgcagcat
180
aggttgcttg aactgtgggt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac
240
caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgcgat
300
catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt
360
cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc
420
aggggagtc aattggtttc gcggggtcga tccgggcccg agcccatcta tcaggctctc
480
ggggcagatg cctccgaagc tt
502

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<210> 586

<211> 167

<212> PRT

<213> Homo sapiens

<400> 586

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Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val
 1           5           10           15
Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
           20           25           30
His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
           35           40           45
Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
           50           55           60
Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
65           70           75           80
Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
           85           90           95
Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
           100          105          110
Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
           115          120          125
Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
           130          135          140
Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
145          150          155          160
Gly Asp Asp Ala Ser Glu Ala
           165

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<210> 587

<211> 746

<212> DNA

<213> Homo sapiens

<400> 587

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gcgtctctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc
60
gagctgtgctg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggcccga
120
tgccctgcagc gctctgaccc ggccctctac ggggggtgtcc aggcgcgcct ccttggcgcc
180
ttcagcttcc gccactgtgc ggggttctctg tgccactgcc ctctcggtt tgaggggagcc
240
gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc
300
caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt
360
gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgac
420
actgtggcag gctatatctg caggtgcccc gagacctggg gtggggcgca ctgttctgtg
480
cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcac ccctatcttc
540
gagtcctgggg tccacagtta cgtctgccac tgcccacctg gtaccactgg accgttctgt
600
ggccagaata ccacctctc tgtgatggct gggagcccca ttcaggcatc agtgccagct
660
ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgcctg gaccttggcc
720

```

actcgcaatg acaccaagga aagctt
746

<210> 588

<211> 248

<212> PRT

<213> Homo sapiens

<400> 588

Ala Ser Cys Leu Glu Gly Leu Gly Ser Phe Arg Cys Leu Cys Trp Pro
1 5 10 15
Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser
20 25 30
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala
35 40 45
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg
50 55 60
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala
65 70 75 80
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn
85 90 95
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro
100 105 110
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu
115 120 125
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly
130 135 140
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val
145 150 155 160
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys
165 170 175
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro
180 185 190
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val
195 200 205
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu
210 215 220
Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala
225 230 235 240
Thr Arg Asn Asp Thr Lys Glu Ser
245

<210> 589

<211> 381

<212> DNA

<213> Homo sapiens

<400> 589

atctcacaag tacaattaca gtctcaagaa ctgagctatc agcaaaagca aggtcttcag
60
ccagtacctc tgcaagccac tatgagtgtc gcaactggta tccagccatc gcctgtaaat
120
gtgggttggtg taacttcagc tttaggtcag cagccttcca ttccagttt ggctcaaccc
180

cagctaccat attctcaggc ggctcctcca gtgcaaaactc cccttcaggc ggcaccacca
 240
 ccccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggcaccaggc
 300
 catgtcaaat cagtgaactca aaatcctgct tcagagtatg tacaacagca gccaatcttt
 360
 caaacagcaa tgcctccgg a
 381

<210> 590

<211> 127

<212> PRT

<213> Homo sapiens

<400> 590

Ile	Ser	Gln	Val	Gln	Leu	Gln	Ser	Gln	Glu	Leu	Ser	Tyr	Gln	Gln	Lys
1				5					10					15	
Gln	Gly	Leu	Gln	Pro	Val	Pro	Leu	Gln	Ala	Thr	Met	Ser	Ala	Ala	Thr
			20					25					30		
Gly	Ile	Gln	Pro	Ser	Pro	Val	Asn	Val	Val	Gly	Val	Thr	Ser	Ala	Leu
		35					40					45			
Gly	Gln	Gln	Pro	Ser	Ile	Ser	Ser	Leu	Ala	Gln	Pro	Gln	Leu	Pro	Tyr
		50				55				60					
Ser	Gln	Ala	Ala	Pro	Pro	Val	Gln	Thr	Pro	Leu	Pro	Gly	Ala	Pro	Pro
65				70						75				80	
Pro	Gln	Gln	Leu	Gln	Tyr	Gly	Gln	Gln	Gln	Pro	Met	Val	Ser	Thr	Gln
			85					90						95	
Met	Ala	Pro	Gly	His	Val	Lys	Ser	Val	Thr	Gln	Asn	Pro	Ala	Ser	Glu
			100					105					110		
Tyr	Val	Gln	Gln	Gln	Pro	Ile	Leu	Gln	Thr	Ala	Met	Ser	Ser	Gly	
		115					120					125			

<210> 591

<211> 684

<212> DNA

<213> Homo sapiens

<400> 591

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 120
 cgcgattcca ttccgggtcct cttccaccgc cagggggccgg gggaaaaatc cgtatcgaaa
 180
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 240
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 300
 gccaccgcgc cggtacgcaa cgagcagaag ctgggcccga acgaactgtg ctactgcggt
 360
 tcgggcaaga agtacaagca ctgccacggt cagatcagct aaggtcttta ccgatactg
 420
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 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttggttctgg
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 660
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 684

<210> 592
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 592
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 20 25 30
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 35 40 45
 His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg
 50 55 60
 Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His
 65 70 75 80
 Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val
 85 90 95
 Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly
 100 105 110
 Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys
 115 120 125
 His Gly Gln Ile Ser
 130

<210> 593
 <211> 615
 <212> DNA
 <213> Homo sapiens

<400> 593
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 gataccatcc ccgcgccgt aggccagcca cgatggtcga cggccaccat ccagacccca
 180
 gtcataccta ctacacgtgg tcgattcgtg atcgcccccg tcatgatgcg caccatcgac
 240
 ccggtttggca tggcccgcca tcacaccgat ctcggtcagg ttgcgaagt cattgtcacg
 300
 ccaaggatcg tcgatttggg cgctccggg gagctcgggg gtcagggtt cgacacaagg
 360
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 420

accggagact cgggtgcgacg cattcaactgg cgctccaccg ctcaccgcgg ggacctcatg
 480
 gtccgatacgg agggagcaggc ctggaacecca tccgtcgtca tctgtgtgga ttctcggggc
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<210> 594

<211> 205

<212> PRT

<213> Homo sapiens

<400> 594

Xaa	Arg	Val	Gln	Thr	Ala	Arg	Ser	Leu	Ala	Pro	Val	Arg	Ile	Ala	Leu
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Gly	Ser	Gln	Thr	Cys	Glu	Thr	Val	Thr	Val	Glu	Arg	Arg	Gly	Gly	Leu
			20					25					30		
Pro	Leu	Arg	Ala	Ala	Arg	Phe	Thr	Asp	Thr	Ile	Pro	Ala	Pro	Leu	Gly
		35					40					45			
Gln	Pro	Arg	Trp	Ser	Thr	Ala	Thr	Ile	Gln	Thr	Pro	Val	Ile	Pro	Thr
		50				55					60				
Thr	Arg	Gly	Arg	Phe	Val	Ile	Gly	Pro	Val	Met	Met	Arg	Thr	Ile	Asp
		65			70					75				80	
Pro	Phe	Gly	Met	Ala	Arg	His	His	Thr	Asp	Leu	Gly	Gln	Val	Ala	Glu
			85						90					95	
Val	Ile	Val	Thr	Pro	Arg	Ile	Val	Asp	Leu	Gly	Ala	Ser	Gly	Glu	Leu
			100					105						110	
Gly	Gly	Gln	Gly	Phe	Asp	Thr	Arg	Ser	Ser	Ala	Ile	His	Ala	Gly	Arg
		115				120						125			
Arg	Gly	Pro	Asp	Asp	Ala	Met	Val	Arg	Asp	Trp	His	Thr	Gly	Asp	Ser
		130			135						140				
Val	Arg	Arg	Ile	His	Trp	Arg	Ser	Thr	Ala	His	Arg	Gly	Asp	Leu	Met
				150					155					160	
Val	Arg	Cys	Glu	Glu	Gln	Ala	Trp	Asn	Pro	Ser	Val	Val	Ile	Val	Leu
				165				170						175	
Asp	Ser	Arg	Ala	Arg	Arg	His	Ala	Gly	Thr	Gly	Pro	Asp	Ala	Ser	Phe
			180					185						190	
Glu	Trp	Ala	Val	Asn	Ala	Val	Ala	Ser	Ile	Ser	Thr	Arg			
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<210> 595

<211> 303

<212> DNA

<213> Homo sapiens

<400> 595

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 120
 gcctgtgccc gcaaccgccc cgaattctc tccctggcac cgtgtcgcgt ttacggagcc
 180

cgaggaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgcctg tcatcaggca
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 300
 gga
 303

<210> 596
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 596
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 Ala Ile Gly Pro Arg Arg Ala Gly Ala Phe Ala Arg Ala Ser Ala Glu
 20 25 30
 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val
 35 40 45
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln
 50 55 60
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp
 65 70 75 80
 Asp Gln Gly Pro Arg Asp Leu Val
 85

<210> 597
 <211> 2709
 <212> DNA
 <213> Homo sapiens

<400> 597
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 aagaaccaca tgggtggagaa gacctacgaa tgtaagaat gcgggaaatc ctttggcgat
 120
 ctggtgtccc ggaggaaaca catgaggatt cacatcgta agaaacccgt ggaatgtcgg
 180
 cagtgcggga agaccttcgg aaaccagtcc atccttaaga ctcacatgaa ctctcacatc
 240
 ggagagaaac catacgggtg cgatctctgc gggaaagctt tcagcgcgag ttcaaaccct
 300
 accgcacaca ggaagataca cagcaagag agacgctacg aatgcgcgcg ctgcgggaaa
 360
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 420
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 480
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 540
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1140
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1320
gaaatacttc ctgtcatctg cccctttcca gaaaacttg gccgacctt ggtctacagc
1380
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1440
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gatgctgcta agtcggctcc agcacacagg agccccccac aacgaagagt tagtgcccc
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1680
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1740
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1800
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1860
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1980
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2040
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2100
ttctcagtc cactttgtta ctggtacctg atgcacacgg attgcgacca gagcatgatg
2160
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2220
tagtgacttc cccggtatcc actctcatct tcttccaata tcaagagaat ccagggtctg
2280

tcagattagtg aagggtgtgct aatctaaatt ttaaaaaatc tcttacaggt tttcttgcag
 2340
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 2400
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 2460
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 2520
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 2580
 agcgaccctg gcctcccctg tggcctcttt gagggtctgc agcagccctg gacttcagaa
 2640
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 2700
 aaaaaaaaaa
 2709

<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

Xaa	Ala	Cys	Thr	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Trp	Lys	Ser	Asn	Phe
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Asn	Leu	His	Lys	Lys	Asn	His	Met	Val	Glu	Lys	Thr	Tyr	Glu	Cys	Lys
		20					25						30		
Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met
		35					40					45			
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys
	50					55					60				
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr
	65				70					75				80	
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala
			85					90						95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg
		100						105					110		
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg
		115				120					125				
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg
		130				135					140				
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met
			145		150					155				160	
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys
			165						170					175	
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr
		180					185						190		
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp
		195				200						205			
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu
		210				215					220				
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu
					230						235				240

<210> 599
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 599
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 ttcggcgctca tggcgacaggt gctaggcgtg gccgtgcacg tgagctcga ccgctttggc
 120
 caggcatgtt tgcggggcgg catcccttgc acttgcagtc cgtggcctat cggccgaggg
 180
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgag aggagcgtgt tggcagacta
 240
 tggggctcgt cggaggacga ggatgtgagt ggcatggct ttgcgcgact gggcgatttc
 300
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 340

<210> 600
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 600
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 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His
 20 25 30
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
 35 40 45
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
 50 55 60
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
 65 70 75 80
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
 85 90 95
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
 100 105 110

<210> 601
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 601
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 ccgcgctcca ccattttgat ggacggcgct ccgctggcgg tcgcgcctta cggccagccg
 120
 cagctgtcga tggccccgct gtctatcggt aatctgcaat cgggtggagct ggtgcgcggc
 180
 ggccggcgcg tgcgctacgg gccgcagaac gtcggcgcggt tgatcaactt cgttaccgga
 240

gacattccca aaacgttttg cggtgccgcc agcgtacaaa cccagggtgc cagccacggc
 300
 ggccctgaaga ccctgaccag cgcctccgtg ggccggcaccg cagacaacgg cctcggcgcc
 360
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 421

<210> 602

<211> 140

<212> PRT

<213> Homo sapiens

<400> 602

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Ser	Arg	Leu	Ser	Pro	Arg	Ser	Thr	Ile	Leu	Met	Asp	Gly	Val	Pro	Leu
		20						25					30		
Ala	Val	Ala	Pro	Tyr	Gly	Gln	Pro	Gln	Leu	Ser	Met	Ala	Pro	Leu	Ser
		35				40						45			
Ile	Gly	Asn	Leu	Gln	Ser	Val	Asp	Val	Val	Arg	Gly	Gly	Gly	Ala	Val
	50				55					60					
Arg	Tyr	Gly	Pro	Gln	Asn	Val	Gly	Gly	Val	Ile	Asn	Phe	Val	Thr	Arg
	65			70					75				80		
Asp	Ile	Pro	Lys	Thr	Phe	Gly	Gly	Ala	Ala	Ser	Val	Gln	Thr	Gln	Gly
			85					90					95		
Ala	Ser	His	Gly	Gly	Leu	Lys	Thr	Leu	Thr	Ser	Ala	Ser	Val	Gly	Gly
		100						105					110		
Thr	Ala	Asp	Asn	Gly	Leu	Gly	Ala	Glu	Leu	Leu	Tyr	Ser	Gly	Leu	His
	115					120							125		
Gly	Gln	Gly	Tyr	Arg	Asp	Asn	Asn	Asp	Asn	Thr	Asp				
	130					135					140				

<210> 603

<211> 309

<212> DNA

<213> Homo sapiens

<400> 603

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 120
 gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcggt
 180
 ggcaaacccg aagacctcgt agagggtgtg cgccgcggtg tggacatgtt cgattgcgtg
 240
 atgccaaacc gtaatgcccg caatgggcat ctgttcacg atacaggcgt gctgaagatc
 300
 cgtaacgcy
 309

<210> 604

<211> 103

<212> PRT

<213> Homo sapiens

<400> 604

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Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu
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Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
      20           25           30
Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
      35           40           45
Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
      50           55           60
Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
      65           70           75           80
Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
      85           90           95
Val Leu Lys Ile Arg Asn Ala
      100

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<210> 605

<211> 428

<212> DNA

<213> Homo sapiens

<400> 605

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120
caccacatc acatttcagt accttggcta tcttcaatcg gaaaaaaga ttggagtaaa
180
tggtgagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg
240
attccacgtg caaagggtccc catgctacat cctgcgacaa tgaggccggt agcacgttta
300
ttgcctcgct gctttgccga acgccaacct ctgtaccgat acgctgatac tgattgttga
360
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420
aagtcttg
428

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<210> 606

<211> 135

<212> PRT

<213> Homo sapiens

<400> 606

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Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile
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Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser
      20           25           30
Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
  50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
  65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100              105              110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115              120              125
Asn Tyr Pro Ile Val Asn Ala
      130              135

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<210> 607

<211> 366

<212> DNA

<213> Homo sapiens

<400> 607

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  120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
  180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attgaaaata cttgtacttg
  240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
  300
ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta ttgcccgcag
  360
gacgcg
  366

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<210> 608

<211> 122

<212> PRT

<213> Homo sapiens

<400> 608

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Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
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Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
      65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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                100                105                110
Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala
      115                120

<210> 609
<211> 291
<212> DNA
<213> Homo sapiens

<400> 609
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tgggtcgggtt ggaacgagtc cgtcatgagc ccggtcgcca tggacgactc cagcagtcgg
120
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ccgaagcctc aaacttcccc cgccccgtac gccggggcgg ctccgaagac accggccaca
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291

<210> 610
<211> 69
<212> PRT
<213> Homo sapiens

<400> 610
Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp
1          5          10          15
Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro
20        25        30
Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
35        40        45
Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
50        55        60
Trp Arg Val Glu Pro
65

<210> 611
<211> 393
<212> DNA
<213> Homo sapiens

<400> 611
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120
acgcgcacatca ggccatcaaa aggtcaggta gcgactcttg agcaagcgct tgatgcagggt
180
gcgaaatgtc ctgcaattct tcagcagctt cgggccgttc gtggcgagct caacggattg
240
atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc
300

```

gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag
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 aggcaccagg gtgtcctcgg tgagggcaaa ttt
 393

<210> 612
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 612
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 20 25 30
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly
 35 40 45
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro
 50 55 60
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu
 65 70 75 80
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser
 85 90 95
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser
 100 105 110
 Ile Val Arg Ser Tyr Leu Arg
 115

<210> 613
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 613
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 120
 acactggata aagagagtgg agaaaagcctc agagtgttga gtgtcaaatg cattttttac
 180
 tagaataatca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga
 240
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctggtca atgactggtt
 300
 agacacacaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt
 360
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga
 420
 tttatgtggc tatttggagg aagaagagga aagtaccacc gtccaaaaat ttatagacca
 480
 tctgtccatc aaaaatgttg tagattctgc aatgatggaa gatcttgaa ggaaggaaaa
 540
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 567

<210> 614
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 614
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 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr
 20 25 30
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala
 35 40 45
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
 50 55 60
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
 65 70 75 80
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
 85 90 95
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
 100 105 110
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
 115 120 125
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
 130 135 140
 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu
 145 150 155 160
 Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg
 165 170 175
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp
 180 185

<210> 615
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 615
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 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc
 240
 ctgttttaacg tcatcatgga taaagctttg gcagtgtcgt gggtagctgt agaagccgac
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 gaatgcgcat ggttggggat gcaggaggca gatatcagcg gcttgaggcg tgcctgggtg
 360
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 420
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 480

atcgtggcca aagtggccag ggatcgcatc atgacgccta tggacgccga gattcctggg
 540
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<210> 616

<211> 213

<212> PRT

<213> Homo sapiens

<400> 616

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Ala	Arg	Ala	Gly	Leu	Gly	Pro	Val	Ala	Gly	Cys	Asp	Glu	Ala	Gly	Arg
			20					25					30		
Gly	Ala	Cys	Ala	Gly	Pro	Leu	Val	Ala	Ala	Ala	Val	Ile	Leu	Asp	Asp
		35				40					45				
Arg	Arg	Ser	Gly	Arg	Ile	Ala	Gly	Leu	Ala	Asp	Ser	Lys	Thr	Leu	Ser
	50				55					60					
Ala	Ala	Lys	Arg	Glu	Ala	Leu	Phe	Asn	Val	Ile	Met	Asp	Lys	Ala	Leu
	65			70					75					80	
Ala	Val	Ser	Trp	Val	Arg	Val	Glu	Ala	Asp	Glu	Cys	Asp	Arg	Leu	Gly
			85				90							95	
Met	Gln	Glu	Ala	Asp	Ile	Ser	Gly	Leu	Arg	Arg	Ala	Val	Val	Arg	Leu
	100						105						110		
Gly	Val	Glu	Pro	Gly	Tyr	Val	Leu	Ser	Asp	Gly	Phe	Pro	Val	Asp	Gly
	115					120						125			
Leu	Thr	Val	Pro	Asp	Leu	Gly	Met	Trp	Lys	Gly	Asp	Ser	Val	Cys	Ala
	130				135					140					
Cys	Val	Ala	Ala	Ala	Ser	Ile	Val	Ala	Lys	Val	Ala	Arg	Asp	Arg	Ile
	145			150					155					160	
Met	Ile	Ala	Met	Asp	Ala	Glu	Ile	Pro	Gly	Tyr	Asp	Phe	Ala	Val	His
			165						170					175	
Lys	Gly	Tyr	Ala	Thr	Ala	Leu	His	Gln	Arg	Arg	Leu	Lys	Glu	Leu	Gly
	180					185						190			
Pro	Ser	Arg	Gln	His	Arg	Met	Ser	Tyr	Ala	Asn	Val	Arg	Arg	Ala	Ala
	195					200						205			
Arg	Leu	His	Ser	Ser											
	210														

<210> 617

<211> 337

<212> DNA

<213> Homo sapiens

<400> 617

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 120

tcggcgccaa cgccagcgc caggccatgt tctcgaaaa cggttccggc cttcccggag
 180
 cgaatcctcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcacaaagc
 240
 gctgcaacgt cgtgccaatc gagatggccg aggagttcca gcgtcgcggc gtcgcgctcg
 300
 tctcgatcat ctgcgtggcg cactcgcagg cgtcgac
 337

<210> 618

<211> 112

<212> PRT

<213> Homo sapiens

<400> 618

Xaa	Thr	Cys	Leu	Ala	Arg	Gly	Thr	Arg	Gly	Ser	Trp	Ser	Arg	Lys	Cys
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Gly	Arg	Ala	Thr	Ala	Arg	Phe	Pro	Ala	Ser	Thr	Pro	Ser	Ser	Ser	Cys
			20				25						30		
Arg	Cys	Arg	Ser	Thr	Thr	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ser	Ala	Arg
			35				40					45			
Pro	Cys	Ser	Ser	Lys	Thr	Phe	Pro	Ala	Phe	Pro	Glu	Arg	Ile	Leu	Arg
			50			55					60				
Asn	Phe	Asp	Leu	Ser	Gln	Gln	Asp	Ser	Ala	Leu	Val	Ile	Ser	Ser	Ser
65					70					75				80	
Ala	Ala	Thr	Ser	Cys	Gln	Ser	Arg	Trp	Pro	Arg	Ser	Ser	Ser	Val	Ala
				85					90					95	
Ala	Ser	Ala	Ser	Ser	Arg	Ser	Ser	Arg	Trp	Arg	Thr	Arg	Arg	Arg	Arg
			100					105						110	

<210> 619

<211> 425

<212> DNA

<213> Homo sapiens

<400> 619

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 120
 gttttatagc atctttgtca gaaggcaaac ctgccaaacc agatgaatcg atgccactct
 180
 caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgctta ccgcttccag
 240
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 300
 caatagaagc ccgctcattt ttaaagctca gtatgtcact aatgcctttt tcgaagtggc
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 420
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 425

<210> 620

<211> 137

<212> PRT

<213> Homo sapiens

<400> 620

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Met Ala Ser His Ser Asn Gln Ser Ala Ser Asn Met Ala Gln Gly Ile
 1             5             10             15
Trp Ser His Phe Glu Lys Gly Ile Ser Asp Ile Leu Ser Phe Lys Asn
      20             25             30
Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys
      35             40             45
Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly
 50             55             60
His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly
65             70             75             80
Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile
      85             90             95
Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu
      100            105            110
Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu
      115            120            125
Glu His Lys Ile Gly Ile Lys Asn Ala
130                        135

```

<210> 621

<211> 453

<212> DNA

<213> Homo sapiens

<400> 621

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120
gtcggttgagg aactcgacat gttcccggtc gaatgcgtcg tgcgggggcta cctcaccggt
180
tcagggtggg ccgaatatca gcgcaaccag gccgtgtgcg gaateccgct tcccaggggg
240
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300
ggagaacatg acgagaacat cgactatcta cgcctggtag aactcgtcgg tccngatgn
360
tcagcgcgag tgcgtgacct ttcgctgcgg gtctaccagc gtgcagagga gatcgctcgg
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aagcgaggca tcctcctggc ggataccaag ctt
453

```

<210> 622

<211> 151

<212> PRT

<213> Homo sapiens

<400> 622

```

Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

```

```

1           5           10           15
Gln Leu Ala Asp Ile Val Asp Asn His Leu Val Ser Val Asp Val Pro
20
Ala Glu Val Ala Gly Arg Ala Met Val Val Glu Glu Asp Met Phe
35
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
50
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
65
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
85
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
100
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
115
Leu Arg Val Tyr Gln Arg Ala Glu Glu Ile Ala Arg Lys Arg Gly Ile
130
Leu Leu Ala Asp Thr Lys Leu
145
150

```

<210> 623

<211> 345

<212> DNA

<213> Homo sapiens

<400> 623

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cgaggaacta tcaggccgcg caatcagttg tggcgaaatt cgacgcgggc accattgccc
120
aagccgaaga cctgccacct gacgacaccc acacggggggc ggaactggta aagagcgtgg
180
tcaacagcat cacctgtgtg tcacccctgt acatcgaaga ttaccacc atagagatcc
240
aggggctggg actgcactgt gtcaggctct gggcgcttgg gctgctcgcc ctgtcactgc
300
ccagcgacc catcggggca caccgccgct acgccgcata tggcg
345

```

<210> 624

<211> 111

<212> PRT

<213> Homo sapiens

<400> 624

```

Met Ser Thr Glu Asp Met Leu Asp Leu Ser Asn Val Ser Tyr Tyr
1           5           10           15
Ala Arg Asn Tyr Gln Ala Ala Gln Ser Val Val Ala Lys Phe Asp Ala
20
Gly Thr Ile Ala Gln Ala Glu Asp Leu Pro Pro Asp Asp Thr His Thr
35
Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
50
Pro Leu Tyr Ile Glu Asp Phe Thr Thr Ile Glu Ile Gln Gly Leu Gly
55           60

```

```

65              70              75              80
Leu His Cys Val Arg Leu Trp Ala Pro Gly Leu Leu Ala Leu Ser Leu
      85              90              95
Pro Ser Ala Pro Met Arg Ala His Pro Arg Tyr Ala Ala Tyr Gly
      100              105              110

```

<210> 625

<211> 339

<212> DNA

<213> Homo sapiens

<400> 625

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120
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180
gcccaaccac tcccatgaga gacaggctct ccctgcctga gcttgggacc agggcccttc
240
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300
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339

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<210> 626

<211> 105

<212> PRT

<213> Homo sapiens

<400> 626

```

Met Gly Gln Met Gln Cys Cys Gly Gly Cys His Pro Val Thr Ser Gln
1          5          10          15
Ser Ser Met Cys Ser Glu Leu Ser Arg Glu Gly Ala Trp Val Gln Ala
      20          25          30
Gln Ala Gly Arg Ala Cys Leu Ser Trp Glu Val Val Gly Trp Val Gly
      35          40          45
Ala Gln Cys Lys Gly Arg Gln Thr Cys Trp Ser Leu Gly Tyr Asp Pro
      50          55          60
Glu Gln Ser Gly Gly Ala Glu Ser Ser Cys Leu Trp Ala Ser Ile Ala
      65          70          75          80
Leu Pro Val Asn Tyr Arg Pro Trp Lys Asn His Leu Cys Ile Gln Gln
      85          90          95
Met Ser Ser Ser Ile Met Leu Gly Thr
      100          105

```

<210> 627

<211> 10319

<212> DNA

<213> Homo sapiens

<400> 627

```

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60

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120
atctctagcg tcctcttttt tggtgctgct ggtttctcca gacctcgct cctctcgatt
180
gctctctcgc ettcctatctt cttttttttt tttttaaaca aaaacaaca cccctcccc
240
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300
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420
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720
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<211> 1294

<212> PRT

<213> Homo sapiens

<400> 628

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Ala Leu Leu Leu Leu His Leu Ser Pro Gly Ala Ala Gly Ser Ser Arg
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<211> 411

<212> DNA

<213> Homo sapiens

<400> 629

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      65           70           75           80
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<210> 632

<211> 87

<212> PRT

<213> Homo sapiens

<400> 632

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Lys Glu Ala Leu Leu Ile Leu Ser Lys Glu Leu Asp Thr Cys Gln Gln
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Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
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<212> DNA

<213> Homo sapiens

<400> 633

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<213> Homo sapiens

<400> 634

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 Met Gly Xaa Gln Val Val Glu Leu Gly Pro Val Asn Ala Thr Ile His
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<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

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 Ile His Ala Phe Ser Ala Gly Leu Gly Gly Ala Ile Gly Tyr Val Leu
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 Gly Gly Leu Asp Trp Thr Gln Thr Phe Leu Gly Ser Trp Phe Arg Thr
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 Gln Asn Gln Val Leu Phe Phe Phe Ala Ala Ile Ile Phe Thr Val Ser
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 100 105 110
 Gln Glu Arg Ser Ala Glu Glu Pro Gly Ala Leu Asp Gly Gly Glu Pro
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 His Gly Val Pro Ala Phe Pro Asp Glu Val Gln Ser Glu His Glu Leu
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 Ala Leu Asp Tyr Pro Asp Val Asp Ile Met Arg Ser Lys Ser Asp Ser
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His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser				
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Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met				
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Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu				
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Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Thr Thr Asp Phe Met				
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Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr				
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Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu				
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Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys				
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Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly				
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Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly				
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Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr				
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Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly				
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<212> DNA

<213> Homo sapiens

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120

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180

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<210> 638

<211> 99

<212> PRT

<213> Homo sapiens

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			20					25					30		
Pro	Trp	Cys	Phe	Cys	Arg	Pro	Leu	Leu	Phe	Phe	Gly	Met	Val	Arg	Phe
		35					40					45			
Ile	Ala	Ile	Pro	Val	Phe	Leu	Thr	Val	Pro	Asn	Ile	Ile	Asn	Ile	Gly
	50				55					60					
Ile	Gln	Ala	Ala	Val	Val	Ala	Ile	Met	Ala	Phe	Gly	Met	Thr	Phe	Val
	65				70				75					80	
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Ser Ala Met

<210> 639

<211> 330

<212> DNA

<213> Homo sapiens

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<212> PRT

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Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
 35           40           45
Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
 50           55           60
Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
 65           70           75           80
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<210> 641

<211> 491

<212> DNA

<213> Homo sapiens

<400> 641

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<210> 642

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<400> 642

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Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His
 1           5           10           15
His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly
 20           25           30
Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
 35           40           45
Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```

```

      50              55              60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65      70      75      80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85      90      95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100      105      110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115      120      125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130      135      140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145      150      155      160
Leu Gln Cys

```

<210> 643

<211> 628

<212> DNA

<213> Homo sapiens

<400> 643

```

nagatctttg acatctacgt ggtaaccgct gactacctgc ccctaggggc tgagcaggat
60
gccatcacgc tgcgggaagc ccagtatgtg gaggtcctgg atgcagccca cccactgcgc
120
tggtctgttc gcaccaagcc caccaagtcc agccccctcac ggcagggtctg ggtgtcacca
180
gcctacctgg acaggaggct caagctgtca cctgagtggg gggccgctga gggccctgag
240
ttccctgggg aggcctgtgtc tgaagacgaa tacaaggcaa ggctgagctc tgtgatccag
300
gagctgctga gttctgagca ggccttcgtg gaggagctgc agttcctgca gagccaccac
360
ctgcagcacc tggagcgctg cccccacgtg cccatagctg tggccggcca gaaggcagtc
420
atcttccgca atgtgcggga catcgcccg cttccacgca gcttcctgca ggagtgtcag
480
cagtcgcaca cggacgacga cgtggccatg tgcttcatca agaaccaggc ggcctttgag
540
cagtaacctg agttctcggt gggacgtgtg caggctgagt cggtggctgt cagcacggcc
600
atccaggagt tctacaagaa atacgcgt
628

```

<210> 644

<211> 209

<212> PRT

<213> Homo sapiens

<400> 644

```

Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1      5      10      15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

```

	20		25		30									
Leu	Asp	Ala	His	Pro	Leu	Arg	Trp	Leu	Val	Arg	Thr	Lys	Pro	Thr
	35		40		45									
Lys	Ser	Ser	Pro	Ser	Arg	Gln	Gly	Trp	Val	Ser	Pro	Ala	Tyr	Leu
	50		55		60									
Arg	Arg	Leu	Lys	Leu	Ser	Pro	Glu	Trp	Gly	Ala	Ala	Glu	Ala	Pro
	65		70		75									
Phe	Pro	Gly	Glu	Ala	Val	Ser	Glu	Asp	Glu	Tyr	Lys	Ala	Arg	Leu
	85		90		95									
Ser	Val	Ile	Gln	Glu	Leu	Leu	Ser	Ser	Glu	Gln	Ala	Phe	Val	Glu
	100		105		110									
Leu	Gln	Phe	Leu	Gln	Ser	His	His	Leu	Gln	His	Leu	Glu	Arg	Cys
	115		120		125									
His	Val	Pro	Ile	Ala	Val	Ala	Gly	Gln	Lys	Ala	Val	Ile	Phe	Arg
	130		135		140									
Val	Arg	Asp	Ile	Gly	Arg	Phe	His	Ser	Ser	Phe	Leu	Gln	Glu	Leu
	145		150		155									
Gln	Cys	Asp	Thr	Asp	Asp	Val	Ala	Met	Cys	Phe	Ile	Lys	Asn	Gln
	165		170		175									
Ala	Ala	Phe	Glu	Gln	Tyr	Leu	Glu	Phe	Leu	Val	Gly	Arg	Val	Gln
	180		185		190									
Glu	Ser	Val	Val	Val	Ser	Thr	Ala	Ile	Gln	Glu	Phe	Tyr	Lys	Lys
	195		200		205									

Ala

<210> 645

<211> 417

<212> DNA

<213> Homo sapiens

<400> 645

atccataggc attgccagag tattcacttc ctgttggagg cacacagggg agaggcctgt
60gaggggaagg gcatcaatgc agggctgggg tgtgggaagg tctgcagggc tggcaatggg
120caagctcagg aatggtgggg gagacagtgg gagccacggc agggacaatg gagctcagaa
180ggtccctctg tcattcccttt tggaaacctt tgatctggaa aatttggggc agtgccttt
240tccgtaggta ctggaggcac tggcttgaca tactacagcc ctcccaggag gcccagaagg
300tagatgttat aactaccccc attttccaga tgaagaaact gagcctctgg gatctgcgga
360agctcccaga gctggagcag ttagtccctg ggccttacac tcacagcaca gtttccc
417

<210> 646

<211> 95

<212> PRT

<213> Homo sapiens

<400> 646

Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

```

1           5           10           15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
      20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
      35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
      50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
      85           90           95

```

<210> 647

<211> 421

<212> DNA

<213> Homo sapiens

<400> 647

```

acgcgtttcg gttcttgagc gcttccacca attcagcggg ggtgagcggc cctgtgcat
60
cgcgagcagc ggtgatcaga taggcgatat ccgcctcggt cagttgcacg gtgtcgttat
120
cggttagccat gcgtggcgaa ctcccttggc atgggaaaaa cgggtgaggg caacgggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaaacacgtc agtatagcgc gtttccgccg
240
gggatttcctg tgaatgaagg caagaagtcg ggacgcacgc cacctgctac cgctcggtgg
300
tacgatagcc gcggcgccac caggttggtc acattccaaa cgcaacgcag gaaccgcgat
360
gaacagcggtt tttcgcaaca aaccctttat gacgctgggt ctggggcatt tcagtgtcga
420
c
421

```

<210> 648

<211> 90

<212> PRT

<213> Homo sapiens

<400> 648

```

Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
1           5           10           15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
      20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
      35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
      50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
      85           90

```

<210> 649
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 649
 cgcaacatgc ataaacacat gtgctcctcc gagactcagc tacttccctt gccctctctg
 60
 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc
 120
 cagttctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag
 180
 gaggggaagg caccaatgga aggtgggggc aggggaaggag gtacgcttga caagttccaa
 240
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttcctgtc
 300
 tctctcgctc aagcacgtcc ctcttaagag cccctctctg cagacgcccc cagtggaaac
 360
 aagcctagat tcgctgccaa gaaggccgac attttttaga cttgccagct taaaggggac
 420
 tgcacaggca cgcaactcaa tccccccctc catgtcctcc gctgtgacac attcaggcaa
 480
 cccgaaacac acaaagacac ggttgacac agcggccacc tgtgcacaca ggaggtagca
 540
 catggagcgc atctgacccc ggg
 563

<210> 650
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 650
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
 1 5 10 15
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu
 20 25 30
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
 35 40 45
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
 50 55 60
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
 65 70 75 80
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
 85 90 95
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
 100 105

<210> 651
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac
 60
 cataatggag tccatggggt caaagttatc tccctggagct cagcagttga tggatatggt
 120
 taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa
 180
 ttctggatgc aagcatatga ttggactaca atcctcatct accttaggaa ccttaaaaca
 240
 gtgcgtctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
 300
 cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c
 351

<210> 652

<211> 95

<212> PRT

<213> Homo sapiens

<400> 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1			5					10					15		
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
		20						25				30			
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
		35				40					45				
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
	50				55					60					
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65			70					75					80		
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
		85						90					95		

<210> 653

<211> 399

<212> DNA

<213> Homo sapiens

<400> 653

nncccggggt gggctggggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac
 60
 caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgctca
 120
 cactcttctc ctggagaggg agcgagcccc caaatgttcc aactgtgtgc ccaggggccc
 180
 cctctgtccc gccctccctg tcgagttcct cctacaactc cacttaattgg gggctctggc
 240
 tcccttcccc cagaaccacc ctccagtttc caggcctttc cactctagc aggccctggg
 300
 gggetttttc ccccaagget tgctgaccca gtccctctgt ggggcagtag cagccccctg
 360
 ttcctcccaa ggggcaatgc cccctctcca gccccacct
 399

<210> 654

<211> 133

<212> PRT

<213> Homo sapiens

<400> 654

```

Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
 1             5             10             15
Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
      20             25             30
Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
      35             40             45
Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
      50             55             60
Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
65             70             75             80
Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
      85             90             95
Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
      100            105            110
Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
      115            120            125
Ser Pro Ala Pro Pro
      130

```

<210> 655

<211> 368

<212> DNA

<213> Homo sapiens

<400> 655

```

tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
60
gatgagggtgg gaagtgcact gggatctggg ggaagaagcc cgggggttcaa gactcagcta
120
ctgactgcat ggtgtcaaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
180
gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
240
cttgacaaat gcaaggtgcc atacaaacag gaaactgcaca atctcaccgc cgggcactact
300
cagcattgtt atttttacct ttacatctat atgaagatgt agttccatto cttttaactg
360
ttgttttc
368

```

<210> 656

<211> 108

<212> PRT

<213> Homo sapiens

<400> 656

```

Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
 1             5             10             15
Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

```

      20              25              30
Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
      35              40              45
Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
      50              55              60
Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
      65              70              75              80
Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
      85              90              95
His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
      100              105

```

<210> 657

<211> 330

<212> DNA

<213> Homo sapiens

<400> 657

```

gtcgaccacg gcatgaaaaa gccgggggatg atcctcatca acaacccttg gggcgagttcc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cggtgtcgag
120
cgtatttcagg acagcgacct ggacgtgggt ccgcaattga ccccgctcta aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cgccctctcg gcacaggtgg tcaagtcctt
240
ggaccgcatg ggttgggacg tgcctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

```

<210> 658

<211> 102

<212> PRT

<213> Homo sapiens

<400> 658

```

Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
      1              5              10              15
Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
      20              25              30
Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
      35              40              45
Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
      50              55              60
Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
      65              70              75              80
Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
      85              90              95
Trp Arg Ala Gly Gly Ala
      100

```

<210> 659

<211> 1505

<212> DNA

<213> Homo sapiens

<400> 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg
60
ctggccggct gcatcgccgc caccgggatg gacatgtgga gaccccagga cctgtacgac
120
aaccccgctca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttcacgc catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcacc gtctctgggtg ccattggcct cctggatatcc
300
atcttttccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct cgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct
420
gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaact gtacaccggc
480
atgggtggga tggcgagac gtgtcagacc aggtacacat ttggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cactactaatt ggggggtgta tgatgtgcat cgcctgccgg
600
ggcctggcac cagaagaac caactacaaa gccgtttctt atcatgcctc agggccacagt
660
gttgcttaca agcctggagg ctccaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta tccttccaag
780
cacgactatg tgtaatgctc taagacctct cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tccatcttag atttcttctt gcttttgact cacagctgga
900
agtttagaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg
960
tctctaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
tttttaatct tctctccat tttgatgatt tagacagact cccctctctc ctctagtca
1140
ataaacccat tgatgatcta ttcccagct tatccccaa aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctggt tgaattttgt ctccccacc ccaactggc
1260
tagtaataaaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccatgatct cggttttctt acactgtgat cttaaaagt accaaaacca agtcattttc
1380
agtttgaggc aaccaaaccct ttctactgct gttgacatct tcttattaca gcaacaccat
1440
tctaggagtt tctgagctc tccactggag tctctccctt ctgtcgtctt ctgcgacggg
1500

taccc
1505

<210> 660
<211> 261
<212> PRT
<213> Homo sapiens

<400> 660
Met Ser Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1 5 10 15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20 25 30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35 40 45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65 70 75 80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85 90 95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100 105 110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115 120 125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130 135 140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145 150 155 160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165 170 175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180 185 190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195 200 205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210 215 220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225 230 235 240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245 250 255
Lys His Asp Tyr Val
260

<210> 661
<211> 451
<212> DNA
<213> Homo sapiens

<400> 661
nnacgcgtgt agtttgtgta tcggcgcgga actcgcgcgcg tctgatctcg aggagcttcc
60
cccatggacg agattttaac cttgcttgcc ggaggcgggtg acgacgagcc agagtggcat
120

gacaaggcat tatgtgcca gactgatccg gaggcattct tccctgaaa gggaggatcc
 180
 acccgtgagg ccaagcgcac ctgtgagtc tgtgaggtcc gccaggagtg cttggagtag
 240
 gcccttcgca atgacgagag gtccggaatc tggggcgcat tgtccgagat ggagaggcgt
 300
 cgggtgcgca agcgggctgt acctgacgtc ggagcgcggt tattgacacg gcccggtaaa
 360
 atgcctctgc tgcccgagat ggctgtctgc acgatgcggc atatgcgag atcgacagacg
 420
 tgggtgtcat cccgtgtctc atgacgtcga c
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10				15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala
				20				25				30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys
				35				40				45		
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn
				50			55				60			
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg
65					70					75			80	
Leu	Arg	Lys	Arg	Ala										
				85										

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

ctcagcgtc tcgacgccga cgcgcgccag ggagccaagg aagacctctc gcagcgcgac
 60
 ccctacgacg tgctcgtcgt aggggagggt cccgcgggtg ccgcggccgc cgtgtacgag
 120
 gctcgaagg gcattcgac cgccatgggtc gggctctcga tcggcgccca ggtactcgat
 180
 accgaggcca tcgacaacct catctcgggt cgcacacaca ccggctccgc tctggccgac
 240
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc
 300
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgccccgc
 360
 cgctcagtc tcgtggccac cgggtgccgc tggcgcaacc ttggcgtacc tggcgaggag
 420
 gaataccgca ccaagggtgt gacctactgc ccgcaactgc atggcccgtc attcacaggc
 480

aaaaagggtgg cgcgcgcgcg aggtggaac tccggtattg aggcgcgtat cgacctcgcc
 540
 ggcgcgcgcg ac
 552

<210> 664
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 664
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
 1 5 10 15
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
 20 25 30
 Gly Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
 35 40 45
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
 50 55 60
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
 65 70 75 80
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
 85 90 95
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
 100 105 110
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
 115 120 125
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Tyr Arg Thr
 130 135 140
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
 145 150 155 160
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
 165 170 175
 Ile Asp Leu Ala Gly Val Val Asp
 180

<210> 665
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 665
 acgcgtacag ttcgccgcgc aggttgaaca ccacgatcgg tgtaccggtc acttcgctcga
 60
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 120
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<210> 666
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 666
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 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
 35 40 45
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
 50 55 60
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly
 65 70 75 80
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
 85 90 95
 Val Gln Pro Arg Arg Arg Thr Val Arg
 100 105

<210> 667
 <211> 391
 <212> DNA
 <213> Homo sapiens

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 gccgtgttgt cgcgcactctg cgaaccggaa cgccagatca tttccgggt gccgtgggtt
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 360
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<210> 668
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 668
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 20 25 30
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35              40              45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
  50              55              60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
  65              70              75              80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85              90              95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100              105              110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115              120              125
Asp Ala
      130

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<210> 669

<211> 707

<212> DNA

<213> Homo sapiens

<400> 669

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  600
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<210> 670

<211> 170

<212> PRT

<213> Homo sapiens

<400> 670

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Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
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Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

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                20                25                30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
   35                40                45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
   50                55                60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
   65                70                75                80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
   85                90                95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
  100                105                110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
  115                120                125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
  130                135                140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
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<210> 671

<211> 444

<212> DNA

<213> Homo sapiens

<400> 671

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444

```

<210> 672

<211> 103

<212> PRT

<213> Homo sapiens

<400> 672

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Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
  20                25                30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

      35              40              45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
  50              55              60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
  65              70              75              80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
      85              90              95
Gly Ala Ile Cys Trp Ala Pro
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<210> 673
 <211> 452
 <212> DNA
 <213> Homo sapiens

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acgttcaaat actgtgcact tgaacgtcc gggccgcac acctgggtga ctttgtgcga
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 452

```

<210> 674
 <211> 134
 <212> PRT
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<400> 674
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Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
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Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
      35              40              45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
      50              55              60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
  65              70              75              80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
      85              90              95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
      100              105              110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly

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115
Gly Asp Trp Gly Gly Pro
130

120

125

<210> 675
<211> 8564
<212> DNA
<213> Homo sapiens

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 8280
 ggaaggactt acccagattt actgctgctg tgcttttgat ctctgcttac cgttcaagag
 8340
 gcgtgtgcag gccacagtc ggtgacccca tcaactcgag gaccaagggg gcggggactg
 8400
 ctggctcaag ccccgctgtg tccctccctcc ctcccttcct tgggcagaat gaattcgatg
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<210> 676

<211> 2518

<212> PRT

<213> Homo sapiens

<400> 676

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Pro	Arg	Tyr	Pro	Pro	His	Ser	Leu	Ser	Tyr	Pro	Val	Gln	Ile	Ala	Arg
			20					25					30		
Thr	His	Thr	Asp	Val	Gly	Leu	Leu	Glu	Tyr	Gln	His	His	Ser	Arg	Asp
			35				40				45				
Tyr	Ala	Ser	His	Leu	Ser	Pro	Gly	Ser	Ile	Ile	Gln	Pro	Gln	Arg	Arg
	50				55					60					
Arg	Pro	Ser	Leu	Leu	Ser	Glu	Phe	Gln	Pro	Gly	Asn	Glu	Arg	Ser	Gln
65					70				75					80	
Glu	Leu	His	Leu	Arg	Pro	Glu	Ser	His	Ser	Tyr	Leu	Pro	Glu	Leu	Gly
			85					90					95		
Lys	Ser	Glu	Met	Glu	Phe	Ile	Glu	Ser	Lys	Arg	Pro	Arg	Leu	Glu	Leu
			100				105						110		
Leu	Pro	Asp	Pro	Leu	Leu	Arg	Pro	Ser	Pro	Leu	Leu	Ala	Thr	Gly	Gln
		115					120					125			
Pro	Ala	Gly	Ser	Glu	Asp	Leu	Thr	Lys	Asp	Arg	Ser	Leu	Thr	Gly	Lys
		130				135				140					
Leu	Glu	Pro	Val	Ser	Pro	Ser	Pro	Pro	His	Thr	Asp	Pro	Glu	Leu	
145				150					155					160	
Glu	Leu	Val	Pro	Pro	Arg	Leu	Ser	Lys	Glu	Glu	Leu	Ile	Gln	Asn	Met

165										170										175																																																																																																																																																																
Asp	Arg	Val	Asp	Arg	Glu	Ile	Thr	Met	Val	Glu	Gln	Gln	Ile	Leu	Ser	Lys	180	185	190	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995	1000
Leu	Lys	Lys	Lys	Gln	Gln	Gln	Leu	Glu	Glu	Glu	Ala	Ala	Lys	Pro	Pro	Pro	200	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995	1000		
Glu	Pro	Glu	Lys	Pro	Val	Ser	Pro	Pro	Pro	Ile	Glu	Ser	Lys	His	Arg	Arg	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905																								

595				600				605							
Glu	Leu	Asn	Glu	Ser	Ser	Arg	Trp	Thr	Glu	Glu	Glu	Met	Glu	Thr	Ala
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Lys	Lys	Gly	Leu	Leu	Glu	His	Gly	Arg	Asn	Trp	Ser	Ala	Ile	Ala	Arg
625				630				635				640			
Met	Val	Gly	Ser	Lys	Thr	Val	Ser	Gln	Cys	Lys	Asn	Phe	Tyr	Phe	Asn
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Tyr	Lys	Lys	Arg	Gln	Asn	Leu	Asp	Glu	Ile	Leu	Gln	Gln	His	Lys	Leu
				660				665				670			
Lys	Met	Glu	Lys	Glu	Arg	Asn	Ala	Arg	Arg	Lys	Lys	Lys	Lys	Ala	Pro
				675				680				685			
Ala	Ala	Ala	Ser	Glu	Glu	Ala	Ala	Phe	Pro	Pro	Val	Val	Glu	Asp	Glu
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Glu	Met	Glu	Ala	Ser	Gly	Val	Ser	Gly	Asn	Glu	Glu	Glu	Met	Val	Glu
				705				710				715			
Glu	Ala	Glu	Ala	Leu	His	Ala	Ser	Gly	Asn	Glu	Val	Pro	Arg	Gly	Glu
				725				730				735			
Cys	Ser	Gly	Pro	Ala	Thr	Val	Asn	Asn	Ser	Ser	Asp	Thr	Glu	Ser	Ile
				740				745				750			
Pro	Ser	Pro	His	Thr	Glu	Ala	Ala	Lys	Asp	Thr	Gly	Gln	Asn	Gly	Pro
				755				760				765			
Lys	Pro	Pro	Ala	Thr	Leu	Gly	Ala	Asp	Gly	Pro	Pro	Pro	Gly	Pro	Pro
				770				775				780			
Thr	Pro	Pro	Arg	Arg	Thr	Ser	Arg	Ala	Pro	Ile	Glu	Pro	Thr	Pro	Ala
				785				790				795			
Ser	Glu	Ala	Thr	Gly	Ala	Pro	Thr	Pro	Pro	Pro	Ala	Pro	Pro	Ser	Pro
				805				810				815			
Ser	Ala	Pro	Pro	Pro	Val	Val	Pro	Lys	Glu	Glu	Lys	Glu	Glu	Glu	Thr
				820				825				830			
Ala	Ala	Ala	Pro	Pro	Val	Glu	Glu	Gly	Glu	Glu	Gln	Lys	Pro	Pro	Ala
				835				840				845			
Ala	Glu	Glu	Leu	Ala	Val	Asp	Thr	Gly	Lys	Ala	Glu	Glu	Pro	Val	Lys
				850				855				860			
Ser	Glu	Cys	Thr	Glu	Glu	Ala	Glu	Glu	Gly	Pro	Ala	Lys	Gly	Lys	Asp
				865				870				875			
Ala	Glu	Ala	Ala	Glu	Ala	Thr	Ala	Glu	Gly	Ala	Leu	Lys	Ala	Glu	Lys
				885				890				895			
Lys	Glu	Gly	Gly	Ser	Gly	Arg	Ala	Thr	Ala	Lys	Ser	Ser	Gly	Ala	
				900				905				910			
Pro	Gln	Asp	Ser	Asp	Ser	Ser	Ala	Thr	Cys	Ser	Ala	Asp	Glu	Val	Asp
				915				920				925			
Glu	Ala	Glu	Gly	Gly	Asp	Lys	Asn	Arg	Leu	Leu	Ser	Pro	Arg	Pro	Ser
				930				935				940			
Leu	Leu	Thr	Pro	Thr	Gly	Asp	Pro	Arg	Ala	Asn	Ala	Ser	Pro	Gln	Lys
				945				950				955			
Pro	Leu	Asp	Leu	Lys	Gln	Leu	Lys	Gln	Arg	Ala	Ala	Ala	Ile	Pro	Pro
				965				970				975			
Ile	Gln	Val	Thr	Lys	Val	His	Glu	Pro	Pro	Arg	Glu	Asp	Ala	Ala	Pro
				980				985				990			
Thr	Lys	Pro	Ala	Pro	Pro	Ala	Pro	Pro	Pro	Gln	Asn	Leu	Gln	Pro	
				995				1000				1005			
Glu	Ser	Asp	Ala	Pro	Gln	Gln	Pro	Gly	Ser	Ser	Pro	Arg	Gly	Lys	Ser
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Arg	Ser	Pro	Ala	Pro	Pro	Ala	Asp	Lys	Glu	Ala	Phe	Ala	Ala	Glu	Ala

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 Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro Phe
 1045 1050 1055
 Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro Asp
 1060 1065 1070
 Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu Gly
 1075 1080 1085
 Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile Ser
 1090 1095 1100
 Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu Glu
 1105 1110 1115 1120
 Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His Val
 1125 1130 1135
 Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met Gly
 1140 1145 1150
 Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly Val
 1155 1160 1165
 Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu Ser
 1170 1175 1180
 Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr Ala
 1185 1190 1195 1200
 Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser Thr
 1205 1210 1215
 Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr His
 1220 1225 1230
 Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile
 1235 1240 1245
 Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu
 1250 1255 1260
 Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu Ser
 1265 1270 1275 1280
 Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly Arg
 1285 1290 1295
 Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr Tyr
 1300 1305 1310
 Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser Ile
 1315 1320 1325
 Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro His
 1330 1335 1340
 His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly Ile
 1345 1350 1355 1360
 Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu Ala
 1365 1370 1375
 Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Ser Arg
 1380 1385 1390
 Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys Leu
 1395 1400 1405
 Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg
 1410 1415 1420
 Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu
 1425 1430 1435 1440
 Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr
 1445 1450 1455
 Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His

1460 1465 1470
 Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro Val
 1475 1480 1485
 His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys
 1490 1495 1500
 Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly
 1505 1510 1515 1520
 Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly Lys
 1525 1530 1535
 Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe Ala
 1540 1545 1550
 Gly His Leu Pro Arg Gly Ser Pro Val Thr Thr Arg Glu Pro Thr Pro
 1555 1560 1565
 Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp Arg
 1570 1575 1580
 Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser Thr
 1585 1590 1595 1600
 Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu
 1605 1610 1615
 Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala
 1620 1625 1630
 Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala
 1635 1640 1645
 Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His
 1650 1655 1660
 Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu
 1665 1670 1675 1680
 Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met
 1685 1690 1695
 His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg
 1700 1705 1710
 Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly
 1715 1720 1725
 Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu
 1730 1735 1740
 Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala
 1745 1750 1755 1760
 Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser
 1765 1770 1775
 Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr
 1780 1785 1790
 Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 1795 1800 1805
 Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Val Glu His
 1810 1815 1820
 Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly
 1825 1830 1835 1840
 Ser Ser Ser Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser
 1845 1850 1855
 His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu
 1860 1865 1870
 Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile
 1875 1880 1885
 Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr

1890					1895					1900					
Ser	Ser	Pro	Val	Arg	Pro	Ala	Ala	Thr	Phe	Pro	Pro	Ala	Thr	His	Cys
1905					1910					1915					1920
Pro	Leu	Gly	Gly	Thr	Leu	Asp	Gly	Val	Tyr	Pro	Thr	Leu	Met	Glu	Pro
					1925					1930					1935
Val	Leu	Leu	Pro	Lys	Glu	Ala	Pro	Arg	Val	Ala	Arg	Pro	Glu	Arg	Pro
					1940					1945					1950
Arg	Ala	Asp	Thr	Gly	His	Ala	Phe	Leu	Ala	Lys	Pro	Pro	Ala	Arg	Ser
					1955					1960					1965
Gly	Leu	Glu	Pro	Ala	Ser	Ser	Pro	Ser	Lys	Gly	Ser	Glu	Pro	Arg	Pro
					1970					1975					1980
Leu	Val	Pro	Pro	Val	Ser	Gly	His	Ala	Thr	Ile	Ala	Arg	Thr	Pro	Ala
1985					1990					1995					2000
Lys	Asn	Leu	Ala	Pro	His	His	Ala	Ser	Pro	Asp	Pro	Pro	Ala	Pro	Pro
					2005					2010					2015
Ala	Ser	Ala	Ser	Asp	Pro	His	Arg	Glu	Lys	Thr	Gln	Ser	Lys	Pro	Phe
					2020					2025					2030
Ser	Ile	Gln	Glu	Leu	Glu	Leu	Arg	Ser	Leu	Gly	Tyr	His	Gly	Ser	Ser
					2035					2040					2045
Tyr	Ser	Pro	Glu	Gly	Val	Glu	Pro	Val	Ser	Pro	Val	Ser	Ser	Pro	Ser
					2050					2055					2060
Leu	Thr	His	Asp	Lys	Gly	Leu	Pro	Lys	His	Leu	Glu	Glu	Leu	Asp	Lys
2065					2070					2075					2080
Ser	His	Leu	Glu	Gly	Glu	Leu	Arg	Pro	Lys	Gln	Pro	Gly	Pro	Val	Lys
					2085					2090					2095
Leu	Gly	Gly	Glu	Ala	Ala	His	Leu	Pro	His	Leu	Arg	Pro	Leu	Pro	Glu
					2100					2105					2110
Ser	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Leu	Gln	Thr	Ala	Pro	Gly	Val	Lys
					2115					2120					2125
Gly	His	Gln	Arg	Val	Val	Thr	Leu	Ala	Gln	His	Ile	Ser	Glu	Val	Ile
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Thr	Gln	Asp	Tyr	Thr	Arg	His	His	Pro	Gln	Gln	Leu	Ser	Ala	Pro	Leu
2145					2150					2155					2160
Pro	Ala	Pro	Leu	Tyr	Ser	Phe	Pro	Gly	Ala	Ser	Cys	Pro	Val	Leu	Asp
					2165					2170					2175
Leu	Arg	Arg	Pro	Pro	Ser	Asp	Leu	Tyr	Leu	Pro	Pro	Pro	Asp	His	Gly
					2180					2185					2190
Ala	Pro	Ala	Arg	Gly	Ser	Pro	His	Ser	Glu	Gly	Gly	Lys	Arg	Ser	Pro
					2195					2200					2205
Glu	Pro	Asn	Lys	Thr	Ser	Val	Leu	Gly	Gly	Gly	Glu	Asp	Gly	Ile	Glu
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Pro	Val	Ser	Pro	Pro	Glu	Gly	Met	Thr	Glu	Pro	Gly	His	Ser	Arg	Ser
2225					2230					2235					2240
Ala	Val	Tyr	Pro	Leu	Leu	Tyr	Arg	Asp	Gly	Glu	Gln	Thr	Glu	Pro	Ser
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Arg	Met	Gly	Ser	Lys	Ser	Pro	Gly	Asn	Thr	Ser	Gln	Pro	Pro	Ala	Phe
					2260					2265					2270
Phe	Ser	Lys	Leu	Thr	Glu	Ser	Asn	Ser	Ala	Met	Val	Lys	Ser	Lys	Lys
					2275					2280					2285
Gln	Glu	Ile	Asn	Lys	Lys	Leu	Asn	Thr	His	Asn	Arg	Asn	Glu	Pro	Glu
					2290					2295					2300
Tyr	Asn	Ile	Ser	Gln	Pro	Gly	Thr	Glu	Ile	Phe	Asn	Met	Pro	Ala	Ile
2305					2310					2315					2320
Thr	Gly	Thr	Gly	Leu	Met	Thr	Tyr	Arg	Ser	Gln	Ala	Val	Gln	Glu	His

2325 2330 2335
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met
 2340 2345 2350
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
 2355 2360 2365
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
 2370 2375 2380
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly
 2385 2390 2395 2400
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys
 2405 2410 2415
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser
 2420 2425 2430
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn
 2435 2440 2445
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro
 2450 2455 2460
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro
 2465 2470 2475 2480
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His
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 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu
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<211> 345

<212> DNA

<213> Homo sapiens

<400> 677

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 gccaacggta tcttgaatgt gagcgcaaaag gataaggcta ccggtaagga acagaagatt
 180
 cgcacgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
 240
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
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 345

<210> 678

<211> 110

<212> PRT

<213> Homo sapiens

<400> 678

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 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

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Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35                40                45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50                55                60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
      65                70                75                80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85                90                95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
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<210> 679

<211> 362

<212> DNA

<213> Homo sapiens

<400> 679

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120
ggtagacagcc tggatttcaa gcgtgccatt gctgacgtca cgcagtgtcc acccgaacgc
180
caaaaaagtc tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgacg gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
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360
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362

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<210> 680

<211> 100

<212> PRT

<213> Homo sapiens

<400> 680

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      20                25                30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35                40                45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
      50                55                60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
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Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85                90                95
Lys Ala Lys Asp
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<210> 681
 <211> 357
 <212> DNA
 <213> Homo sapiens

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 120
 ggtttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa
 180
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta
 240
 attgcagaag gcaatatcga tacacctgaa aaggtgaaac gtgtgcttga gttaggcgcg
 300
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcattcacgaa aaaattt
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<210> 682
 <211> 119
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<400> 682
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 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
 20 25 30
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
 35 40 45
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
 50 55 60
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
 65 70 75 80
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
 85 90 95
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
 100 105 110
 Gln Leu Ile Thr Lys Lys Phe
 115

<210> 683
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 <212> DNA
 <213> Homo sapiens

<400> 683
 nctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
 60
 aatattgttt tgcccgacgc gtggttgcatt gattgcgtca gttaccctaa aaaccatgta
 120
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
 180

aattacccca aacaatactt attagcaatt catcatgcaa ttccagcgca cagtgctcagt
 240
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
 300
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtatgccagt acagcgccca
 360
 ctatatcttg aagttgaccc ctccagcgag acacgatctc tagtctgcat g
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5					10					15	
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
		20						25					30		
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
		35					40				45				
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50				55					60					
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
	65			70					75					80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
		85						90						95	
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
		100					105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115				120						125			
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
	130					135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgctg ttcgaggatg aaccggaac gatggatgga ttgacactat tcggcctgtt
 60
 cgccgtcact gcgatgtctg tctgctatgc catggaggac cgcagccact gggttcgtgtt
 120
 gctgttcgag gccgcttgcc gctcggttcg gcctacggct tcttccaagg cgcttgccg
 180
 ttcggcttcg tcgaggcgat atgggagctc gttgcctcgc gcgtgggtgga cgatcaggcc
 240
 gcgatgaccg catcgtccgg cttaagcccg gaaacgaaa cgaccagtgc gctgggtttga
 300
 tgggcgccgc gtcgtggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
 360
 gtgcgatgccg acgctgtcgc tcacgcgct acgctcgacc acggcgccgc gcaatag
 417

<210> 686
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 686
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro
 1 5 10 15
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
 20 25 30
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
 35 40 45
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
 50 55 60
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
 65 70 75 80
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
 85 90 95
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
 100 105 110

<210> 687
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 687
 nnacgcgtga cgcaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgcac
 60
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacett atcagccggt
 120
 ctogatgaaa cccacgttg tgcacgacg gagcttcggg taccacctgc gtgcgcgggt
 180
 caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc
 240
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg
 300
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
 360
 ccagtcggtt atattggcgg ggttttccgc gacatttttg ccgacgacta ga
 412

<210> 688
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 688
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
 1 5 10 15
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
 20 25 30
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg


```

      35              40              45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
  50              55              60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
  65              70              75              80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85              90              95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100              105              110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115              120              125
Phe Arg Asp Ile Phe Ala Asp Asp
      130              135

```

<210> 689

<211> 499

<212> DNA

<213> Homo sapiens

<400> 689

```

cgcgctgcggt tactcgacgt cgatttttcat cacggtaacg gcacccagaa cattttttac
  60
ccgcgcgaatg acgtgatggt catatcgctg cacggcgagc cggccgtgtc ctatccctac
  120
tattcggggt tcagcgatga agtcggcgca ggtgttgagg aagggttcaa cctcaactac
  180
ccgctgcgca aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcctgcagg
  240
aaactccagc aattctcgcc gcaggatttg gtgatctcac tgggggtcga caccctcaag
  300
gacgacccga tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
  360
atagcgagtg tggggtgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
  420
atcggaaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
  480
gcccgaagac ggcgtgata
  499

```

<210> 690

<211> 157

<212> PRT

<213> Homo sapiens

<400> 690

```

Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
  1              5              10              15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20              25              30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35              40              45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50              55              60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
      85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
      100         105         110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
      115         120         125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
      130         135         140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691

<211> 336

<212> DNA

<213> Homo sapiens

<400> 691

```

ntgctgctgtg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggccccctg ggagttggcc tgcgacatcg cgctgccgtg cgccacccag
120
aacgaactgg acgccgacgc cgcccgcacg ctgctgcgca acggctgcct ttgctgtggct
180
ggaggcgcgca atatgccgcc gcgccttgag gctgtggata tctttatcga ggcggggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggccggcgtgg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccattgcgcct gctgtggacc gccggc
336

```

<210> 692

<211> 112

<212> PRT

<213> Homo sapiens

<400> 692

```

Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1      5      10      15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
      20      25      30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
      35      40      45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
      50      55      60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65      70      75      80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
      85      90      95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
100         105         110

```

<210> 693

<211> 580

<212> DNA

<213> Homo sapiens

<400> 693

ngggcaaccc ggaaggtccg gcgtcccagc cgcctacctc gctgggaccc tggctcttgct
 60
 gtcccccgct ggctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
 120
 gccacctcgc cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
 180
 aagagtattg aaattgccaa aaacagagga gcaagataca ggcttgacc agagctggaa
 240
 atatgaggct gcggatgttg ggatcattat tacgagtcgg acacctctt gcaactgttt
 300
 caagtcctag cgcccttgt ggagtctccc gtcactcagg acatcatctg cgacgtgggg
 360
 atacctgtaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggag
 420
 atcctgtctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
 480
 tgggtcaccc cgtggtcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
 540
 gttaaagcacc tccgtgtgt gtagccttgg gtcctgatca
 580

<210> 694

<211> 136

<212> PRT

<213> Homo sapiens

<400> 694

Met	Gly	Arg	Lys	Val	Thr	Val	Ala	Thr	Cys	Ala	Leu	Asn	Gln	Trp	Ala
1				5					10				15		
Leu	Asp	Phe	Glu	Gly	Asn	Leu	Gln	Arg	Ile	Leu	Lys	Ser	Ile	Glu	Ile
			20					25					30		
Ala	Lys	Asn	Arg	Gly	Ala	Arg	Tyr	Arg	Leu	Gly	Pro	Glu	Leu	Glu	Ile
			35				40					45			
Cys	Gly	Cys	Gly	Cys	Trp	Asp	His	Tyr	Tyr	Glu	Ser	Asp	Thr	Leu	Leu
	50				55						60				
His	Ser	Phe	Gln	Val	Leu	Ala	Ala	Leu	Val	Glu	Ser	Pro	Val	Thr	Gln
	65				70					75				80	
Asp	Ile	Ile	Cys	Asp	Val	Gly	Ile	Pro	Val	Met	His	Arg	Asn	Val	Arg
			85						90					95	
Tyr	Asn	Cys	Arg	Val	Ile	Phe	Leu	Asn	Arg	Lys	Ile	Leu	Leu	Ile	Arg
			100					105					110		
Pro	Lys	Met	Ala	Leu	Ala	Asn	Glu	Gly	Asn	Tyr	Arg	Glu	Leu	Arg	Trp
		115					120						125		
Phe	Thr	Pro	Trp	Ser	Arg	Ser	Arg								
	130						135								

<210> 695

<211> 439

<212> DNA

<213> Homo sapiens

<400> 695
 ntggtagactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc
 60
 atcatggctc tgctgagggc tgattacctg ctcgatatcg agacttcgggt gcccggtatc
 120
 ggcgacaagt tcgtcccggc cgtctggggc aaactcaaac tcggcaagga caacgagcac
 180
 accgctctgc cctggctactt cggccccgttc gtcgtgacgt acaacaagga cattttcaag
 240
 gatgttggcc tcgatcccg aatccccggc aagacgatga ccgagtacct cgacttcggc
 300
 aagaaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc
 360
 gcggaatggc gtgccctcgg cgtcaaggtc atgaatgacg atttcaccaa gttcactttt
 420
 gcctcggaat ccaacgcgt
 439

<210> 696
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 696
 Xaa Val Thr Gln Ala Ser Asn Gly Thr Met Ala Asp Val Val Asn Met
 1 5 10 15
 Pro Ser Ser Thr Ile Met Ala Leu Ser Arg Ala Asp Tyr Leu Leu Asp
 20 25 30
 Ile Glu Thr Ser Val Pro Gly Ile Gly Asp Lys Phe Val Pro Asp Val
 35 40 45
 Trp Gly Lys Leu Lys Leu Gly Lys Asp Asn Glu His Thr Ala Leu Pro
 50 55 60
 Trp Tyr Phe Gly Pro Phe Val Val Thr Tyr Asn Lys Asp Ile Phe Lys
 65 70 75 80
 Asp Val Gly Leu Asp Pro Glu Ile Pro Pro Lys Thr Met Thr Glu Tyr
 85 90 95
 Leu Asp Phe Ala Lys Lys Ile Thr Ala Ala Gly Lys Gln Ala Val Tyr
 100 105 110
 Gly Asn Thr Ser Trp Tyr Met Leu Ala Glu Trp Arg Ala Leu Gly Val
 115 120 125
 Lys Val Met Asn Asp Asp Phe Thr Lys Phe Thr Phe Ala Ser Glu Ser
 130 135 140
 Asn Ala
 145

<210> 697
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 697
 nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggg
 60

tgcggtgat ggggtcggag atgtgcacct ccacaaactt gaacttgatc ggaccaaccc
 120
 ttccaccct ggagagactc gcctgccttg aaagtcttct tgcccttctt gggaactga
 180
 tcgcccctcc gaacgagata atccaagctc aagcgaccgc ccaccttgctc gcgcgcctcc
 240
 acaccgacgg aatcgatgc cgggatcgca tcgatgctag cggcggtgcg tgcaatgaca
 300
 atcttgctct cagcagcga tacggggccc cgttggaat cgaacacaaa caccttgaaag
 360
 gcgttgtn
 368

<210> 698

<211> 108

<212> PRT

<213> Homo sapiens

<400> 698

Met	Pro	Met	Lys	Arg	Leu	Ser	Val	Met	Gly	Ser	Glu	Met	Ser	Pro	Ser
1			5					10					15		
His	Asn	Leu	Asn	Leu	Ile	Gly	Pro	Thr	Leu	Ser	Thr	Leu	Glu	Arg	Leu
		20					25					30			
Ala	Cys	Leu	Glu	Ser	Leu	Leu	Ala	Leu	Gly	Gln	Leu	Ile	Ala	Leu	
		35				40				45					
Pro	Asn	Glu	Ile	Ile	Gln	Ala	Gln	Ala	Thr	Ala	His	Leu	Val	Ala	Arg
	50				55					60					
Leu	His	Thr	Asp	Gly	Met	Arg	Cys	Arg	Asp	Arg	Ile	Asp	Ala	Ser	Gly
65			70					75					80		
Gly	Ala	Cys	Asn	Asp	Asn	Leu	Val	Phe	Thr	Gln	Arg	Tyr	Gly	Pro	Ala
		85					90						95		
Val	Gly	Ile	Glu	His	Lys	His	Leu	Glu	Gly	Val	Val				
		100					105								

<210> 699

<211> 363

<212> DNA

<213> Homo sapiens

<400> 699

nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc
 60
 cacacctcag attggcaact ggggatgact cggcactacc tgcgaagcg cggcgacgac
 120
 gaccacacgg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacggt
 180
 gccgggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aaccacaaat
 240
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg
 300
 tacttgctgc ccggaatca cgacagctta gagccggggt gtctctggga tgggccagaa
 360
 ttc
 363

<210> 700
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 700
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met
 1 5 10 15
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His
 20 25 30
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala
 35 40 45
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu
 50 55 60
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn
 65 70 75 80
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile
 85 90 95
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro
 100 105 110
 Gly Cys Leu Trp Asp Gly Pro Glu Phe
 115 120

<210> 701
 <211> 585
 <212> DNA
 <213> Homo sapiens

<400> 701
 nacgcgtccg ggcacacccgt caccgaggcg acgttccacg gccacccccc gctgatctat
 60
 ttccggtacg tccattgcgc gcatgtctgc ccgctgacac tgggcaacat ggtctcggcc
 120
 ctcgatcgcc tggggtcccg ggccgacggc atcgttccga tcttcatctc cgtcgatccg
 180
 gcccgcgaca ccccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcgcatcgtc
 240
 ggcgtgaccg gcaccgcagc gcagctggcg ccggtactgg cggagtcca catcaccgcy
 300
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgcgctga ccacagcgcc
 360
 ctctctatc tcatggacgg caacaaccgc ctgttgccgg tcatggcggc cagcgccgac
 420
 gctgcctcgc tgacgcacca gctggcgccc ggctggccg gggcaagaat gagaccatga
 480
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggctg ttcggcatca
 540
 tctgtgctgt cggcatcgcc ggcgtgctcg atttcgtcga ccggt
 585

<210> 702
 <211> 159
 <212> PRT

<213> Homo sapiens

<400> 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
          20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
          35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
          50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
          85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
          100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
          115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
          130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145          150          155

```

<210> 703

<211> 390

<212> DNA

<213> Homo sapiens

<400> 703

```

ttctctgctc catcacacc tcagcagaat ggcacgcgcg agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagt ctggcctgaa
120
gccattgata ctgcttgcac caccatcaac cgcgtttatc ttcaacaagg tttggagaaa
180
acctcttatg agttcctaac tggttaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaa ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaaactgt ggaatgtgcgn
390

```

<210> 704

<211> 130

<212> PRT

<213> Homo sapiens

<400> 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

                20                25                30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35                40                45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50                55                60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
      65                70                75                80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85                90                95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100                105                110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115                120                125
Val Arg
      130

```

```

<210> 705
<211> 513
<212> DNA
<213> Homo sapiens

```

```

<400> 705
acgcgtatatt cgtccaaatg attcaaatca aaacgcgcc gttaaaaacg atgcaggcga
60
agacaatgcg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgacaaag ttgagaaaga ctatgcaaatt tatggggatg aagctacttt cgggtggcgg
240
aaatcaattc gtgatggtat gggtcaaaat cctaatgtga caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcgggtatta aaaatgggta tatttttaag attggtaaag ctggaacccc agatataatg
420
gataacgttg acatcatcat tgggtgaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

```

<210> 706
<211> 140
<212> PRT
<213> Homo sapiens

```

```

<400> 706
Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1          5          10          15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20          25          30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35          40          45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```



```

      50              55              60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65              70              75              80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
      85              90              95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
      100             105             110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
      115             120             125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
      130             135             140

```

<210> 707

<211> 409

<212> DNA

<213> Homo sapiens

<400> 707

```

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat tttcatggca gtgtctatgg acggctcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgccca cccctgcccc tttttgtctt cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggt ttcccagcct gtctggccat cacccccag cccagccccct cctgctgggt
360
gacgtgctca gttcggcccc tgctgtactg ggagggggct aggagcata
409

```

<210> 708

<211> 136

<212> PRT

<213> Homo sapiens

<400> 708

```

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
1              5              10              15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
      20              25              30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
      35              40              45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
      50              55              60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
      65              70              75              80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
      85              90              95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
      100             105             110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu

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115              120              125
Trp Trp Ser Glu Asp Ala Thr Arg
130              135

<210> 709
<211> 771
<212> DNA
<213> Homo sapiens

<400> 709
acgcgtctga cggagagcct cctgagtctc cccacgcaga ggactcagaa agggaatcgg
60
tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc
120
tccccctcca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaag
180
acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaa
240
ccagtgaaca cgaagggtta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt
300
ttaaactctc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtgcgat
360
cggatgatga aagaatagat caggttgaag atgacggaga tcaggttgaa gatgatggag
420
agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtccctc
480
gtcctgagag gggaaagggg cccagtggcg aggacagatg gttggtactg ggggagggcc
540
tgtgtgattt caggctgcaa gcaccccagg catctgtgac agctccttca gagcagacca
600
cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttgatg aaacagctgc
660
caggcccccag tgggtggtgag gaagaaaaac cgatgggaaa tgggagtcga agccccctc
720
ctggcacatc cctggacaat cctgtaccca gccctcccc ttctgagatc t
771

<210> 710
<211> 205
<212> PRT
<213> Homo sapiens

<400> 710
Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu
1          5          10          15
Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His
20          25          30
Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp
35          40          45
Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile
50          55          60
Pro Glu Val Ala Ser Asp Asp Glu Arg Ile Asp Gln Val Glu Asp Asp
65          70          75          80
Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu

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      85              90              95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg
      100              105              110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly
      115              120              125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro
      130              135              140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys
      145              150              155
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu
      165              170              175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser
      180              185              190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile
      195              200              205

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<210> 711
 <211> 432
 <212> DNA
 <213> Homo sapiens

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<400> 711
nnggatccga cggcgcaaag ccttaaatgaa gggtaggcag ttacctcttt ttctgtagga
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attctctctgt tttatatcta ctcccccta ggttcatect actcctcat cttctgagct
120
aatgtgcccc ctttatttgc acttgcatgg aatatgatta tgaacacagt tttatcatt
180
gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga ggggtataag
240
gtcgttgggt aaacggacaa cggttgtgac gcgatccaaa tggttcgcga atgcctgccg
300
gacctgatca tcctggatat cagcatcccc aaactcgacg gctcgaagt gctctgccga
360
ttcaacgcc aagaacacatc catgaaaacc ctgattctta ccgccagag tccgacgttg
420
ttcgccacgc gt
432

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<210> 712
 <211> 93
 <212> PRT
 <213> Homo sapiens

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<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
1      5      10      15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
20     25     30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
35     40     45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
50     55     60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

```

65              70              75              80
Ile Leu Thr Ala Gln Ser Pro Thr Leu Phe Ala Thr Arg
      85              90

<210> 713
<211> 465
<212> DNA
<213> Homo sapiens

<400> 713
atcctgatcg ccaacggtgg tatgcagaac ccggtgggcg cggtgttcaa ccccgacacc
60
atgcgcgatgg aaatgaccga cttcgccgcg gtgatcttca acccggtggc gcaggccaag
120
ttcgtgcata cggtcagcgc gggctacgtg gccggcgcca tgttcgtcat gtcgatcagc
180
gcctggtacc tgctcaaggg ccgccacacc gacctggcca agcgctcgat ggcggtcgcc
240
gccagcttgc gcctggcgtc ggcgctgtcg gtcgtcgtgc tgggtgacga aagcggttat
300
ctcaccacgc aacaccagaa gatgaagatc gcggccatgg aatccatgtg gcacaccgag
360
ccggcgccgc cgtccttcaa cctgatcgcg ctgcccaacc aggcgaacg caagaacgac
420
ttcgccatcg agattcccta cgtcatgngc ctcateggca cgcgt
465

<210> 714
<211> 155
<212> PRT
<213> Homo sapiens

<400> 714
Ile Leu Ile Ala Asn Gly Gly Met Gln Asn Pro Val Gly Ala Val Phe
1      5      10      15
Asn Pro Asp Thr Met Arg Met Glu Met Thr Asp Phe Ala Ala Val Ile
20     25     30
Phe Asn Pro Val Ala Gln Ala Lys Phe Val His Thr Val Ser Ala Gly
35     40     45
Tyr Val Ala Gly Ala Met Phe Val Met Ser Ile Ser Ala Trp Tyr Leu
50     55     60
Leu Lys Gly Arg His Thr Asp Leu Ala Lys Arg Ser Met Ala Val Ala
65     70     75     80
Ala Ser Phe Gly Leu Ala Ser Ala Leu Ser Val Val Val Leu Gly Asp
85     90     95
Glu Ser Gly Tyr Leu Thr Thr Glu His Gln Lys Met Lys Ile Ala Ala
100    105    110
Met Glu Ser Met Trp His Thr Glu Pro Ala Pro Ala Ser Phe Asn Leu
115    120    125
Ile Ala Leu Pro Asn Gln Ala Glu Arg Lys Asn Asp Phe Ala Ile Glu
130    135    140
Ile Pro Tyr Val Met Xaa Leu Ile Gly Thr Arg
145    150    155

```

<210> 715
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 715
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 60
 cagaccggcc tgctgctca ggcactgggt cgtttgcgcc aggcagcgcc gacggtggag
 120
 tgcaagttgg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg
 180
 gactcggcga tcattcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta
 240
 ctgcgcaagg agccgtttgt gttgatcgtg cccagggcgg tcgggggtga tgaccggttg
 300
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg ctctgtttgg cggg
 354

<210> 716
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 716
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala
 1 5 10 15
 Ile Thr Thr Ala Gln Thr Gly Leu Pro Gln Ala Leu Val Arg Leu
 20 25 30
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser
 35 40 45
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile
 50 55 60
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val
 65 70 75 80
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly
 85 90 95
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp
 100 105 110
 Arg Ala Ser Phe Gly Gly
 115

<210> 717
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 717
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 60
 ccgttaagtc atctaataag gccattctgt ggctctccat cagtaagaac caaatccata
 120
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca
 180

atataatcaa gctgacaata ctgatcaaac cactcgcacg aaagctacta cgcgttgacc
 240
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag
 300
 accaggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgat
 360
 attcaacggc gtagcaccag cacagcaaca tagccactag t
 401

<210> 718

<211> 130

<212> PRT

<213> Homo sapiens

<400> 718

Met	Leu	Leu	Cys	Trp	Cys	Tyr	Ala	Val	Glu	Ser	His	Trp	Ile	Ser	Phe
1			5					10					15		
His	Phe	Leu	Glu	Arg	Pro	Ile	Phe	Asn	Leu	Ala	Thr	Thr	Trp	Ser	Ser
		20					25					30			
Phe	Leu	Leu	Trp	Thr	Ile	Leu	Phe	Leu	Ser	Ile	Ser	Leu	Val	Phe	Ser
		35				40					45				
Ala	Trp	Trp	Ser	Ser	Gly	Ser	Ser	Phe	His	Ala	Ser	Gly	Leu	Ile	Ser
	50				55					60					
Ile	Val	Ser	Leu	Ile	Ile	Leu	Ser	His	Phe	Ser	Val	Ser	Gln	His	Gln
65				70				75					80		
Phe	Asp	Ala	Leu	Leu	Ser	Ala	Gln	Leu	Leu	Trp	Ile	Trp	Phe	Leu	
			85					90					95		
Leu	Met	Glu	Ser	His	Arg	Met	Ala	Tyr	Leu	Asp	Asp	Leu	Thr	Ala	Leu
		100					105					110			
Pro	Gly	Arg	Arg	Ala	Leu	Asn	Glu	Lys	Leu	Val	Gly	Leu	Pro	Lys	Arg
		115				120						125			
Tyr	Ala														
	130														

<210> 719

<211> 685

<212> DNA

<213> Homo sapiens

<400> 719

tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcggtca
 60
 ctcttggaag cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc
 120
 aatctccctg cgttggtaac tgggcataag aaagacctct cgactccagc aacctcatcg
 180
 tgcaaatgcc gtggcgtggt caactctgac ggcttggaag ctgcagacct tgtcaaagga
 240
 cctcgccga aattcaccct tgatctcttt gtcttgtcca actctgtgcc ctgagaatga
 300
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgtc gaatcacgtc
 360
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag
 480
 cataaaaagg tattctcgga cgggaaatgt aaagtctgag cttaggtgca gagtaccgcc
 540
 atcgatcagt gtctgatact gcttgctcgc gactttcttg cagagcaatg ggtatagcgt
 600
 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat
 660
 gaccacgtca tcgatgggat ttgct
 685

<210> 720

<211> 161

<212> PRT

<213> Homo sapiens

<400> 720

Met	Ser	Leu	Thr	Arg	Arg	Asn	Arg	Gln	Gly	Glu	Gln	Thr	Thr	Ala	Ser
1				5					10					15	
Thr	Trp	Leu	Lys	Thr	Leu	Tyr	Pro	Leu	Leu	Gly	Lys	Glu	Val	Ala	Asp
			20					25					30		
Lys	Gln	Tyr	Gln	Thr	Leu	Ile	Asp	Gly	Gly	Thr	Leu	His	Leu	Ser	Ser
			35				40					45			
Asp	Phe	Thr	Phe	Pro	Val	Ala	Glu	Tyr	Leu	Phe	Met	Leu	Arg	Pro	Val
			50			55					60				
Glu	Gln	Glu	Val	Phe	Glu	Leu	Gly	Phe	Asn	Ala	Lys	Ser	Leu	Arg	Ser
					70				75					80	
Gly	Val	Val	Glu	Gly	Val	Leu	Ala	Gly	Ser	Arg	Ala	Ala	Leu	Ala	Gly
				85				90						95	
Leu	Gln	Asn	Gly	Asp	Val	Ile	Gln	His	Phe	Ser	Arg	Val	Ser	Val	Ala
			100					105					110		
Leu	Met	Asp	Ser	Gln	Lys	Thr	Val	Ser	Phe	Ser	Gly	Thr	Arg	Val	Gly
			115				120					125			
Gln	Asp	Lys	Glu	Ile	Lys	Gly	Glu	Phe	Arg	Pro	Arg	Ser	Phe	Asp	Lys
			130			135					140				
Val	Cys	Ser	Phe	Gln	Ala	Val	Arg	Val	Asp	His	Ala	Thr	Ala	Phe	Ala
					150					155					160
Arg															

<210> 721

<211> 579

<212> DNA

<213> Homo sapiens

<400> 721

aagcttggga tcagggtgtg gcagtggtgg gggagtgtgg aggtcctgcc ctgctcacgg
 60
 attgccaca ttgagcgagc ccacaagccc tacacagagg acctcaccgc ccatgtccgc
 120
 aggaacgcct tcagggtggc tgaagtctgg atggatgaat taaaagcca cgtctactgg
 180
 catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct
 240

ctcaggaaac agctgcagtg caagaccttc cgggtgtacc tggtcagcgt gtacccagag
 300
 atgaggatgt actccgacat cattgcctat ggagtgtctgc agaattctct gaagactgat
 360
 ttgtgtcttg accagggggc agatacagag aatgtcccca tcatgtacat ctgccatggg
 420
 atgacgcctc agaacgtgta ctacacgagc agtcagcaga tccatgtggg cattctgagc
 480
 cccaccgtgg atgatgatga caaccgatgc ctggtggagc tcaacagccg gccccggctc
 540
 atcgaatgca gctacgcca agccaagagg atgaagctt
 579

<210> 722

<211> 193

<212> PRT

<213> Homo sapiens

<400> 722

Lys Leu Gly Ile Arg Val Trp Gln Cys Gly Gly Ser Val Glu Val Leu
 1 5 10 15
 Pro Cys Ser Arg Ile Ala His Ile Glu Arg Ala His Lys Pro Tyr Thr
 20 25 30
 Glu Asp Leu Thr Ala His Val Arg Arg Asn Ala Leu Arg Val Ala Glu
 35 40 45
 Val Trp Met Asp Glu Phe Lys Ser His Val Tyr Trp His Gly Thr Tyr
 50 55 60
 Gln Glu Asp Ser Gly Ile Asp Ile Gly Asp Ile Thr Ala Arg Lys Ala
 65 70 75 80
 Leu Arg Lys Gln Leu Gln Cys Lys Thr Phe Arg Trp Tyr Leu Val Ser
 85 90 95
 Val Tyr Pro Glu Met Arg Met Tyr Ser Asp Ile Ile Ala Tyr Gly Val
 100 105 110
 Leu Gln Asn Ser Leu Lys Thr Asp Leu Cys Leu Asp Gln Gly Pro Asp
 115 120 125
 Thr Glu Asn Val Pro Ile Met Tyr Ile Cys His Gly Met Thr Pro Gln
 130 135 140
 Asn Val Tyr Tyr Thr Ser Ser Gln Gln Ile His Val Gly Ile Leu Ser
 145 150 155 160
 Pro Thr Val Asp Asp Asp Asp Asn Arg Cys Leu Val Asp Val Asn Ser
 165 170 175
 Arg Pro Arg Leu Ile Glu Cys Ser Tyr Ala Lys Ala Lys Arg Met Lys
 180 185 190
 Leu

<210> 723

<211> 384

<212> DNA

<213> Homo sapiens

<400> 723

acgcgtcctc ttacgctcag ttttgacaat gcgtgctggc agccaaccga agccgtaaaa
 60

ctcaacgaaa tgetctcgct taaaccgtgc gaaggaaccc caccgcaatg gcgcttatcc
 120
 cggaaggagg attaccaaat gcgcattgat acgcgctccg gaacgcctac gctgatgctt
 180
 accgtacaaa gtgtaaccga caaacctgtt acggacgtca ctcgacaatg tccataatgg
 240
 gacggcaagc cctcaccct tgacgtaacg aatacatctc cggaaggctc cgtcgtagca
 300
 gactcttaca gcaagcaaac cgctatgggt gactcaaggta aaatcacact tcagcctgccc
 360
 gctaacagca atggcctgct gctg
 384

<210> 724

<211> 128

<212> PRT

<213> Homo sapiens

<400> 724

Thr	Arg	Pro	Leu	Thr	Leu	Ser	Phe	Asp	Asn	Ala	Cys	Trp	Gln	Pro	Thr
1			5					10					15		
Glu	Ala	Val	Lys	Leu	Asn	Glu	Met	Leu	Ser	Leu	Lys	Pro	Cys	Glu	Gly
			20					25				30			
Thr	Pro	Pro	Gln	Trp	Arg	Leu	Phe	Arg	Glu	Gly	Asp	Tyr	Gln	Met	Arg
			35			40					45				
Ile	Asp	Thr	Arg	Ser	Gly	Thr	Pro	Thr	Leu	Met	Leu	Thr	Val	Gln	Ser
			50			55					60				
Val	Thr	Asp	Lys	Pro	Val	Thr	Asp	Val	Thr	Arg	Gln	Cys	Pro	Lys	Trp
65					70					75				80	
Asp	Gly	Lys	Pro	Leu	Thr	Leu	Asp	Val	Thr	Asn	Thr	Phe	Pro	Glu	Gly
					85					90				95	
Ser	Val	Val	Arg	Asp	Phe	Tyr	Ser	Lys	Gln	Thr	Ala	Met	Val	Gln	Gln
			100					105					110		
Gly	Lys	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Asn	Ser	Asn	Gly	Leu	Leu	Leu
			115					120					125		

<210> 725

<211> 521

<212> DNA

<213> Homo sapiens

<400> 725

tcctgactgt ctttattgca gtggtctgga actgttgat ggaacgaatt ttatctagag
 60
 cctggtgaac agcttccag gtgtgcattt agggcctcct agggatcacc aaagttttta
 120
 gaaaataggt ttccttcttc cacaggcatg gagaaggaag gaaattttgc actggccttt
 180
 gggaagctga agaagagctg gggggaggct tggtctgaca aaatagtgc tctctccctg
 240
 ctgaaatgt cccacagaag gctgtttctg gttcacattt gccctctag gtcaccctcc
 300
 tccccctcat cctgctcact gccagagaga ctatgctggg agtgggtgcat cggtggtctc
 360

caggcccttt taggctcaag gtgttcattc cctggctcct tccctgccat gtctttgttc
 420
 cttctcctct ccttcccatc ccagcagcca cctcctcct tccaccagac ctgggaacca
 480
 tcatcccaac cacaatcacc ccgtggttct attacacgcg t
 521

<210> 726

<211> 124

<212> PRT

<213> Homo sapiens

<400> 726

Met	Glu	Lys	Glu	Gly	Asn	Phe	Ala	Leu	Ala	Phe	Gly	Lys	Leu	Lys	Lys
1				5					10					15	
Ser	Trp	Gly	Glu	Ala	Cys	Ser	Asp	Lys	Ile	Val	Thr	Leu	Ser	Leu	Leu
			20					25					30		
Glu	Met	Ser	His	Arg	Arg	Leu	Phe	Leu	Val	His	Ile	Cys	Pro	Ser	Arg
			35				40					45			
Ser	Thr	Pro	Ser	Pro	Ser	Ser	Cys	Ser	Leu	Pro	Glu	Arg	Leu	Cys	Trp
	50					55					60				
Glu	Trp	Cys	Ile	Gly	Gly	Leu	Gln	Ala	Leu	Leu	Gly	Ser	Arg	Cys	Ser
	65				70					75				80	
Phe	Pro	Gly	Ser	Phe	Pro	Ala	Met	Ser	Leu	Phe	Leu	Pro	Pro	Ser	Phe
				85					90					95	
Pro	Ser	Gln	Gln	Pro	Pro	Ser	Ser	Phe	His	Gln	Thr	Trp	Glu	Pro	Ser
			100						105				110		
Ser	Gln	Pro	Gln	Ser	Pro	Arg	Gly	Ser	Ile	Thr	Arg				
			115				120								

<210> 727

<211> 629

<212> DNA

<213> Homo sapiens

<400> 727

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 60
 tctgttgctt gacggcacgg tggtctcagga ctgcgatctcg ggaaccttgg cgactcgcg
 120
 tgccattatc gacgctggtg agttgaaggc tccagcgcacg cgggcggttg cgtcaatcacg
 180
 tgccgcccgc cagcaggttc aaggagaact cgaatgaatc cgaatgacta cctggtgctc
 240
 tcggcgatct tggttcgatc cggcatcggt ggcttcctga cgaggcgtaa tgccttggtg
 300
 gcctttatgt cggtggaggt gatgctcaac gccgcgaacc tggcgctggt gactttcgct
 360
 cagctacacg gctctctcga cggacaggtc ggggttttct tcgtgatgat cgtggcagcc
 420
 gctgaggtgg ttgtcggttt ggcgatcacc gtcactatct tccgttcccc tcgcaccact
 480
 tcggtggacg acaccaacct gctgaagttc tgaggagagt accgtgactg tcttggaaac
 540

cggcttggtc aacgtggcct ggctcatgat tgcggtgccca ctgggtggttg ccgcgctgct
 600
 attggtgctg ggacgccgca gcgacgcgt
 629

<210> 728
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 728
 Met Asn Pro Asn Asp Tyr Leu Val Leu Ser Ala Ile Leu Phe Ala Ile
 1 5 10 15
 Gly Ile Val Gly Phe Leu Thr Arg Arg Asn Ala Leu Val Ala Phe Met
 20 25 30
 Ser Val Glu Leu Met Leu Asn Ala Ala Asn Leu Ala Leu Val Thr Phe
 35 40 45
 Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val
 50 55 60
 Met Ile Val Ala Ala Ala Glu Val Val Val Gly Leu Ala Ile Ile Val
 65 70 75 80
 Thr Ile Phe Arg Ser Arg Arg Thr Thr Ser Val Asp Asp Thr Asn Leu
 85 90 95
 Leu Lys Phe

<210> 729
 <211> 4716
 <212> DNA
 <213> Homo sapiens

<400> 729
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 60
 ttaagggaat gctgcaggac agggaatccc aaaatcaaaa gtctacagtt ccgtcaagaa
 120
 ggagaatgta ttcttttgat gatgtgctgg aggaaggaaa gcgacccccct acaatgactg
 180
 gtgcagaagc aagttaccag agtgagagag tagaagagaa gggagcaact tattcttcag
 240
 aaattcccaa agaagattct accacttttg caaaaagaga ggacccgtgt aacaactgaa
 300
 attcagcttc cttctcaaag tctgtggaa gaacaaagcc cagcctcttt gtcttctctg
 360
 cgttcacgga gcacacaaat ggaatcaact cgtgtttcag cttctctccc cagaagttac
 420
 cggaaaaactg atacagtcag gttaacatct gtggtcacac caagaccctt tggctctcag
 480
 acaaggggaa tctcatcact cccagatct tacacgatgg atgatgcttg gaagtataat
 540
 ggagatgttg aagacattaa gagaactcca aacaatgtgg tcagaccccc tgcaccaagc
 600
 ccgacgcaa gccaaactggc ttcaagctta tctagccaga aagaggtagc agcaacagaa
 660

gaagatgtga caaggctgcc ctctcctaca tcccccttct catctcttcc ccaagaccag
720
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<212> PRT

<213> Homo sapiens

<400> 730

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<211> 364

<212> PRT

<213> Homo sapiens

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65				70					75					80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85					90						95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
	115						120					125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130				135					140					
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145				150						155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165						170					175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
		180						185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
	195						200					205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215						220			
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225				230						235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245						250					255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
	260						265						270		
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

```

      275              280              285
Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
  290              295              300
Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
  305              310              315              320
Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
      325              330              335
Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
      340              345              350
Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg
  355              360

```

<210> 735

<211> 597

<212> DNA

<213> Homo sapiens

<400> 735

```

gtcgactagc caaaccgccc gggaaagtct tgtaccaccg atcctgggtt atcgggatct
60
catcgccacc atggactcgc gcaatctgga aaccgccaac cttattccag aaaaaataat
120
tgcttgggtg cctcgatccc gctctgaccg ccaactggac cgctcaaccc aggacatcct
180
cagtgcctac cagcagctgg ctgcaccgct ggcaactacc atcttcgttg tgggtgccac
240
agcgcgcgac attctgctga cacacgtgtt cggtatcgag accggagctg ccacgctcga
300
cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
360
gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac
420
gagcgacaac acgatcgccc ggccaatcga tctcatccca ttcggcggga tcgaacagcc
480
gccagccacc atcaaatggc cgcccagatc ggctgtcatg atgaatgttg ctggctacgc
540
agatgcctgg cgggccgcag tcgaagtaga gtttgtgccc gggcgcagca tacgcgt
597

```

<210> 736

<211> 175

<212> PRT

<213> Homo sapiens

<400> 736

```

Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile
  1              5              10              15
Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser
      20              25              30
Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
      35              40              45
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
      50              55              60
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

```

```

65              70              75              80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
                        85              90              95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
                        100             105             110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
                        115             120             125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
                        130             135             140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145              150              155              160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
                        165              170              175

```

<210> 737

<211> 497

<212> DNA

<213> Homo sapiens

<400> 737

```

ntgcgcctgg ccaattccgg cgccatcctc gggcacgacg tggggaaaaa ctccatgggt
60
cgcgcgggca tcgttgggta cggatacgat cccaaccctc acgccgacgc tgccgaccta
120
caccctgccc tgtcctggat cagccacgtc acctctgcta aaactgtcag tgtgggggat
180
accatcggtc acggcagaaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcgggttacg ccgacggact gtcccaggga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatc tgcattggacc aattcatggt cgatcttggc
360
ccgattcca acgtcacggt gggagatgag gtggtgctca ttggaaccca ggaggacgaa
420
actctgacgc ctgatgacat ggccgaactc ctoggaacca ttagctacga gatcattgct
480
gccatttcca aacgcgt
497

```

<210> 738

<211> 165

<212> PRT

<213> Homo sapiens

<400> 738

```

Xaa Arg Leu Ala Asn Ser Gly Ala Ile Leu Gly His Asp Leu Gly Lys
1           5           10           15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
20          25          30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
35          40          45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
50          55          60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

```

```

65          70          75          80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
      85          90          95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
      100         105         110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
      115         120         125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
      130         135         140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145          150          155          160
Ala Ile Ser Lys Arg
      165

```

<210> 739

<211> 438

<212> DNA

<213> Homo sapiens

<400> 739

```

cggtgctgctggg aagagcgggg gcacgcgctc aagaccaagg aaaagctggc acagaccggc
60
acggcctcat cagcagctgt gggctcaggc cccctcccg aggcggagca ggcgtggcgg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc cccctctctg cgggcccgag gacgacgccc agctccagct ggcctctagt
240
ttgagccgag aagagcatga taaggaggag cggatccgct gcggggatga cctgcggcgtg
300
cagatggcaa tcgaggagag caaggaggag actggggggc aggaggagtc gtcctcatg
360
gaccttgctg acgtcttcac gccccagct cctgccccga ccacagaccc ctggggggggc
420
ccagcaccga tggctgct
438

```

<210> 740

<211> 146

<212> PRT

<213> Homo sapiens

<400> 740

```

Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
1      5      10      15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
      20      25      30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Glu Leu
      35      40      45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
      50      55      60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65      70      75      80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp

```

```

      85              90              95
Asp Leu Arg Leu Gln Met Ala Ile Glu Glu Ser Lys Arg Glu Thr Gly
      100              105              110
Gly Lys Glu Glu Ser Ser Leu Met Asp Leu Ala Asp Val Phe Thr Pro
      115              120              125
Pro Ala Pro Ala Pro Thr Thr Asp Pro Trp Gly Gly Pro Ala Pro Met
      130              135              140
Ala Ala
145

```

```

<210> 741
<211> 726
<212> DNA
<213> Homo sapiens

```

```

<400> 741
gctctctccc gaccgcgttg ttgtaaggat gtcgcgacgg tgcgcacaaa tgaatatgtg
60
aatttgcggg tcactctgcct cgctggggccc actgctagcg gaaaatcagg gctagcgggtg
120
cgagtggtgc gccgcttgta tgctgatgag caccgcggcg aaattattaa tactgactcg
180
atggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgcg cgagcagcgc
240
acggtagtagc atcacctggt gtcgattctt gatgtgactg tgccctcctc gctagtactg
300
atgcagacgc tggcccgtag tgccgtcgag gattgtctgt cgcgtgggtg catccctgtc
360
ttggtgggag ggtctgcgct gtacaccaag gccatcattg acgaaatgtc catcccgcca
420
actgatccgg aagtgagggc tcggtggcag gagaagctag atgccagagg gccgcgagtt
480
ctgcatgacg agcttgcccc tcgcatcccc aaggcggctg agtcaatctt gcccggaac
540
ggcaggcgaa tcgtttcgtg ccctcgaagt ttattgaccc tgacagggtc ctttactgcc
600
accgatcccc gacgggaccc tccactggcc aagacgggtg aaatgggctt agaactgtcg
660
cgcaaaagaca tagaccagcg tattgccgat cggggtgacc agatgtgggc atacggtttc
720
gtcgac
726

```

```

<210> 742
<211> 242
<212> PRT
<213> Homo sapiens

```

```

<400> 742
Ala Ser Leu Arg Pro Arg Cys Cys Lys Asp Val Ala Thr Val Arg Lys
1          5          10          15
Asn Glu Tyr Val Asn Leu Pro Val Ile Cys Leu Val Gly Pro Thr Ala
20         25         30
Ser Gly Lys Ser Gly Leu Ala Val Arg Val Cys Arg Arg Leu Tyr Val

```



```

      35              40              45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
  50              55              60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
  65              70              75              80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85              90              95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100              105              110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115              120              125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Thr Asp Pro Glu
      130              135              140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
      145              150              155              160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165              170              175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180              185              190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195              200              205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210              215              220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
      225              230              235              240
Val Asp

```

<210> 743

<211> 430

<212> DNA

<213> Homo sapiens

<400> 743

```

naaaaaagtg atgggttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
  60
gatgagggca acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
  120
aagctattgg tacgagtgtg cccggcgcac gtgtactcag aggagcccga tggcactatt
  180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcggttgc tgcgccaggg
  240
tcgcttgaat ggcactatcc cgcaggtgca atgggtatctt cggtccagaga aggatgaagt
  300
ccttggtggc gactgtaaag cgacatggcc gtcgctcggt aggaggaatt gtggtgtccg
  360
caccaaaatg tgctcaggat gaagttcgtc atggaaaatcc ggctccaacc gtttcggggg
  420
ctgggtcgca
  430

```

<210> 744

<211> 98

<212> PRT

<213> Homo sapiens

<400> 744

```

Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
 1           5           10           15
His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
      20           25           30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
      35           40           45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
      50           55           60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
65           70           75           80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
      85           90           95
Glu Gly

```

<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

```

cggccgattg aagcgctcgt gcggtttgag tcggtgatgg atcgcggtgga cggtgcttcg
60
gcgctcggtg ggcgcattgg gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
120
tatgagcagg cggcgctttac ccgcgatctg gaaagctcgc tgatcaaggg cctgatccct
180
gccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
240
tacttgattc gcgcgcggca gtacatccac gacaacgccc gcgaagccgt gcactctggaa
300
gacctggaaa ccgctgccgg ggtatcgagg ttcaagtgt tcgatcgctt tcgcaaatac
360
tt
362

```

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

```

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1           5           10           15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
      20           25           30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
      35           40           45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
50           55           60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```

```

65              70              75              80
Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val
                        85              90              95
Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr
                100              105

```

```

<210> 747
<211> 416
<212> DNA
<213> Homo sapiens

```

```

<400> 747
nacgcgttga tcgcccgcga cgttttcac cgcgaatcac cgcacatggc ggcctatttt
60
ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcctgggcc
120
gccgtgttca aacgtatcgc caaggaagga cgggacgcgc tgtaccacgg gccgattggc
180
gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
240
ctcaaggctt acaccgcaa ggaacgcacg ccgctgtgca ccgactaca gcaatatcag
300
gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
360
ctgcaggccg tggaagcccg cgacccacgc ctggccatcg ccccatgaa accggt
416

```

```

<210> 748
<211> 138
<212> PRT
<213> Homo sapiens

```

```

<400> 748
Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
1           5           10          15
Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
20          25          30
Leu Leu Lys Asn Pro Ala Leu Ala Val Phe Lys Arg Ile Ala Lys
35          40          45
Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
50          55          60
Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
65          70          75          80
Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
85          90          95
Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
100         105         110
Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
115         120         125
Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
130         135

```

```

<210> 749
<211> 1211

```

<212> DNA

<213> Homo sapiens

<400> 749

nagtcctaga cgccagaccc gctcagaccc tcctgccagg tgacagccgc caagatgggg
 60
 tcttggggcc tgctgtggcc tcccctgctg ttcaccgggc tgctcgccgc acccccgggg
 120
 accatggccc aggccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac
 180
 acaaatgtca cagagccgct ggtggacatc cacgtcccg aggccaggga ggtgacctc
 240
 ggagccttgt ccaccccctt tgcatttcgg atccagggaa accagctgtt tctcaactg
 300
 actcctgatt acgaggagaa gtcactgctt gaggtcagc tgctgtgtca gagcgaggc
 360
 acattggta cccagctaag ggtgttcgtg tcagtgtg agtcaatga caatgcccc
 420
 gaattcccc ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccac
 480
 gtcatcccc agacgcaact gcaggctgag gaccgcgaca aggaacgacat tctgttctac
 540
 accctccagg aatgacagc aggtgccagt gactacttct ccttggtgag tgtaaacctg
 600
 cccgcctga ggctggaccg gccctggac ttctacgagc ggccgaacat gaccttctg
 660
 ctgctgtgc gggacactcc gggggagaat gtggaaccca gccacactgc caccgccaca
 720
 ctagtgtga acgtggtgcc cgccgacctg cggccccgt ggttctgccc ctgcacctc
 780
 tcagatggt acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata
 840
 ctgccatctc cctcgtctc gcgtcccgga ccatctacg ctgaggacg agaccgcggc
 900
 atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc
 960
 caccagact cgggcaacct caccgtggcc aggagtgtcc ccagccccat gaccttctt
 1020
 ctgctggtga agggccaaca ggccgacctt gcccgctact cagtgaacca ggtcaccgtg
 1080
 gagggctgtg gctgcggccg gagccccgc ccgcttcccc cagagctgt atcgtggcac
 1140
 cgtggcgct ggcgtggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc
 1200
 tctgaggatc c
 1211

<210> 750

<211> 385

<212> PRT

<213> Homo sapiens

<400> 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

1	5	10	15
Leu Val Arg Pro	Pro Gly Thr Met	Ala Gln Ala Gln Tyr Cys Ser Val	
20	25	30	
Asn Lys Asp Ile	Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro		
35	40	45	
Leu Val Asp Ile	His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala		
50	55	60	
Leu Ser Thr Pro	Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu		
65	70	75	80
Asn Val Thr Pro	Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu		
85	90	95	
Leu Cys Gln Ser	Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val		
100	105	110	
Ser Val Leu Asp	Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr		
115	120	125	
Lys Glu Ile Arg	Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile		
130	135	140	
Pro Glu Thr Gln	Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu		
145	150	155	160
Phe Tyr Thr Leu	Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser		
165	170	175	
Leu Val Ser Val	Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp		
180	185	190	
Phe Tyr Glu Arg	Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr		
195	200	205	
Pro Gly Glu Asn	Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val		
210	215	220	
Leu Asn Val Val	Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys		
225	230	235	240
Thr Phe Ser Asp	Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala		
245	250	255	
Val Pro Thr Gly	His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly		
260	265	270	
Pro Ile Tyr Ala	Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile		
275	280	285	
Tyr Ser Ile Phe	Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro		
290	295	300	
Asp Ser Gly Asn	Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr		
305	310	315	320
Phe Leu Leu Leu	Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser		
325	330	335	
Val Thr Gln Val	Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala		
340	345	350	
Pro Leu Pro Pro	Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp		
355	360	365	
Ser Gly Arg Cys	Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu		
370	375	380	
Asp			
385			

<210> 751

<211> 345

<212> DNA

<213> Homo sapiens

<400> 751
 cgcgctgcgg tcacgtgcaa cgacatgagc gaggtcaaca tcgacgcggc gctgggtggcg
 60
 gcaggcgggc ggctgtgcgc caccgaggag aagctcgtcg agatgtcgaa cggctgcacg
 120
 tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggcccg
 180
 ttcgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgcgggt cgccgcccag
 240
 ttcgatttcc gtgaccagga cggcgtctcg ctgcgcgacg tcgcgcgggt ggataccatg
 300
 gtcaccgctg tcgacgccgc gtccttctcg cgcgactacg gctcg
 345

<210> 752
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 752
 Arg Val Ala Val Ile Val Asn Asp Met Ser Glu Val Asn Ile Asp Ala
 1 5 10 15
 Ala Leu Val Ala Ala Gly Gly Gly Leu Ser Arg Thr Glu Glu Lys Leu
 20 25 30
 Val Glu Met Ser Asn Gly Cys Ile Cys Cys Thr Leu Arg Asp Asp Leu
 35 40 45
 Met Gln Glu Val Ala Arg Leu Ala Gly Glu Gly Arg Phe Asp Ala Leu
 50 55 60
 Val Ile Glu Ser Thr Gly Val Ser Glu Pro Met Pro Val Ala Ala Thr
 65 70 75 80
 Phe Asp Phe Arg Asp Gln Asp Gly Val Ser Leu Ala Asp Val Ala Arg
 85 90 95
 Leu Asp Thr Met Val Thr Val Val Asp Ala Ala Ser Phe Leu Arg Asp
 100 105 110
 Tyr Gly Ser
 115

<210> 753
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 753
 gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc
 60
 gcgtcggact agtcacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg
 120
 atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg
 180
 cctatggtag cgcgatcccc gggtacgccc ttcgacggag ctttcgctt ccatgtcgcg
 240
 cgcggcaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg
 300

accgacggct atatcagccc gagctggtag gccgaccgc agggaccaca gt
352

<210> 754

<211> 91

<212> PRT

<213> Homo sapiens

<400> 754

Met	His	Pro	Asn	Arg	Ala	Phe	Arg	Phe	Ala	Asp	Asp	Val	Ser	Met	Leu
1			5						10				15		
Asp	Phe	Ala	Ala	Lys	Arg	Ala	Phe	Ala	His	Ile	Phe	Val	Ser	Thr	Pro
		20					25					30			
Glu	Gly	Pro	Met	Val	Ala	His	Ala	Pro	Val	Thr	Pro	Phe	Asp	Gly	Ala
		35				40				45					
Phe	Arg	Phe	His	Val	Ala	Arg	Gly	Asn	Arg	Ile	Ala	Arg	His	Leu	Asp
	50				55				60						
Gly	Ala	Thr	Leu	Leu	Leu	Ser	Ile	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Ser
65			70						75					80	
Pro	Ser	Trp	Tyr	Ala	Asp	Pro	Gln	Gly	Pro	Gln					
			85					90							

<210> 755

<211> 301

<212> DNA

<213> Homo sapiens

<400> 755

tgggatgcag ggtctttctt ctccaaggat ttcattctctg gagggagaaa agggccccag
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ctgtctgcc tcaaacggg ttgccgggct ggagctcttc ccaggcccggt gtgaggaaga
120
gcaaaggccg gcaggggctc gatgggacca gtcgctcgct caggccccagg aaaaccacac
180
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca
240
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccc cctaccccg
300
g
301

<210> 756

<211> 99

<212> PRT

<213> Homo sapiens

<400> 756

Met	Gln	Gly	Leu	Ser	Ser	Pro	Arg	Ile	Ser	Phe	Leu	Glu	Gly	Glu	Lys
1			5					10				15			
Gly	Pro	Ser	Cys	Leu	Pro	Ser	Asn	Arg	Val	Ala	Gly	Leu	Glu	Leu	Leu
		20					25					30			
Pro	Gly	Pro	Cys	Glu	Glu	Gln	Arg	Pro	Ala	Gly	Ala	Arg	Trp	Asp	
		35				40				45					
Gln	Ser	Leu	Ala	Gln	Ala	Gln	Glu	Asn	His	Thr	Ala	Gly	Gly	Cys	Gln

```

      50              55              60
Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
65              70              75              80
His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
      85              90              95
Tyr Pro Gly

```

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<210> 757
<211> 311
<212> DNA
<213> Homo sapiens

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<400> 757
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60
gtctccgatg ttctctacgt catcgaggcc aacccaggg catcgcgcac agtccccttc
120
gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
180
acgatcgccct cgctcaggcg ctccggccac ctgcccaggg ccgacgcccg cgtcaccgat
240
cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc
300
gaggggacgcg t
311

```

```

<210> 758
<211> 103
<212> PRT
<213> Homo sapiens

```

```

<400> 758
Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
1      5      10      15
Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
20      25      30
Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
35      40      45
Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
50      55      60
Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp
65      70      75      80
Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
85      90      95
Phe Arg Thr Thr Glu Gly Arg
100

```

```

<210> 759
<211> 391
<212> DNA
<213> Homo sapiens

```

```

<400> 759

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attgccgagg gcaagaccta cacccgcaac tcgccgaaca tgtgtgccat gttgccgctc
120
gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg
180
ggctaccgca cgcctgcgtc ggaactgcac gctgccggcc tgacagcgct ggatategac
240
actggtaaaq tgcgtgggca ctaccagttc acccaccatg acctgtggga catggacgtg
300
ggcggccagc cgagcctgat cgacatcaag accgccggcg gcgtgaaaca agccgtgatg
360
gcctcgacca agcaaggcag catctacgcg t
391

<210> 760
<211> 130
<212> PRT
<213> Homo sapiens

<400> 760
Val His Thr Gly Lys Leu Val Trp Asn Trp Asp Ser Gly Asn Pro Asp
1 5 10 15
Asp Thr Thr Pro Ile Ala Glu Gly Lys Thr Tyr Thr Arg Asn Ser Pro
20 25 30
Asn Met Trp Ser Met Phe Ala Val Asp Glu Lys Leu Gly Met Leu Tyr
35 40 45
Leu Pro Met Gly Asn Gln Thr Pro Asp Gln Phe Gly Gly Tyr Arg Thr
50 55 60
Pro Ala Ser Glu Leu His Ala Ala Gly Leu Thr Ala Leu Asp Ile Asp
65 70 75 80
Thr Gly Lys Val Arg Trp His Tyr Gln Phe Thr His His Asp Leu Trp
85 90 95
Asp Met Asp Val Gly Gly Gln Pro Ser Leu Ile Asp Ile Lys Thr Ala
100 105 110
Ala Gly Val Lys Gln Ala Val Met Ala Ser Thr Lys Gln Gly Ser Ile
115 120 125
Tyr Ala
130

<210> 761
<211> 324
<212> DNA
<213> Homo sapiens

<400> 761
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ctaggagagg ccaatccttc cctgccccac agctccttct ctgcaaagct cagggggcaa
120
tcaggtaact cctgcccaag agggcccccatt gggtcctcgc ctaaggaagg cagggcgagg
180
cattgggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg
240

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtagc tgcaaaattt
 300
 tcctcccat ccccatcca caga
 324

<210> 762
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 762
 Met Gly Asp Gly Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe
 1 5 10 15
 Pro Leu Gly Pro Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp
 20 25 30
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala
 35 40 45
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val
 50 55 60
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu
 65 70 75 80
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys
 85 90 95
 Lys Val Arg Pro Leu Trp Ala Tyr Leu
 100 105

<210> 763
 <211> 301
 <212> DNA
 <213> Homo sapiens

<400> 763
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 60
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 120
 ccgcgggtgc cgccaccggc ttaccgagg ccaccggcgg cctcggtctg ttctgctgtg
 180
 gcgctgcctt gggcaccatt gccggccttg ccatgagcaa cattggcgcg gacacaggcg
 240
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 300
 t
 301

<210> 764
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 764
 Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu
 1 5 10 15
 His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg

	20				25					30			
Pro	Ala	Met	Val	Pro	Lys	Ala	Ala	Pro	Ser	Arg	Lys	Gln	Pro
	35					40					45		
Pro	Val	Ala	Ser	Val	Lys	Pro	Val	Ala	Ala	Thr	Ala	Ala	Val
	50				55					60			
Pro	Ala	Val	Ile	Ala	Ile	Leu	Ala	Ala	Thr	Ser	Ser	Thr	Pro
	65			70					75				80
Met	Ser	Ala	Ile	Ile	Glu	Val	Trp	Asp	Ser	Ala	Ser	Pro	Ile
			85					90					95
Ala	His	Asn	Ala										
			100										

<210> 765

<211> 831

<212> DNA

<213> Homo sapiens

<400> 765

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taacattgtt gttcctgtat ttaaggccct ataacaggga agatgcgccca cctcatcagt
120
agcctccaga atcacatca ccagctgaaa ggggagggtcc tgagatataa gcggaaattg
180
agagaagccc agtctgacct gaacaagaca cgccctgcgt gtggtagtgc cctcctgcag
240
tcccagtcct gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
300
gacttatcct ccagtcctc agcttcaaa gcatctcagg aggatgccaa tgaaatcaag
360
tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
420
agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
480
aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
540
gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaa
600
gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
660
cagctgatgg cagctgagaa gaagtctaa gacagattgg aagatctaa gcaaaagact
720
aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
780
aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a
831

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<210> 766

<211> 243

<212> PRT

<213> Homo sapiens

<400> 766

Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

```

      1           5           10           15
Gly Glu Val Leu Arg Tyr Lys Arg Lys Leu Arg Glu Ala Gln Ser Asp
      20           25           30
Leu Asn Lys Thr Arg Leu Arg Ser Gly Ser Ala Leu Leu Gln Ser Gln
      35           40           45
Ser Ser Thr Glu Asp Pro Lys Asp Glu Pro Ala Glu Leu Lys Pro Asp
      50           55           60
Ser Gly Asp Leu Ser Ser Gln Ser Ser Ala Ser Lys Ala Ser Gln Glu
      65           70           75           80
Asp Ala Asn Glu Ile Lys Ser Lys Arg Asp Glu Glu Glu Arg Glu Arg
      85           90           95
Glu Arg Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Lys Glu
      100          105          110
Lys Glu Arg Glu Arg Glu Lys Gln Lys Leu Lys Glu Ser Glu Lys Glu
      115          120          125
Arg Asp Ser Ala Lys Asp Lys Glu Lys Gly Lys His Asp Asp Gly Arg
      130          135          140
Lys Lys Glu Ala Glu Ile Ile Lys Gln Leu Lys Ile Glu Leu Lys Lys
      145          150          155          160
Ala Gln Glu Ser Gln Lys Glu Met Lys Leu Leu Leu Asp Met Tyr Arg
      165          170          175
Ser Ala Pro Lys Glu Gln Arg Asp Lys Val Gln Leu Met Ala Ala Glu
      180          185          190
Lys Lys Ser Lys Ala Glu Leu Glu Asp Leu Arg Gln Arg Leu Lys Asp
      195          200          205
Leu Glu Asp Lys Glu Lys Lys Glu Asn Lys Lys Met Ala Asp Glu Asp
      210          215          220
Ala Leu Arg Lys Ile Arg Ala Val Glu Glu Gln Ile Glu Tyr Leu Gln
      225          230          235          240
Lys Lys Leu

```

<210> 767

<211> 431

<212> DNA

<213> Homo sapiens

<400> 767

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120
gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttctctggc tgcgtcccta
180
ggtcgggtgg cagccttcaa ggtcgccacg ccgtattccc tgtatgtctg tcccgagggg
240
cagaacgtca ccctcacctg caggctcttg ggccctgtgg acaaagggca cgatgtgacc
300
ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccgg
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420
aacaccagcc a
431

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<210> 768
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 768
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser
 1 5 10 15
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala
 20 25 30
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
 35 40 45
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
 50 55 60
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Arg Gly Glu Val
 65 70 75 80
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
 85 90 95
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser
 100 105 110

<210> 769
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 769
 tgtacacctc gtaatacatg atcgcgatac cgcccgcgat gaccctaagc aactcattct
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 cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctgggtttcc gtagaaaga
 120
 acggtatggt ttgtatgtcg cggccctgcc actcaaacct caccgtgtca cccacctcaa
 180
 aaaaatcccc ggtcggccca caaataaate aattgcgccc ctctctcgag ttcttccatg
 240
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaagggtg
 300
 acgttgaccg gactgatttc ggaccagttg gcgtcgggat tgggggcagg gtagttaccg
 360
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 420
 an
 422

<210> 770
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 770
 Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro
 1 5 10 15
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```

                20                25                30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
      35                40                45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
      50                55                60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
      65                70                75                80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
      85                90                95
Pro Asp Xaa

```

<210> 771

<211> 369

<212> DNA

<213> Homo sapiens

<400> 771

```

gcctacgcgc aattcctcgc gggatatggcg tttacaatg cgtctctcgg gtatgtgcat
60
gcaatggcgc atcagctggg cgggtttttac gatctgccgc acggcgtgtg caatgcgata
120
ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gccaggccca tgggtgtcga tgtcagtcga atgacagcag aacagggcgc acagggcgtgt
240
atcgagagaga ttgcgtctctt ggcacgtcag gtgaatatcc cgggtgggatt gcgtgacctc
300
aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

```

<210> 772

<211> 123

<212> PRT

<213> Homo sapiens

<400> 772

```

Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
  1                5                10                15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
      20                25                30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
      35                40                45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
      50                55                60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
      65                70                75                80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
      85                90                95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
      100                105                110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

```

115

120

<210> 773
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 773
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 60
 gggttacttga tccgcgtgga gccgggcgta caaactccgg aattcaccct ggaaaacgcc
 120
 tccggttcct gccgggattc ggcggtggtg ctggtgcaac tgctgcgcaa cctgggcctg
 180
 gcggcgcatg ttgtgtctgg ctatctgacg caactgaccg ccgacgtcaa agccctcgac
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 ggcccgtccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgattttg
 300
 cccggcgcc
 309

<210> 774
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 774
 Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu
 1 5 10 15
 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr
 20 25 30
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala
 35 40 45
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe
 50 55 60
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp
 65 70 75 80
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys
 85 90 95
 Glu Val Tyr Leu Pro Gly Ala
 100

<210> 775
 <211> 4125
 <212> DNA
 <213> Homo sapiens

<400> 775
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 120
 gctaccagcg aagactccga cctgagcatg cgcacactga gcacgcccag cccagccctg
 180

atatgtccac cgaatctccc aggatctcag aatggaagg gctcgtccac ctccctgtcc
240
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300
ccgctcatcc ggctcgctc cagaccccag aaggatcagg ccagcataga ccggctcccc
360
gaccactcca tgggtcagat ctctctcttc ctgcccacca accagctgtg ccgctgcgcg
420
cgagtgtgcc gccgtggta caacctggcc tgggacccgc ggctctggag gactatccgc
480
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660
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780
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1200
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1260
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1620
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1680
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1740
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1800

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1980
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2100
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2160
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2400
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gcaaagccca gatccccca tcagttgctt ttactcagt ttttcaaata ggagtaaagg
2580
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2640
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2880
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2940
gaagagggaa cacactgaga tgacttagac tctgggtccac caaccagacc cttggaaaag
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3060
tggatagaag tctatattct agcctcattt gcatgaagtc agatagccag aagaaattcc
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3180
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3240
aaaatgccca ttatccaat gcgaacctc tgcactcca agccagttat gctgaatttg
3300
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caaacatcat ggctctccat ccaatcaaca tcatacaatt acatgtgtaa tcaaggctct
 3480
 gtgccatggg ggaaatgaat catttagcta ggccaggatc tagtgaaagc cacagagttt
 3540
 aaaaccatga aagaagtga aggcagcatt cctcagctct gtgacttggt accctatttg
 3600
 aagtttcagg atttgggtgt cacaaggat tgtccctaat ccttggccct ggggtcttcc
 3660
 gagtgcgctg gtttaatact ctgagaatga gcaggagat ccagagaatg aatccctgac
 3720
 cgcatacct aaactgtctt ccaaacatga gacaaagctg actgttcaca ctgattgccc
 3780
 agcacatacc gtcttgccag tttcttcttt tctccagtc tctgttcat ccattctggt
 3840
 ctcccttggg gtgggaatct atgatggagg ttactgggga aacagctcag cagatttttg
 3900
 gagaccaaac caaagggtctc actaggaat ttatctgttt taaacattg ctctcttcc
 3960
 ggctctgcta aattgaatgc tcattgtttg ttgttggtgt ttttaattc taatgtcaa
 4020
 atcactgctg gctgtatgaa tctagaaagc cttaatttac taccaagaaa taaagcaata
 4080
 tgttcgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
 4125

<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

Tyr	Gly	Ser	Glu	Gly	Lys	Gly	Ser	Ser	Ser	Ile	Ser	Ser	Asp	Val	Ser
1				5					10					15	
Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
			35				40					45			
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
			50			55				60					
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
				85				90						95	
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
			100					105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
			115			120					125				
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
			130			135					140				
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
				150					155					160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
				165				170						175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

```

      180              185              190
Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
      195              200              205
Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
      210              215              220
Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
      225              230              235              240
Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
      245              250              255
Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
      260              265              270
Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
      275              280              285
Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
      290              295              300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
      305              310              315              320
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
      325              330              335
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
      340              345              350
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
      355              360              365
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
      370              375              380
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
      385              390              395              400
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
      405              410              415
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
      420              425              430
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
      435              440              445
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
      450              455              460
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
      465              470              475              480
Ala Phe Phe

```

<210> 777

<211> 705

<212> DNA

<213> Homo sapiens

<400> 777

```

gggtaccatcg tttttaaaccc taattaagat attactcatt cttgttggtg cccaattcca
60
caccaaatctg ctctttaatg ccagactgat ggctctaaca atccttatta actccttttt
120
gtgggttcaa ggaataacaa aaacctcttc tctcattcac cacctctagg ccaggagaaa
180
ttatttttgg ttcaggcttt cacagtgggg gtctgaaagt gaccagtcta gaaaaggatg
240

```

actcagcaaa aggagagctc tgaagggtccc tgaggcggca cggtcagca ttattaggtc
 300
 acatgggtatg acctgaaaca aatacgttct tcccaaatgt ggcaggaccg ggagagcttc
 360
 tcaccaggag ggaaccgccg caatgaccgc cggacgtcca gcaacacttg ttgtagtcc
 420
 ttgctcatct gccgtagggt cttccctgat ataggagggt ggtcattggc attgacattg
 480
 aggagcttgg gccacacttt tcgtctgac tcacagtcga ggagccctcc ttcactgata
 540
 gccatgcgtc taagggcagc cacatcagtg ggcactctgt tcagagcctg gtgtatctct
 600
 aacactttct ttttctttt ggcgttaaag tctgccttct ccgcgcgcgc gtcccagtg
 660
 ccggagggtg gccgtcccct gcgcactccg gaggccatcc ccggg
 705

<210> 778

<211> 134

<212> PRT

<213> Homo sapiens

<400> 778

Met	Ala	Ser	Gly	Val	Arg	Arg	Gly	Arg	Pro	Thr	Ser	Gly	His	Trp	Asp
1				5					10				15		
Gly	Gly	Ala	Glu	Lys	Ala	Asp	Phe	Asn	Ala	Lys	Arg	Lys	Lys	Lys	Val
		20					25					30			
Leu	Glu	Ile	His	Gln	Ala	Leu	Asn	Ser	Asp	Pro	Thr	Asp	Val	Ala	Ala
	35					40					45				
Leu	Arg	Arg	Met	Ala	Ile	Ser	Glu	Gly	Gly	Leu	Leu	Thr	Asp	Glu	Ile
	50				55					60					
Arg	Arg	Lys	Val	Trp	Pro	Lys	Leu	Leu	Asn	Val	Asn	Ala	Asn	Asp	Pro
65					70				75					80	
Pro	Pro	Ile	Ser	Gly	Lys	Asn	Leu	Arg	Gln	Met	Ser	Lys	Asp	Tyr	Gln
			85					90					95		
Gln	Val	Leu	Leu	Asp	Val	Arg	Arg	Ser	Leu	Arg	Arg	Phe	Pro	Pro	Gly
		100					105						110		
Glu	Lys	Leu	Ser	Arg	Ser	Cys	His	Ile	Trp	Glu	Glu	Arg	Ile	Cys	Phe
		115					120					125			
Arg	Ser	Tyr	His	Val	Thr										
	130														

<210> 779

<211> 322

<212> DNA

<213> Homo sapiens

<400> 779

tcggacatg tgcaacaat tcaatgatgt ggtgcgtcga catgggtgtgc atcactctgt
 60
 gactgtgagt gattctgagg ataccgttgc gccgtcccag ctggttcgat cccctcgtaa
 120
 cgccttgccct ttgaaggaac ccagtgggaa ggctagacca agtaaatatg aatcaccaaa
 180

cgccagcaac ttcacgtgca ggcattgtggc aactggcaaa gagggcactg atgatgagta
 240
 tgctaactca aactactact actcgtatgc tgccaatcga ctaggagacg aggaaacgga
 300
 ggaaatgata ggtttggcta cc
 322

<210> 780
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 780
 Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His
 1 5 10 15
 Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu
 20 25 30
 Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys
 35 40 45
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val
 50 55 60
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn
 65 70 75 80
 Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu
 85 90 95
 Thr Glu Glu Met Ile Gly Leu Ala Thr
 100 105

<210> 781
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 781
 nntcgctgctg ctggaatgtg tgtctgtgta tgtgtgtgta tgtatgtgtg tatggaatgt
 60
 gtgtgtatgn gaatatgtgt gtgtatgnga atgtgtgtgt gtgtttggaa tgtgtgtatg
 120
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatngaa tgtgtgtgtg tgtttggaat
 180
 gtatcgaaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg
 240
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tngaatgtg tgtgtgt
 297

<210> 782
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 782
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Met Tyr Val
 1 5 10 15
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```

                20                      25                      30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
      35                      40                      45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
      50                      55                      60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
      65                      70                      75                      80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
      85                      90                      95
Cys Val Cys

```

<210> 783

<211> 612

<212> DNA

<213> Homo sapiens

<400> 783

```

accggtgacg taactgctcc cgctggcagc ttcgaggcgc atgtcgattt gcgtgcccg
60
caccgggtcg agtgagctgc ccagcagcaa gccaccaca tcggtgacca gaccgatcac
120
tttgtttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggt
180
ccgcacaaaa atcggctggg tgctgatcaa ctgcgggttg ccaatcgag aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgctggct ttgttgga gctgcacaaa gccctgaatc aggttgaaca
360
gttgagggtt gacgtccagg gcgctcttgt ccgtgcggtt ttgtatatgt atcaggtcgc
420
ccagggtcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg ccagcttga gcacatcgat ggcgccctgg atcaactggc
540
cgacggtcgc gtcggtcttg agcaactggc cgtagttgcc ggcgctgacg ttgaggcgga
600
tggccgacgc gt
612

```

<210> 784

<211> 190

<212> PRT

<213> Homo sapiens

<400> 784

```

Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
  1              5              10              15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
      20              25              30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
      35              40              45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

```

```

      50              55              60
Phe Ala Arg Phe Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65              70              75              80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85              90              95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100             105             110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115             120             125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130             135             140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145             150             155             160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165             170             175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180             185             190

```

<210> 785

<211> 408

<212> DNA

<213> Homo sapiens

<400> 785

```

accttggaact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
60
cttcaggcgcg ccacgcctcg tggctctgtca gtactgctcg acgggggtgtt caaccacgtc
120
tcgcgtcgca accgcacgtg gcaggatgcg cagagtgcctg ggccagattc agacgccggc
180
cgtatgggttc gctgggtgtga gggggcgcttc gacgttttcg aggggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgacgtgcgg gaacatgtca cccggatcat gaactattgg
300
tgccggtcgcg gtgttgacgg ctggcggctg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggg gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

```

<210> 786

<211> 134

<212> PRT

<213> Homo sapiens

<400> 786

```

Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

```

```

65              70              75              80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
      85              90              95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
      100             105             110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
      115             120             125
Glu Arg Ser Ala Leu Thr
      130

```

<210> 787

<211> 310

<212> DNA

<213> Homo sapiens

<400> 787

```

acgcgtgaag gggaatgaaa gggtttttcc tggatcaaaa tgatgcttgt ggcagacaca
60
gttggaaacca cagacgatgc cagccttggt tcagcagtgc gacactggcc cactggcgtg
120
ccttggtctc tcctcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagcttttatg tcacaacatt gaggctggcg gagaaagacc ggccccctta cccacacctta
240
gacttctcgg aaggggccgc cgggtccaca acctggcccg ttaactccct gggcagctgc
300
tggggggagaa
310

```

<210> 788

<211> 90

<212> PRT

<213> Homo sapiens

<400> 788

```

Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1          5          10          15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
      20          25          30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
      35          40          45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
      50          55          60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65          70          75          80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
      85          90

```

<210> 789

<211> 369

<212> DNA

<213> Homo sapiens

<400> 789

acgcgtgaag ttgcagcagc aagcaatctg cctcgcttct ggtgccacc gaaaccaagg
 60
 tctgccagac agcagcgctg ggacctctcc cctccccagc aggatggggc ggctctggaa
 120
 gcacgaggtg ttccaaagtg caaacaagct gctgttaaat aattattccc aaacgccaaa
 180
 gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg
 240
 gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcagcg tgtttctgt
 300
 gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc
 360
 cccatttcc
 369

<210> 790

<211> 114

<212> PRT

<213> Homo sapiens

<400> 790

Met Asp Trp Gln Ser Ala Leu Gln Gly Asn Thr Gly Ile His Ser Gln
 1 5 10 15
 Glu Thr Pro Cys Phe Ile Thr His Asn Lys Lys Thr Lys Cys Gln
 20 25 30
 Tyr Ser Ala Leu Ala Ile Ser Val Arg Gly Lys Lys Arg Lys Lys Gln
 35 40 45
 Ala Ser Lys Pro Ala Arg Ala Leu Ala Phe Gly Asn Asn Tyr Leu Thr
 50 55 60
 Ala Ala Cys Leu His Phe Gly Thr Pro Arg Ala Ser Arg Ala Gly Pro
 65 70 75 80
 Ser Cys Trp Gly Gly Glu Arg Ser Gln Arg Cys Cys Leu Ala Asp Leu
 85 90 95
 Gly Phe Gly Gly His Gln Lys Arg Gly Arg Leu Leu Ala Ala Thr
 100 105 110
 Ser Arg

<210> 791

<211> 420

<212> DNA

<213> Homo sapiens

<400> 791

nctctgacca aaaggaaggt atatgaaaac acaacactag gcttcattgt tgaagttgaa
 60
 ggtcttccag ttcttggtgt gaaatgggtat cgaataaaat ctttactaga gccagatgaa
 120
 agaatcaaaa tggaaagagt gggtaaatgt tgttcactgg aaatttctaa cattcaaaaa
 180
 ggagaagggg gagagtacat gtgtcatgct gtaaacatca taggggaagc aaagagcttt
 240
 gcaaatgtag acataatgcc ccaggaagaa agagtgggtgg cactaccacc tccagtaaca
 300

catcagcatg tcattggagtt tgatttggaa cacaccacat catcaagaac accttctctt
 360
 caagaaattg tccttgaagt tgaattaagt gaaaagacg ttaaagaatt tgagaagcag
 420

<210> 792
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 792
 Thr Lys Arg Lys Val Tyr Glu Asn Thr Thr Leu Gly Phe Ile Val Glu
 1 5 10 15
 Val Glu Gly Leu Pro Val Pro Gly Val Lys Trp Tyr Arg Asn Lys Ser
 20 25 30
 Leu Leu Glu Pro Asp Glu Arg Ile Lys Met Glu Arg Val Gly Asn Val
 35 40 45
 Cys Ser Leu Glu Ile Ser Asn Ile Gln Lys Gly Glu Gly Glu Tyr
 50 55 60
 Met Cys His Ala Val Asn Ile Ile Gly Glu Ala Lys Ser Phe Ala Asn
 65 70 75 80
 Val Asp Ile Met Pro Gln Glu Glu Arg Val Val Ala Leu Pro Pro Pro
 85 90 95
 Val Thr His Gln His Val Met Glu Phe Asp Leu Glu His Thr Thr Ser
 100 105 110
 Ser Arg Thr Pro Ser Pro Gln Glu Ile Val Leu Glu Val Glu Leu Ser
 115 120 125
 Glu Lys Asp Val Lys Glu Phe Glu Lys Gln
 130 135

<210> 793
 <211> 479
 <212> DNA
 <213> Homo sapiens

<400> 793
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 60
 ccgcgaacag tactgcggga acccaaacga tcatttttaa cccagacgt ccttgaacca
 120
 aagccaaagt ctacaggtca ctggggcaga ggccgccga aaccagcttc cctcccgcc
 180
 ctaggcgcgc caggtcccg cccagccggg gcgatccttt ggtcggacag tgagggtggg
 240
 agccccaccg acccaagtcc gccgcatcca cccggcgag gcgaccccc acgggcagcc
 300
 gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttcccta
 360
 gcggaggctg ggccggcgcc ttccgcctg cctcagctc ccatccgtg gcccggggga
 420
 tggagcccg tgccgcgaga ggctcggga ggtccagcc aggtgcctg gaactgtga
 479

<210> 794

<211> 159

<212> PRT

<213> Homo sapiens

<400> 794

```

Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val
 1           5           10           15
Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe
      20           25           30
Leu Thr Pro Asp Val Pro Glu Pro Lys Ser Thr Gly His Trp
      35           40           45
Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
      50           55           60
Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly
      65           70           75           80
Ser Pro Pro His Pro Ser Pro Pro His Pro Gly Ala Gly Asp Pro
      85           90           95
Arg Arg Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
      100          105          110
Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser
      115          120          125
Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu
      130          135          140
Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val
      145          150          155

```

<210> 795

<211> 1418

<212> DNA

<213> Homo sapiens

<400> 795

```

gccggcgcg gggaggccgg ggctgcagg cccccgtac gacaagatcc ggactccggc
60
ccggactacg aggcgctgcc ggctggagcc actgtcacca cgcacatggt ggcaggcgcc
120
gtggcaggga tcctggagca ctgcgtgatg taccccatcg actgcgtcaa gaccgggatg
180
cagagtctac agcctgacct agctgcccgc tatcgcaatg tgttgagggc cctctggagg
240
attataagaa cggaggccct atggaggccc atgagggggc tgaacgtcac agcaacaggc
300
gcagggcctg cccacgccct ttatcttgcc tgctacgaaa agttaaaaa gacattgagt
360
gatgtaatcc accctggggg caatagccat attgccaatg gtgcggccgg gtgtgtggca
420
acattacttc atgatgcagc catgaacctc gcggaaggct gatctgctga cttggggctc
480
tgaatctgga tactctccat caccggttgg ctgctgtcac catttcttc ctogttgatg
540
gcactactag tggtaagca gaggatgcag atgtacaact caccatacca ccgggtgaca
600
cgtgtgtgac gggcagtggt gcaaaatgaa ggggcggggg ccttttaccg cagctacacc
660

```

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accagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg
720
caggagcact ttaaccccca gagacggtag aacccaagct cccagctcct ctctggagct
780
tgcgaggag ctgtagctgc cgcagccaca acccactgg acgtttgcaa aacactgctc
840
aacaccagg agtccttggc ttgaaactca cacattacag gacatatcac aggcattggc
900
agtgccttca ggacggtata tcaagtaggt ggggtgaccg cctatttcgg aggggtgacg
960
gccagagtaa ttaccagat cccctccaca gccatcgcat ggtctgtgta tgagtcttc
1020
aaatacctaa tcactaaaag gcaagaagag tggagggctg gcaagtgaag tagcactgaa
1080
cgaagccagg ggttcagatg acactgctgc atcctgggtca cattctctgt ctccctggaat
1140
gtcctccact caagtggagt tagaaggaag gtagaggggc tctccccacg gattttgggt
1200
ttttgactaa caccagtccc tgccaacctc tgttgccacc acctttcctt ccaggcccta
1260
agcacgtgca gcaaagcaca ccacagcacc ttgtataacc tctctccate ctgggcctga
1320
tgacctgctc tagactgtta tagagggata agcagctcat tcccctgggt cctaataaaa
1380
agcctttaa ttaaaaaaaaa aaaaaaaaaa aaaaaaaa
1418

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<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

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Met Ala Leu Leu Val Val Lys Gln Arg Met Gln Met Tyr Asn Ser Pro
1      5      10      15
Tyr His Arg Val Thr Asp Cys Val Arg Ala Val Trp Gln Asn Glu Gly
20     25     30
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Phe Asn Pro Gln Arg Arg Tyr Asn Pro Ser Ser His Val Leu Ser Gly
65     70     75     80
Ala Cys Ala Gly Ala Val Ala Ala Ala Thr Thr Pro Leu Asp Val
85     90     95
Cys Lys Thr Leu Leu Asn Thr Gln Glu Ser Leu Ala Leu Asn Ser His
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Ile Thr Gly His Ile Thr Gly Met Ala Ser Ala Phe Arg Thr Val Tyr
115    120    125
Gln Val Gly Gly Val Thr Ala Tyr Phe Arg Gly Val Gln Ala Arg Val
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Ile Tyr Gln Ile Pro Ser Thr Ala Ile Ala Trp Ser Val Tyr Glu Phe
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170

175

<210> 797

<211> 585

<212> DNA

<213> Homo sapiens

<400> 797

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<212> PRT

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Ile Ala Cys Gly Pro Arg Gly Glu Val Ala Tyr Ala Leu Glu Gly Ala
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Asp Ser Asn Gly Val Tyr Leu Val Pro Ala Phe Thr Gly Leu Gly Ala
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<213> Homo sapiens

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Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Ser His Leu Tyr
35          40          45
Arg Leu His Ser Thr Lys Asn Lys Ile Thr Leu Asn Gly Lys Pro Leu
50          55          60
Glu Ser Tyr Lys Gly Arg Glu Phe Ala Gln Leu Val Ala Val Leu Thr
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Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
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<213> Homo sapiens

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<211> 1400

<212> PRT

<213> Homo sapiens

<400> 804

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Asp	Pro	Leu	Met	Glu	Arg	Arg	Trp	Asp	Leu	Asp	Leu	Thr	Tyr	Val	Thr
			115				120					125			
Glu	Arg	Ile	Leu	Ala	Ala	Ala	Phe	Pro	Ala	Arg	Pro	Asp	Glu	Gln	Arg
			130			135					140				
His	Arg	Gly	His	Leu	Arg	Glu	Leu	Ala	His	Val	Leu	Gln	Ser	Lys	His
145				150						155				160	
Arg	Asp	Lys	Tyr	Leu	Leu	Phe	Asn	Leu	Ser	Glu	Lys	Arg	His	Asp	Leu
			165					170						175	
Thr	Arg	Leu	Asn	Pro	Lys	Val	Gln	Asp	Phe	Gly	Trp	Pro	Glu	Leu	His
			180					185					190		
Ala	Pro	Pro	Leu	Asp	Lys	Leu	Cys	Ser	Ile	Cys	Lys	Ala	Met	Glu	Thr
			195				200					205			
Trp	Leu	Ser	Ala	Asp	Pro	Gln	His	Val	Val	Val	Leu	Tyr	Cys	Lys	Gly
	210				215						220				
Asn	Lys	Gly	Lys	Leu	Gly	Val	Ile	Val	Ser	Ala	Tyr	Met	His	Tyr	Ser
225				230						235				240	
Lys	Ile	Ser	Ala	Gly	Ala	Asp	Gln	Ala	Leu	Ala	Thr	Leu	Thr	Met	Arg
			245					250						255	
Lys	Phe	Cys	Glu	Asp	Lys	Val	Ala	Thr	Glu	Leu	Gln	Pro	Ser	Gln	Arg
			260				265					270			
Arg	Tyr	Ile	Ser	Tyr	Phe	Ser	Gly	Leu	Leu	Ser	Gly	Ser	Ile	Arg	Met
	275					280						285			
Asn	Ser	Ser	Pro	Leu	Phe	Leu	His	Tyr	Val	Leu	Ile	Pro	Met	Leu	Pro

290		295		300	
Ala Phe Glu Pro Gly Thr	Gly Phe Gln Pro Phe Leu Lys Ile Tyr Gln				
305	310		315		320
Ser Met Gln Leu Val Tyr Thr Ser Gly Val Tyr His Ile Ala Gly Pro					
	325		330		335
Gly Pro Gln Gln Leu Cys Ile Ser Leu Glu Pro Ala Leu Leu Leu Lys					
	340		345		350
Gly Asp Val Met Val Thr Cys Tyr His Lys Gly Gly Arg Gly Thr Asp					
	355		360		365
Arg Thr Leu Val Phe Arg Val Gln Phe His Thr Cys Thr Ile His Gly					
	370		375		380
Pro Gln Leu Thr Phe Pro Lys Asp Gln Leu Asp Glu Ala Trp Thr Asp					
385	390		395		400
Glu Arg Phe Pro Phe Gln Ala Ser Val Glu Phe Val Phe Ser Ser Ser					
	405		410		415
Pro Glu Lys Ile Lys Gly Ser Thr Pro Arg Asn Asp Pro Ser Val Ser					
	420		425		430
Val Asp Tyr Asn Thr Thr Glu Pro Ala Val Arg Trp Asp Ser Tyr Glu					
	435		440		445
Asn Phe Asn Gln His His Glu Asp Ser Val Asp Gly Ser Leu Thr His					
	450		455		460
Thr Arg Gly Pro Leu Asp Gly Ser Pro Tyr Ala Gln Val Gln Arg Pro					
465	470		475		480
Pro Arg Gln Thr Pro Pro Ala Pro Ser Pro Glu Pro Pro Pro Pro Pro					
	485		490		495
Met Leu Ser Val Ser Ser Asp Ser Gly His Ser Ser Thr Leu Thr Thr					
	500		505		510
Glu Pro Ala Ala Glu Ser Pro Gly Arg Pro Pro Pro Thr Ala Ala Glu					
	515		520		525
Arg Gln Glu Leu Asp Arg Leu Leu Gly Gly Cys Gly Val Ala Ser Gly					
	530		535		540
Gly Arg Gly Ala Gly Arg Glu Thr Ala Ile Leu Asp Asp Glu Glu Gln					
	545		550		555
Pro Thr Val Gly Gly Gly Pro His Leu Gly Val Tyr Pro Gly His Arg					
	565		570		575
Pro Gly Leu Ser Arg His Cys Ser Cys Arg Gln Gly Tyr Arg Glu Pro					
	580		585		590
Cys Gly Val Pro Asn Gly Gly Tyr Tyr Arg Pro Glu Gly Thr Leu Glu					
	595		600		605
Arg Arg Arg Leu Ala Tyr Gly Gly Tyr Glu Gly Ser Pro Gln Gly Tyr					
	610		615		620
Ala Glu Ala Ser Met Glu Lys Arg Arg Leu Cys Arg Ser Leu Ser Glu					
	625		630		635
Gly Leu Tyr Pro Tyr Pro Pro Glu Met Gly Lys Pro Ala Thr Gly Asp					
	645		650		655
Phe Gly Tyr Arg Ala Pro Gly Tyr Arg Glu Val Val Ile Leu Glu Asp					
	660		665		670
Pro Gly Leu Pro Ala Leu Tyr Pro Cys Pro Ala Cys Glu Glu Lys Leu					
	675		680		685
Ala Leu Pro Thr Ala Ala Leu Tyr Gly Leu Arg Leu Glu Arg Glu Ala					
	690		695		700
Gly Glu Gly Trp Ala Ser Glu Ala Gly Lys Pro Leu Leu His Pro Val					
	705		710		715
Arg Pro Gly His Pro Leu Pro Leu Leu Leu Pro Ala Cys Gly His His					
					720

725										730					735				
His	Ala	Pro	Met	Pro	Asp	Tyr	Ser	Cys	Leu	Lys	Pro	Pro	Lys	Ala	Gly				
740										745					750				
Glu	Glu	Gly	His	Glu	Gly	Cys	Ser	Tyr	Thr	Met	Cys	Pro	Glu	Gly	Arg				
755										760					765				
Tyr	Gly	His	Pro	Gly	Tyr	Pro	Ala	Leu	Val	Thr	Tyr	Ser	Tyr	Gly	Gly				
770										775					780				
Ala	Val	Pro	Ser	Tyr	Cys	Pro	Ala	Tyr	Gly	Arg	Val	Pro	His	Ser	Cys				
785										790					795				
Gly	Ser	Pro	Gly	Glu	Gly	Arg	Gly	Tyr	Pro	Ser	Pro	Gly	Ala	His	Ser				
805										810					815				
Pro	Arg	Ala	Gly	Ser	Ile	Ser	Pro	Gly	Ser	Pro	Pro	Tyr	Pro	Gln	Ser				
820										825					830				
Arg	Lys	Leu	Ser	Tyr	Glu	Ile	Pro	Thr	Glu	Glu	Gly	Gly	Asp	Arg	Tyr				
835										840					845				
Pro	Leu	Pro	Gly	His	Leu	Ala	Ser	Ala	Gly	Pro	Leu	Ala	Ser	Ala	Glu				
850										855					860				
Ser	Leu	Glu	Pro	Val	Ser	Trp	Arg	Glu	Gly	Pro	Ser	Gly	His	Ser	Thr				
865										870					875				
Leu	Pro	Arg	Ser	Pro	Arg	Asp	Ala	Pro	Cys	Ser	Ala	Ser	Ser	Glu	Leu				
885										890					895				
Ser	Gly	Pro	Ser	Thr	Pro	Leu	His	Thr	Ser	Ser	Pro	Val	Gln	Gly	Lys				
900										905					910				
Glu	Ser	Thr	Arg	Arg	Gln	Asp	Thr	Arg	Ser	Pro	Thr	Ser	Ala	Pro	Thr				
915										920					925				
Gln	Arg	Leu	Ser	Pro	Gly	Glu	Ala	Leu	Pro	Pro	Val	Ser	Gln	Ala	Gly				
930										935					940				
Thr	Gly	Lys	Ala	Pro	Glu	Leu	Pro	Ser	Gly	Ser	Gly	Pro	Glu	Pro	Leu				
945										950					955				
Ala	Pro	Ser	Pro	Val	Ser	Pro	Thr	Phe	Pro	Pro	Ser	Ser	Pro	Ser	Asp				
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Trp	Pro	Gln	Glu	Arg	Ser	Pro	Gly	Gly	His	Ser	Asp	Gly	Ala	Ser	Pro				
980										985					990				
Arg	Ser	Pro	Val	Pro	Thr	Thr	Leu	Pro	Gly	Leu	Arg	His	Ala	Pro	Trp				
995										1000					1005				
Gln	Gly	Pro	Arg	Gly	Pro	Pro	Asp	Ser	Pro	Asp	Gly	Ser	Pro	Leu	Thr				
1010										1015					1020				
Pro	Val	Pro	Ser	Gln	Met	Pro	Trp	Leu	Val	Ala	Ser	Pro	Glu	Pro	Pro				
1025										1030					1035				
Gln	Ser	Ser	Pro	Thr	Pro	Ala	Phe	Pro	Leu	Ala	Ala	Ser	Tyr	Asp	Thr				
1045										1050					1055				
Asn	Gly	Leu	Ser	Gln	Pro	Pro	Leu	Pro	Glu	Lys	Arg	His	Leu	Pro	Gly				
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Pro	Gly	Gln	Gln	Pro	Gly	Pro	Trp	Gly	Pro	Glu	Gln	Ala	Ser	Ser	Pro				
1075										1080					1085				
Ala	Arg	Gly	Ile	Ser	His	His	Val	Thr	Phe	Ala	Pro	Leu	Leu	Ser	Asp				
1090										1095					1100				
Asn	Val	Pro	Gln	Thr	Pro	Glu	Pro	Pro	Thr	Gln	Glu	Ser	Gln	Ser	Asn				
1105										1110					1115				
Val	Lys	Phe	Val	Gln	Asp	Thr	Ser	Lys	Phe	Trp	Tyr	Lys	Pro	His	Leu				
1125										1130					1135				
Ser	Arg	Asp	Gln	Ala	Ile	Ala	Leu	Leu	Lys	Asp	Lys	Asp	Pro	Gly	Ala				
1140										1145					1150				
Phe	Leu	Ile	Arg	Asp	Ser	His	Ser	Phe	Gln	Gly	Ala	Tyr	Gly	Leu	Ala				

1155 1160 1165
 Leu Lys Val Ala Thr Pro Pro Ser Ala Gln Pro Trp Lys Gly Asp
 1170 1175 1180
 Pro Val Glu Gln Leu Val Arg His Phe Leu Ile Glu Thr Gly Pro Lys
 1185 1190 1195 1200
 Gly Val Lys Ile Lys Gly Cys Pro Ser Glu Pro Tyr Phe Gly Ser Leu
 1205 1210 1215
 Ser Ala Leu Val Ser Gln His Ser Ile Ser Pro Ile Ser Leu Pro Cys
 1220 1225 1230
 Cys Leu Arg Ile Pro Ser Lys Asp Pro Leu Glu Glu Thr Pro Glu Ala
 1235 1240 1245
 Pro Val Pro Thr Asn Met Ser Thr Ala Ala Asp Leu Leu Arg Gln Gly
 1250 1255 1260
 Ala Ala Cys Ser Val Leu Tyr Leu Thr Ser Val Glu Thr Glu Ser Leu
 1265 1270 1275 1280
 Thr Gly Pro Gln Ala Val Ala Arg Ala Ser Ser Ala Ala Leu Ser Cys
 1285 1290 1295
 Ser Pro Arg Pro Thr Pro Ala Val Val His Phe Lys Val Ser Ala Gln
 1300 1305 1310
 Gly Ile Thr Leu Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His
 1315 1320 1325
 Tyr Pro Val Asn Ser Ile Thr Phe Ser Ser Thr Asp Pro Gln Asp Arg
 1330 1335 1340
 Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val
 1345 1350 1355 1360
 Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala
 1365 1370 1375
 Glu Leu Asp Pro Asp Gln Pro Ala Gly Ala Ile Val Thr Phe Ile Thr
 1380 1385 1390
 Lys Val Leu Leu Gly Gln Arg Lys
 1395 1400

<210> 805

<211> 550

<212> DNA

<213> Homo sapiens

<400> 805

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 atgggacagac ccaggaaatc tcgccaagta cccattcat gggaggccag cagcacaatt
 120
 agtcatccat ttacttatca agctgttact gtgtgtgcaa gaagcgccag agagatgata
 180
 tcaaggagct cttaccatgg ctggcataga gcggtgatg agtaagtcc gtctgcacaa
 240
 agatcccta agcattcatt cttggctgac attcttggt caggggggtc ccatggcctt
 300
 gttccccctc tcgggtcacc agttcaggtc gagggggcct atgcttgaa gggccacacc
 360
 aatggacctt gccaggacac tcagtcacag gtttcacacc caaagagaag acagcccaac
 420
 ccagaccctc aaaagagagc acctggggga agggagcgtg gaaaccagga ctcagaaga
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cacaagagaa aaagaagctg tacactgggg aggcctccgg ggtacctgtg cctgccatgt
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<210> 806
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 806
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 1 5 10 15
 Ser Leu Ser Ile His Ser Trp Leu Thr Phe Leu Ala Gln Gly Val Ser
 20 25 30
 Met Ala Leu Phe Pro Ser Ser Gly His Gln Phe Arg Ser Arg Gly Pro
 35 40 45
 Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His
 50 55 60
 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg
 65 70 75 80
 Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr
 85 90 95
 Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala
 100 105 110
 Cys His Val Ser Glu Gly
 115

<210> 807
 <211> 287
 <212> DNA
 <213> Homo sapiens

<400> 807
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 ccgaggtgg gagagcgcgc ggcattggcga ccgtaaacgt atcgtgtgccc gatgcgatga
 120
 ccgagtggtg cgaagctcag accgggacag gccgtatac cagcgcgagc gattatatct
 180
 gcgccctgat tcgccaggac caggagcgaa gcgacggcct caggcagctt caaacgttga
 240
 tcacgcgagg gttcgacagc ggcacagcg cctcgtcgct tgaatgac
 287

<210> 808
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 808
 Met Ala Val Ala Leu Pro His Trp Gln Asp Ala Lys Phe Leu Ala Met
 1 5 10 15
 Ile Ser Arg Gly Gly Arg Ala Arg Gly Met Ala Thr Val Asn Val Ser

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      20              25              30
Leu Ser Asp Ala Met Thr Glu Trp Val Glu Ala Gln Thr Gly Thr Gly
      35              40              45
Arg Tyr Thr Ser Ala Ser Asp Tyr Ile Cys Ala Leu Ile Arg Gln Asp
      50              55              60
Gln Glu Arg Ser Asp Gly Leu Arg Gln Leu Gln Thr Leu Ile Thr Glu
      65              70              75              80
Gly Phe Asp Ser Gly Ile Ser Ala Ser Ser Leu Asp Asp
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<210> 809

<211> 405

<212> DNA

<213> Homo sapiens

<400> 809

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gggccccccc ccccccccc cttttttttt ccccgggggg tttattccca gggccaacag
120
gacgcgtggt cgcgtcaaat ggagagacga tcggtgccgc ccttgcccca cgatcctgat
180
ggccccgaga ttcctgacga tgtcaccacc ctgcccacac aggtaatggg tctgccacgt
240
cacctgggta tccactcagc tggaatgggt ctgacgcgag aaccagtagg acgcatctgc
300
cccattgagc cggtcgaaat gtttggtcgc acggggctgc agtgggacaa anaaaactgt
360
gcctggatgg ggttggggaa gtttgatctg cttgggttgg ggatg
405

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<210> 810

<211> 135

<212> PRT

<213> Homo sapiens

<400> 810

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Xaa Gly Gly Gly Gly Gly Val Phe Phe Pro Pro Lys Lys Lys Lys
  1           5           10           15
Gly Gly Gly Gly Gly Pro Pro Pro Pro Pro Leu Phe Phe Pro Arg
      20           25           30
Gly Val Tyr Ser Gln Gly Gln Gln Asp Ala Trp Ser Arg Gln Met Glu
      35           40           45
Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
      50           55           60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
      65           70           75           80
His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
      85           90           95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
      100          105          110
Leu Gln Trp Asp Lys Xaa Asn Cys Ala Trp Met Gly Leu Gly Lys Phe
      115          120          125
Asp Leu Leu Gly Leu Gly Met

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130

135

<210> 811

<211> 642

<212> DNA

<213> Homo sapiens

<400> 811

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 60
 cagtgccaat gactgccaat ggcaaagaag agctccaacc aaacaccagg tgcttcatgg
 120
 tgggtgacaca ttaacaacac ccgggaagca gtactgccaa cacctagata tgagaaaaag
 180
 aaaacaggca cttaagcga ggctaaccga ctttcaggaa tgataaaggg cagaggaccc
 240
 tgtcacctct acccctgcta cttaaaggcgt ggcccacaga gcagcagcac cagcagcaca
 300
 taaaatgggg ttaaatatga caggaaaaac aaggtgacag ggaaatgggg tgaagatcaa
 360
 gttcgtggta ngcttttctt tcctagaggc tttgggcctg agctcttgga gaaagctctc
 420
 caacacctca ggggtgtgct gttccctctg cctgtgggga tgctctttgt acgggtgggt
 480
 gactggctcc cactttctct cgtattgttg tcttgtctct tccctcacia ccatcaaggc
 540
 tctttccctt aattctataa gacagtacct ctggcttaga aattatatgc cctcctttaa
 600
 aaaaacgaaa tgctagagga catagaactt gaggaataat tt
 642

<210> 812

<211> 106

<212> PRT

<213> Homo sapiens

<400> 812

Met Val Val Arg Glu Glu Thr Arg Gln Gln Tyr Gly Gly Lys Trp Glu
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 Pro Val Ser His Pro Tyr Lys Glu His Pro His Arg Ala Gly Glu Gln
 20 25 30
 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys
 35 40 45
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe
 50 55 60
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala
 65 70 75 80
 Ala Gly Ala Ala Ala Leu Trp Ala Thr Pro Leu Val Ala Gly Val Glu
 85 90 95
 Val Thr Gly Ser Ser Ala Leu Tyr His Ser
 100 105

<210> 813

<211> 558

<212> DNA

<213> Homo sapiens

<400> 813

cccggcgcat agtcgcgtgg ggtcatggcg gatgaggggt taagagcgcg ttactgcgg
 60
 cgcccgactc cgatcagccg ttcgaaagg cgagccgaa gatcatgaca ttctcgccg
 120
 gttcgctgac cagcaccggg ccgcccggct gggccgggaa accgtggaac aagggaagcg
 180
 ggggcggcgc gcggggtgac gccttcggcc ccttcgcctt cggtcagcgt gcggcgcaat
 240
 tcgggggtcga ggtatgatccg cgcccttcg atcttgacca cgatctccag ttgcccgcca
 300
 ttgtcttcgc cgccgacatc cagcgtgccg ccgcgacca gcgcctcgct ggcgatcagg
 360
 gcgaggttca gcatcaccctt cagcgcggac ttgggcagcg tctccgttcc caccaccagg
 420
 ttgaattgcy tgcgcttatt gtcggcaacc agccctcgt tcgcgggttt cgcttcgcgc
 480
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 ttgttgccg atacgcgt
 558

<210> 814

<211> 151

<212> PRT

<213> Homo sapiens

<400> 814

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Ala	Gly	Lys	Pro	Trp	Asn	Lys	Gly	Ser	Gly	Gly	Gly	Ala	Arg	Gly	Asp
			20				25					30			
Ala	Phe	Gly	Pro	Leu	Ala	Phe	Gly	Gln	Arg	Ala	Ala	Gln	Phe	Gly	Val
		35				40				45					
Glu	Asp	Asp	Pro	Arg	Pro	Phe	Asp	Leu	Asp	His	Asp	Leu	Gln	Leu	Pro
	50				55					60					
Ala	Ile	Val	Phe	Ala	Ala	Asp	Ile	Gln	Arg	Ala	Ala	His	Gln	Arg	
65				70				75					80		
Leu	Ala	Gly	Asp	Gln	Gly	Glu	Val	Gln	His	His	Leu	Gln	Arg	Gly	Leu
			85					90				95			
Gly	Gln	Arg	Leu	Arg	Phe	His	Pro	Pro	Val	Glu	Leu	Arg	Ala	Leu	Ile
		100				105						110			
Val	Gly	Asn	Gln	Pro	Leu	Val	Arg	Gly	Phe	Arg	Phe	Ala	Arg	Val	Asp
		115				120					125				
Leu	Phe	Ala	Glu	Pro	Ala	Gly	Gly	Ala	Glu	Gly	Glu	Ala	Glu	Glu	Phe
	130				135						140				
Glu	Leu	Val	Gly	Gly	Tyr	Ala									
145					150										

<210> 815

<211> 315

<212> DNA

<213> Homo sapiens

<400> 815

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 caaagtggag gatgagaaaag ctcacgacgc gcttcacacg gatgggtcgg agcctggaca
 120
 agctagcgca ggagaaaagg gagacctcac gtccgaagcg gattcagcaa gtgcacaacc
 180
 ttctacccac gctgagggtt ccagtgaagt tactgctacg tccagtatag atgagcaggt
 240
 agacctcatt gctgcaccgt taagcgaaga gtccaatgtc agcaagctcg ggccgtcccc
 300
 tgaggccgat acatc
 315

<210> 816

<211> 90

<212> PRT

<213> Homo sapiens

<400> 816

Met	Pro	Ser	Asp	Leu	Pro	Lys	Val	Asp	Asp	Glu	Lys	Ala	His	Asp	Ala
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Pro	His	Thr	Asp	Gly	Ser	Glu	Pro	Gly	Gln	Ala	Ser	Ala	Gly	Glu	Ser
			20				25					30			
Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
			35				40				45				
His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
			50			55				60					
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
65				70					75					80	
Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
			85					90							

<210> 817

<211> 321

<212> DNA

<213> Homo sapiens

<400> 817

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 ctgaaaggaa tcacacaata ttatgctttt gttgaagagg ggcagaagggt tcattgctgt
 120
 aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat
 180
 agtgttgtagc tgctggctaa aaaaataact gaactcggtt attcatgctt ctacattcat
 240
 gctaagatgt tgcaagacca cagaaatcga gtattccatg attgtcgtaa tgggtgcttg
 300
 agaaaccttg tgtgcacaga t
 321

<210> 818
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 818
 Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met
 1 5 10 15
 Asp Glu Leu Thr Leu Lys Gly Ile Thr Gln Tyr Tyr Ala Phe Val Glu
 20 25 30
 Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln
 35 40 45
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu
 50 55 60
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His
 65 70 75 80
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg
 85 90 95
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp
 100 105

<210> 819
 <211> 3422
 <212> DNA
 <213> Homo sapiens

<400> 819
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 gagggccctgc agcctggggg gactgccctg gcgcctaaga agaggagccg gaaaggccgg
 120
 gcaggggccc atggactctc caaaggcccg ctggagaagc ggccctatct tggcccggtc
 180
 ctgccccctga ctccccgaga cagggccagt ggcacacaag gggccagtga ggacaactct
 240
 ggtggaggag gcaagaagcc aaagatggag gagctgggcc tggcctccca cccccggag
 300
 ggcaggccct gccagcccca gacaaggcca cagaacagc caggccacac caactacagc
 360
 agctattcca agcggaagcg cctcactcgg ggccgggcca agaaccacc ctcttcaccc
 420
 tgtaaggggc gtgccaagcg acgacgacag cagcaggtgc tgccccctga tcccgagag
 480
 cctgaaatcc gcctcaagta catttctct tgcaagcggc tgaggctaga cagccggacc
 540
 cccgcttctt cacccttcgt cggggtggag aagcgagacg cgttcaccac catatgcact
 600
 gttgtcaact cccctggaga tgcgcccaag cccacagga agccttcctc ctctgcctcc
 660
 tcttctcat cctcgtcttc gttctccttg gatgcagccg gggcctccct ggccacactc
 720
 cctggaggct ccactctgca gccgcggccc tcttgcgcc tctcctccac gatgcacttg
 780

gggcctgtgg tttccaaggc cctgagtacc tcttgccctg tttgctgcct ctgccaaaac
840
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900
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<210> 820

<211> 494

<212> PRT

<213> Homo sapiens

<400> 820

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 Phe Thr Ser Pro Glu Ala Leu Gln Pro Gly Gly Thr Ala Leu Ala Pro
 20 25 30
 Lys Lys Arg Ser Arg Lys Gly Arg Ala Gly Ala His Gly Leu Ser Lys
 35 40 45
 Gly Pro Leu Glu Lys Arg Pro Tyr Leu Gly Pro Ala Leu Pro Leu Thr
 50 55 60
 Pro Arg Asp Arg Ala Ser Gly Thr Gln Gly Ala Ser Glu Asp Asn Ser
 65 70 75 80
 Gly Gly Gly Gly Lys Lys Pro Lys Met Glu Glu Leu Gly Leu Ala Ser

85										90										95												
His	Pro	Pro	Glu	Gly	Arg	Pro	Cys	Gln	Pro	Gln	Thr	Arg	Ala	Gln	Lys	His	Pro	Glu	Gly	Arg	Pro	Cys	Gln	Pro	Gln	Thr	Arg	Ala	Gln	Lys		
100										105										110												
Gln	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
115										120										125												
Thr	Arg	Gly	Arg	Ala	Lys	Asn	Thr	Thr	Ser	Ser	Pro	Cys	Lys	Gly	Arg	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
130										135										140												
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180										185										190												
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225										230										235												
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240										245										250												
Thr	Met	His	Leu	Gly	Pro	Val	Val	Ser	Lys	Ala	Leu	Ser	Thr	Ser	Cys	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
255										260										265												
Leu	Val	Cys	Cys	Leu	Cys	Gln	Asn	Pro	Ala	Asn	Phe	Lys	Asp	Leu	Gly	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
270										275										280												
Asp	Leu	Cys	Gly	Pro	Tyr	Tyr	Pro	Glu	His	Cys	Leu	Pro	Lys	Lys	Lys	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
285										290										295												
Pro	Lys	Leu	Lys	Glu	Lys	Val	Arg	Pro	Glu	Gly	Thr	Cys	Glu	Glu	Ala	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
300										305										310												
Ser	Leu	Pro	Leu	Glu	Arg	Thr	Leu	Lys	Gly	Pro	Glu	Cys	Ala	Ala	Ala	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
315										320										325												
Ala	Thr	Ala	Gly	Lys	Pro	Pro	Arg	Pro	Asp	Gly	Pro	Ala	Asp	Pro	Ala	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
330										335										340												
Lys	Gln	Gly	Pro	Leu	Arg	Thr	Ser	Ala	Arg	Gly	Leu	Ser	Arg	Arg	Leu	His	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	L			

<210> 821

<211> 420

<212> DNA

<213> Homo sapiens

<400> 821

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 120
 cgtttgccgc aaaatgtggt gctaggttcg gaaacgacct cgacggtag cagccgtggt
 180
 gtctacaagt ttctgttgt gctgaagtcc gatgccatct atccccacca tcagtcgtca
 240
 ggctacgaca cagagtattg ttctgtgtcg aacacccccg atgtcgattt cgcctcggc
 300
 gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcgggtgaa
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 420

<210> 822

<211> 133

<212> PRT

<213> Homo sapiens

<400> 822

Met	Asp	Gln	Val	Ser	Cys	Val	Leu	Asp	Asn	Gly	Phe	Ala	Ala	Ile	Met
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Asp	Val	Pro	Gly	Phe	Asn	Tyr	Arg	Ala	His	Arg	Tyr	Thr	Glu	Ala	Tyr
			20				25						30		
Arg	Arg	Leu	Pro	Gln	Asn	Val	Val	Leu	Gly	Ser	Glu	Thr	Thr	Ser	Thr
		35				40						45			
Val	Ser	Ser	Arg	Gly	Val	Tyr	Lys	Phe	Pro	Val	Val	Leu	Lys	Ser	Asp
		50				55					60				
Ala	Ile	Tyr	Pro	Asp	His	Gln	Ser	Ser	Gly	Tyr	Asp	Thr	Glu	Tyr	Cys
65					70				75					80	
Ser	Trp	Ser	Asn	Thr	Pro	Asp	Val	Asp	Phe	Ala	Leu	Ala	Glu	Asp	Tyr
			85					90					95		
Pro	Trp	Thr	Met	Gly	Gln	Phe	Val	Trp	Thr	Gly	Phe	Asp	Tyr	Leu	Gly
		100						105					110		
Glu	Pro	Ser	Pro	Tyr	Asp	Thr	Asp	Ala	Trp	Pro	Ser	His	Ala	Ser	Leu
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Phe	Gly	Ile	Val	Asp											
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<210> 823

<211> 550

<212> DNA

<213> Homo sapiens

<400> 823

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 120

ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt
 180
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 240
 gctttgtaaa tggcatctac ggaagcatca cctggggccac ccacaacgag gccatccttc
 300
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 360
 ggtggaagtg tagtggttgg attctcagga agtgctgtga gccaggctg agtgcttatt
 420
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 540
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<210> 824

<211> 161

<212> PRT

<213> Homo sapiens

<400> 824

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Ala	Leu	Leu	Asn	Lys	Arg	Ile	Ser	Thr	Gln	Pro	Gly	Leu	Thr	Ala	Leu
			20					25				30			
Pro	Glu	Asn	Pro	Asn	Thr	Thr	Leu	Pro	Pro	Phe	Gln	Asp	Thr	Pro	Cys
		35					40				45				
Glu	Leu	Gln	Pro	Arg	Ile	Asp	Pro	Ser	Leu	Gly	Gln	Gln	Val	Lys	Asp
	50				55					60					
Gly	Leu	Val	Val	Gly	Gly	Pro	Gly	Asp	Ala	Ser	Val	Asp	Ala	Ile	Tyr
65				70				75						80	
Lys	Ala	Val	Val	Asp	Ala	Ala	Ser	Lys	Gly	Met	Gln	Val	Val	Ile	Thr
			85					90						95	
Thr	Ala	Val	Asn	Ser	Thr	Thr	Gln	Ile	Ser	Pro	Ile	Pro	Ala	Leu	Ser
			100				105						110		
Ala	Met	Ser	Ala	Phe	Thr	Ala	Ser	Ile	Gly	Asp	Pro	Leu	Asn	Leu	Ser
		115					120				125				
Ser	Ala	Val	Ser	Ala	Val	Ile	His	Gly	Arg	Asn	Met	Gly	Gly	Val	Asp
		130				135				140					
His	Asp	Gly	Arg	Leu	Arg	Asn	Ser	Arg	Gly	Ala	Arg	Leu	Pro	Lys	Asn
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Leu															

<210> 825

<211> 327

<212> DNA

<213> Homo sapiens

<400> 825

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 aaccgcgata tccctcacctc ttcgggtggcg gcgggtatcg cctccatcat cggtacgatt
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<210> 826

<211> 109

<212> PRT

<213> Homo sapiens

<400> 826

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Glu	Gly	Ile	Leu	Gln	Leu	Leu	Asp	Glu	Arg	Glu	Met	Arg	Gly	Val	Leu
			20				25					30			
Gly	His	Glu	Leu	Met	His	Val	Tyr	Asn	Arg	Asp	Ile	Leu	Thr	Ser	Ser
			35				40				45				
Val	Ala	Ala	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Thr	Ile	Ala	Gln	Ile	Leu
	50				55				60						
Ser	Phe	Gly	Ala	Met	Phe	Gly	Gly	Ser	Asn	Arg	Asp	Gly	Glu	Arg	Ser
65				70				75					80		
Asn	Pro	Leu	Ala	Met	Phe	Val	Val	Ala	Met	Leu	Ala	Pro	Ile	Ala	Thr
			85					90					95		
Gln	Val	Ile	Gln	Met	Ala	Ile	Ser	Arg	Thr	Arg	Glu	Phe			
			100					105							

<210> 827

<211> 534

<212> DNA

<213> Homo sapiens

<400> 827

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 240
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 360
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 420
 ggggttagtcg gcataccccc cccacggtcc tcagctccgt cggtggggaca gcacagcgtc
 480

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<210> 828

<211> 174

<212> PRT

<213> Homo sapiens

<400> 828

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20 25 30
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro
35 40 45
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu
50 55 60
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile
65 70 75 80
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu
85 90 95
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu
100 105 110
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro
115 120 125
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly
130 135 140
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val
145 150 155 160
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala
165 170

<210> 829

<211> 492

<212> DNA

<213> Homo sapiens

<400> 829

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atctggctgg acctgaagga ggccgggtgac ttctacttcc agccagctgt gaagaagttt
120
gtcctaaga attatggaga gaaccacagaa gcctacaatg aagaactgaa gaagctggag
180
ttgtctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtgag tgtcctccgc
240
aagtaacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag
300
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggag
360
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420
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480

gcagccggcg cc
492

<210> 830
<211> 164
<212> PRT
<213> Homo sapiens

<400> 830
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Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His
20 25 30
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn
35 40 45
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln
50 55 60
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg
65 70 75 80
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly
85 90 95
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser
100 105 110
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile
115 120 125
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys
130 135 140
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys
145 150 155 160
Ala Ala Gly Ala

<210> 831
<211> 303
<212> DNA
<213> Homo sapiens

<400> 831
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120
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180
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300
gac
303

<210> 832
<211> 101
<212> PRT

<213> Homo sapiens

<400> 832

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 20 25 30
 Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
 35 40 45
 Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
 50 55 60
 Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
 65 70 75 80
 Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
 85 90 95
 Met Thr Val Val Asp
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<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

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 120
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 180
 ggattccacc aggcggggtg gcatgttgcg gcggcggttg agcagcagct gtcggcgctct
 240
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 300
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 360
 gatgcgcgatg tcggaactgg gtggatcgcc agcgagcccc ccgacgatcc cggctgcgaa
 420
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 466

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

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 Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
 20 25 30
 Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
 35 40 45
 Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

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      50              55              60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys
65              70              75              80
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg
      85              90              95
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly
      100              105              110
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His
      115              120              125
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile
      130              135              140

```

<210> 835

<211> 482

<212> DNA

<213> Homo sapiens

<400> 835

```

acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag
60
aagctcagag caaagaacat cacaccacgt ccctcagtga tgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgttaga gacaaaacta
180
aaagtaaaat accaagttaa atcaaagcat cagattgag ccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
420
tgaagaacaa tcccatggcc atgcaggcac tcctcccttc cacctctctg cccttcacgc
480
gt
482

```

<210> 836

<211> 120

<212> PRT

<213> Homo sapiens

<400> 836

```

Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
1              5              10              15
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
      20              25              30
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
      35              40              45
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
      50              55              60
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
65              70              75              80
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

```



```

      85              90              95
Lys Ile Arg  Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu
      100              105              110
Leu Gln Ser  Leu Arg Asp Val Val
      115              120

```

<210> 837
 <211> 509
 <212> DNA
 <213> Homo sapiens

```

<400> 837
acgcgtggag ccccgcttctg cccgcctttg cagtcacgcg cctccctgaa gtcaccgctg
60
cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
120
ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggt
180
gcctggcggt cgagcccctc ttatcctggg gaatgctggg gggcgcttct gagcagacct
240
gcctgctgcc cctgctggct ggcactgccc ctcccccggg gaaaggttgg gtgtccccc
300
caggggaact caaagcaggg gagccccctg agggcccaag tccctggaat atcttggcgc
360
tcagatggcc cccctcgaac accctcacac gggggggcgg cgcggtggga ggtgaccag
420
cagccactct tacttggcga agacttttct cccaatgcga gcgcgggtgg tatcagcctg
480
agccttcagg ttggtgaggc tgggggtacc
509

```

<210> 838
 <211> 119
 <212> PRT
 <213> Homo sapiens

```

<400> 838
Met Ala Pro  Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
1      5      10
Ser Tyr Pro  Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
      20      25      30
Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
      35      40      45
Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
      50      55      60
Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
      65      70      75      80
Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
      85      90      95
Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
      100      105      110
Gln Val Gly Glu Ala Gly Val
      115

```

<210> 839
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 839
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggtca atgtggaggg tcggctccag
 60
 ggccgtctcg acatgccgtt ggaatgaggtg gggcgccgtc aggcactcac agtgggtcaa
 120
 gtcatcgccg agatggaacc tgacgcgac atggcctctc cgctacaacg tgcgcgcgac
 180
 acagctcagg caatcggtgc ttgtgctgga ttggcggtac agctggatga tcgactcacc
 240
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgctg caacgaccc
 300
 gaggatcgag caagtgtggt cagccctatc gattaccggg tcggagn
 347

<210> 840
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 840
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu
 1 5 10 15
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg
 20 25 30
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp
 35 40 45
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala
 50 55 60
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile
 65 70 75 80
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg
 85 90 95
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr
 100 105 110
 Arg Val Gly
 115

<210> 841
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 841
 tccggaactc accccgacgc cgctcattatg gacgtcatga tgccgcgtct agatggcttg
 60
 gaagccaccg ggaatgctgc cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc
 120
 cgcgatgctg tcgacgatcg cgttgacggc ctgcacgctg gcgcccagta ctacatggtc
 180

aagcccttcg cctcgcagca actcctcgct cgcctacgcg ccctcactcg tcgttcccg
 240
 cccgagccag agcaaaacga ggccctgaa caactctcct tcgtgacct cacccttgat
 300
 ccaggcaccg gcgagatcac ccgcgggaac cgtcgcatca gtttgacgcg t
 351

<210> 842

<211> 117

<212> PRT

<213> Homo sapiens

<400> 842

Ser	Gly	Thr	His	Pro	Asp	Ala	Val	Ile	Met	Asp	Val	Met	Met	Pro	Arg
1				5					10					15	
Leu	Asp	Gly	Leu	Glu	Ala	Thr	Arg	Met	Leu	Arg	Ser	Asn	Gly	Asn	Asp
			20					25					30		
Val	Pro	Ile	Leu	Val	Leu	Thr	Ala	Arg	Asp	Ala	Val	Asp	Asp	Arg	Val
		35				40					45				
Asp	Gly	Leu	Asp	Ala	Gly	Ala	Asp	Asp	Tyr	Met	Val	Lys	Pro	Phe	Ala
50					55						60				
Leu	Asp	Glu	Leu	Leu	Ala	Arg	Leu	Arg	Ala	Leu	Thr	Arg	Arg	Ser	Arg
65					70				75					80	
Pro	Glu	Pro	Glu	Gln	Asn	Glu	Ala	Pro	Glu	Gln	Leu	Ser	Phe	Ala	Asp
			85						90					95	
Leu	Thr	Leu	Asp	Pro	Gly	Thr	Arg	Glu	Ile	Thr	Arg	Gly	Asn	Arg	Arg
			100					105						110	
Ile	Ser	Leu	Thr	Arg											
			115												

<210> 843

<211> 393

<212> DNA

<213> Homo sapiens

<400> 843

ctagcccagg ctctcgcca cgaggggctg cgcgctgtgg cctctggggc aaaccgggtc
 60
 ggcctcaagc gcggtatcga gaagggtgtc gacgccgttg tggaggagct ccgctctatc
 120
 tcgcgcgcca tcgacaccac ctcggacatg gccagcgttg ccaccatctc cagccgtgac
 180
 gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggttaagg cgggggttatc
 240
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc
 300
 gacaagggtt acctgtcgcc ctacatggtc accgaccagg ttcgcatgga ggctgtgatc
 360
 gaggatcctt acatcctcat tcaactccgc aag
 393

<210> 844

<211> 131

<212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
      20           25           30
Val Val Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
      35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
      50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
      65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
      85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
      100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
      115          120          125
Ser Arg Lys
      130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

```

gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
ccccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttggagga
180
ggcggctgcc gtgaagacag gcacctctgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gcccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac ccagtttcc
360
tctgcatacg ggtccgagc cctgcactgc ctccagggta gttcccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcg
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1           5           10           15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20           25           30
Lys Ala Pro Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35           40           45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50           55           60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65           70           75           80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85           90           95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100          105          110
Ala Pro Ala Ala Val Ala Leu Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115          120          125
Val Pro
      130

```

<210> 847

<211> 448

<212> DNA

<213> Homo sapiens

<400> 847

```

aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct cgcgatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tctgtaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacagaaga
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatattgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaatc tgagaaatag tgcggttagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848

<211> 149

<212> PRT

<213> Homo sapiens

<400> 848

```

Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
      1           5           10           15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20           25           30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35           40           45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Cys Glu

```

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100              105              110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115              120              125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130              135              140
Asp Val Arg Lys Ile
145

```

<210> 849

<211> 463

<212> DNA

<213> Homo sapiens

<400> 849

```

nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaatgaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggga
180
gctgaagatg gatcatggta ttccccctcg catattgtct caaagtccca ctttgtggat
240
ttggcaggat cagaaagagt aacaaaaacg gggaataactg gtgaacgggt caaagaatcc
300
attcaaatca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccga
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttaccggcgt tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

<210> 850

<211> 154

<212> PRT

<213> Homo sapiens

<400> 850

```

Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1              5              10              15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20              25              30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35              40              45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50              55              60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65              70              75              80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

```

      85              90              95
Phe Lys Glu Ser Ile Gln Ile Asn Ser Gly Leu Leu Ala Leu Gly Asn
      100              105              110
Val Ile Ser Ala Leu Gly Asp Pro Arg Arg Lys Ser Ser His Ile Pro
      115              120              125
Tyr Arg Asp Ala Lys Ile Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly
      130              135              140
Ser Ala Lys Thr Val Met Ile Thr Cys Val
145              150

```

<210> 851

<211> 372

<212> DNA

<213> Homo sapiens

<400> 851

```

aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
60
gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
120
aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
180
ttgcttatgct gataagggtta ttcagcttga cgatttggtc gtggtctttc aaccgttttg
240
cagctggtgc acgatattcc tggtaggaac tacgatagaa gaccagcacc ggaagaactt
300
tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
360
taacccacgc gt
372

```

<210> 852

<211> 110

<212> PRT

<213> Homo sapiens

<400> 852

```

Met Ser Glu Leu Leu Met Gln Phe Leu His Ser Leu Ile Asn Ser Phe
1      5      10      15
Ile Ser His Phe Glu Asn Ser Arg Cys Arg Ile Lys Ala Arg Val Trp
      20      25      30
Gly Pro Ser Pro Gln Leu Arg Leu Arg Asp Phe Leu Asp Leu Val Cys
      35      40      45
Tyr Ala Asp Lys Val Ile Gln Leu Asp Asp Leu Phe Val Val Phe Gln
      50      55      60
Pro Phe Cys Ser Trp Ser Thr Ile Phe Leu Val Gly Thr Thr Ile Glu
      65      70      75      80
Asp Gln His Arg Lys Asn Phe Val Asp Ala Glu Gln Thr Pro Thr Asp
      85      90      95
His Phe Ser Leu Glu Val Arg Val Ile Leu Ser Asn Pro Arg
      100      105      110

```

<210> 853

<211> 423

<212> DNA

<213> Homo sapiens

<400> 853

acgcgttcag aaacttatgg tgaatggcc gaactagaaa acctagtcga cgaatattac
 60
 caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa
 120
 gtccaagaaa cgcatttgtt agaagagctt gcagggcatag aatcaggtga tgatggcgca
 180
 gtgggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgatag aaaagaagca
 240
 cagattcgtc atggattgca tcgtcttga gaattaccag aagacgataa attggccgat
 300
 accttggtcg ccttattgcy tttaccccg ggagtgaca ttaccagcaa gggaattttg
 360
 catgccttaa tggcagattt agagttagaa caagacgatt ttgacccaat gcaaagcacg
 420
 cgt
 423

<210> 854

<211> 141

<212> PRT

<213> Homo sapiens

<400> 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1			5					10					15		
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
	20						25					30			
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
	35					40					45				
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
	50					55				60					
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
65			70					75					80		
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
		85					90						95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
	100						105					110			
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
	115					120						125			
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
	130					135						140			

<210> 855

<211> 338

<212> DNA

<213> Homo sapiens

<400> 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga
 60

tgaatgtctg tgcggatggt gctcacagca agatagtgtc tggagcgatt ggcacttcga
 120
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag
 180
 ctggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcaagtgtaa
 240
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa
 300
 acattgctct gagcccattg gagnetctga gcagaaaag
 338

<210> 856

<211> 93

<212> PRT

<213> Homo sapiens

<400> 856

Met	Asn	Val	Cys	Ala	Asp	Val	Ala	His	Ser	Lys	Ile	Val	Leu	Gly	Ala
1			5						10				15		
Ile	Gly	Thr	Ser	Asn	Lys	Met	Glu	His	Gly	Ala	Asp	Gly	Ala	Leu	Ser
			20				25						30		
Lys	Met	Glu	Arg	Gly	Val	Asp	Arg	Ala	Trp	Ser	Lys	Lys	Glu	Leu	Gln
		35				40					45				
Ala	Arg	Trp	Ser	Leu	Gln	Gln	Val	Leu	Leu	Ser	Val	Arg	Trp	Ser	Ser
	50				55					60					
Glu	Lys	Met	Met	Leu	Arg	Val	Arg	Leu	Ser	Ser	Val	Ile	Gly	Thr	Pro
65				70					75					80	
Asn	Ile	Ala	Leu	Ser	Pro	Leu	Glu	Xaa	Leu	Ser	Arg	Lys			
			85					90							

<210> 857

<211> 435

<212> DNA

<213> Homo sapiens

<400> 857

cggacagtg ggccaccagt gtttgcccc agcaatcatg tcagtgaagc ccaacctcgg
 60
 gagacacccc ggccccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc
 120
 cctgggtgaca ggggtggagac ccctgtgggg gagagagccc caacccctgt ctgagcaagg
 180
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc
 240
 tctgagcagc ctcccaacag cgtcctgcct gacaaaactga aggtgagctg ggagaacccc
 300
 agccccccagg agggccccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag
 360
 acttctgagg ctgccccccag ggaggggtggg aagcccccta cccccccacc caagatctta
 420
 tcagagaaac tgaaa
 435

<210> 858

<211> 145

<212> PRT

<213> Homo sapiens

<400> 858

```

Pro Asp Ser Gly  Pro Pro Val Phe Ala  Pro Ser Asn His Val Ser Glu
 1           5           10           15
Ala Gln Pro  Arg  Glu Thr  Pro Arg  Pro Leu Met  Pro Pro Thr Lys Pro
          20           25           30
Phe Leu Ala  Pro Glu Thr  Thr Ser Pro Gly Asp Arg  Val Glu Thr Pro
          35           40           45
Val Gly Glu  Arg Ala  Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser
          50           55           60
Pro Glu Ser  Gln Glu Asp Ser Glu Thr  Pro Ala  Glu Glu Asp Ser Gly
65           70           75           80
Ser Glu Gln  Pro Pro Asn Ser Val Leu  Pro Asp Lys Leu Lys Val Ser
          85           90           95
Trp Glu Asn  Pro Ser Pro Gln Glu Ala  Pro Ala Ala Glu Ser Ala Glu
          100          105          110
Pro Ser Gln Ala  Pro Cys Ser Glu Thr Ser Glu Ala Ala  Pro Arg Glu
          115          120          125
Gly Gly Lys  Pro Pro Thr Pro Pro Pro Lys Ile  Leu Ser Glu Lys Leu
          130          135          140
Lys
145

```

<210> 859

<211> 561

<212> DNA

<213> Homo sapiens

<400> 859

```

naccgctggt  gtggaatcc  ggtttctggt  ggcgacggct  gccacccttc  gtggcaagac
60
atgcgcgtgc  gtgccgatat  gccatacgaa  gcttgcccta  gtgcgaaaag  ctgcgtggaa
120
ccctcgaaga  ggcagggtcg  gcagggttacc  gtggtcggtg  tacgcatcgt  ttcgacgatg
180
aacccattc  tgggagcaga  tatgacgacg  taccagtacc  tcattgtcgg  tggcgggatg
240
gccgctgatt  ctgccgcccc  cggtatccgc  gacatcgaca  agaaagggtc  gatcgccatc
300
ctcagcgcgt  acgtcgacgc  cccgtatcct  cggccagcgc  tgagcaagaa  gctgtggact
360
gaccttgagt  tcacctggga  ccagggtcac  cttgctactg  tcgctgacac  cggcgcgga
420
ttgcggtcgc  gcactgaggt  gctcagcatt  gaccgtgacg  gcaagaccgt  cctgaccgct
480
tccgggccag  tattcggcta  ccagaagttg  ctgctcggtta  cgggccttac  cccgtcgcgc
540
attgacgacg  acggcgatgc  c
561

```

<210> 860

<211> 187

<212> PRT

<213> Homo sapiens

<400> 860

```

Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro
 1           5           10
Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp
      20           25           30
Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln
      35           40           45
Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu
      50           55           60
Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met
65           70           75           80
Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly
      85           90           95
Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro
      100          105          110
Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln
      115          120          125
Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly
      130          135          140
Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala
      145          150          155          160
Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu
      165          170          175
Thr Pro Ser Arg Ile Asp Asp Gly Asp Ala
      180          185

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<210> 861

<211> 352

<212> DNA

<213> Homo sapiens

<400> 861

```

ccatgggttt ctatgctctg aggtttctatc tgtggggaac agtattgact tacttacaaa
60
gagataatgg tcatacccta tggctcaactca ccatagtctg gcggtacatg gacttctcag
120
ccccagtaag atctgtatcc acaggacact taaagtccac ttacagaggg ctatccagtg
180
gcctgaggcc tatttagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg
240
gatccccagag cctgcctcgg gaatggcaga agctggctgg tgcttggcgt gggctttgcc
300
tgtttcactg ctttcaggga ggccctgccac aggggagaaaa ctgggggggg ga
352

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<210> 862

<211> 116

<212> PRT

<213> Homo sapiens

<400> 862

```

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1           5           10           15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
           20           25           30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
 35           40           45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
 50           55           60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
 65           70           75           80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
           85           90           95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
 100           105           110
Asn Trp Gly Gly
 115

```

<210> 863

<211> 327

<212> DNA

<213> Homo sapiens

<400> 863

```

tccggatcga cccggacgaa ttccacggtc cagccattga cttccaaatg ctctttgaca
 60
tacgccgtga catgttcaat gtccaactta cgcgatgtcca cccgctcacc ggtctcattg
 120
agtttgagct gcgagtagac gttgcggtag ttctcggtga ccgactgctc atacgagatg
 180
tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttggttga catggccgct
 240
tggcggaaca tggtcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
 300
agcatttctg accggcgatg acccatn
 327

```

<210> 864

<211> 108

<212> PRT

<213> Homo sapiens

<400> 864

```

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1           5           10           15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
           20           25           30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
 35           40           45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
 50           55           60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
 65           70           75           80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

85 90 95
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro
 100 105

<210> 865
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 865
 acgcgtcattc ctcattcaag agggccagga ggagcaccac cctccgcata ttgcgcgtgc
 60
 agctctcgtt ctgggtctctg agcatgcccc cggcgctctg cacacagctt ctcagcagcc
 120
 tgggtggtgc caggatcgac acatcactgc ctccgagtgc agaggtttcc tttccacct
 180
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc
 240
 tggcctccgt ctccatcgcc tctcatggc cgtcttccgc cgggtgttcc aagcccagct
 300
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat
 360
 cagaaacat gaggggtgat ctccggaggt catcgatgtg gacagactgc cacagccctc
 420
 cgtggaagcc cacataggct gttcctcttc cccccggga cagttttgtg atgaaataga
 480
 cgaagatacg gtcctcattt tctcgtatgt tggtgatttc atttataaca gaataacttag
 540
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga
 600
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gactactcgg
 660
 tgtcaaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt
 720
 ctaaaattt
 729

<210> 866
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 866
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys
 1 5 10 15
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro
 20 25 30
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro
 35 40 45
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg
 50 55 60
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg
 65 70 75 80
 Thr Ala Gly

<210> 867
 <211> 640
 <212> DNA
 <213> Homo sapiens

<400> 867
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
 60
 tcagggtggac tctcgttggt ggccggcgctc gctggccccc tcgcaccocgg tcccggtgca
 120
 catgctccag ggccgcagctc ttgtccacct ttacctcacc gaaagccttg tttttgcctc
 180
 gggttaatccc ttcattgagg gctttgatcc aggattcctt ctctccccc gtgggtgcct
 240
 ggaatttgat gtcgctgacc ttgttccctg gggatcgag caggataaag cggtgttttc
 300
 gcttgaggag ggcacgaagg tcttggcact tctcatagct gccagctcc acagtctcca
 360
 cacacttctg atcatcctca ttctcataga ccagcagctg ggcttggcag aggagcagat
 420
 atcggctctt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
 480
 ccaccatctg tgctcccccga ggcttctcac cggttctctt cacaccctcc tcctccatgg
 540
 cgaatccgcc gaggtcccg cgtcccgcca ctgcttcca gcgcgcgcgc ggctctgcca
 600
 ccgcgtctac gcccgccag gcggcgactc tccgcgttct
 640

<210> 868
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 868
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
 1 5 10 15
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
 20 25 30
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
 35 40 45
 His Cys Ser Ser
 50

<210> 869
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 869
 ngggtgatgc tgctcgcggc attgagcacc tttgtgctca gcgcgctgtt tatcgacaac
 60

ttcctgtcgc cgctgaatat gcgcgggctg ggccctggcga ttctgacggg gggcatcgct
 120
 gcgtgcacca tgctgttctg cctggcgtcg gggcatttcg acttgctggg gggctcggtg
 180
 atcgctgtg ccggtgtggg cgcggggatt gtgattcgtg acaccgatag cgtggcactc
 240
 ggcgtgtccg ctgcgttggc catgggctg gtagtggggc tgatcaacgg catcgtgatc
 300
 gccaaagctgc gcatcaacgc g
 321

<210> 870

<211> 107

<212> PRT

<213> Homo sapiens

<400> 870

Xaa	Val	Met	Leu	Leu	Ala	Ala	Leu	Ser	Ile	Phe	Val	Leu	Ser	Ala	Leu
1				5					10					15	
Phe	Ile	Asp	Asn	Phe	Leu	Ser	Pro	Leu	Asn	Met	Arg	Gly	Leu	Gly	Leu
			20						25				30		
Ala	Ile	Ser	Thr	Val	Gly	Ile	Ala	Ala	Cys	Thr	Met	Leu	Phe	Cys	Leu
		35					40						45		
Ala	Ser	Gly	His	Phe	Asp	Leu	Ser	Val	Gly	Ser	Val	Ile	Ala	Cys	Ala
	50					55				60					
Gly	Val	Val	Ala	Gly	Ile	Val	Ile	Arg	Asp	Thr	Asp	Ser	Val	Ala	Leu
65					70				75					80	
Gly	Val	Ser	Ala	Ala	Leu	Ala	Met	Gly	Leu	Val	Val	Gly	Leu	Ile	Asn
			85						90					95	
Gly	Ile	Val	Ile	Ala	Lys	Leu	Arg	Ile	Asn	Ala					
			100						105						

<210> 871

<211> 320

<212> DNA

<213> Homo sapiens

<400> 871

agatcttcag agtctctcgtc ttttaaatgg gggtaacagc agcaagtcct cagagggtgc
 60
 ctgagcctca aaacacatcc tggtttgtaa cgctccgcagc ctcagcaggg gctaggcaca
 120
 gaacaagcat tcaggacctg gaaggtacca gcgacacctg gtcctccctt cccaggcaca
 180
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tctcagacca
 240
 ctgccccccac cactaccaca atcatactca cctctcctgg tccatactg acaaaggacc
 300
 tgccacggcc agggagacaa
 320

<210> 872

<211> 98

<212> PRT

<213> Homo sapiens

<400> 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1             5             10             15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
 20             25             30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
 35             40             45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
 50             55             60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
 65             70             75             80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
 85             90             95
Arg Gln

```

<210> 873

<211> 363

<212> DNA

<213> Homo sapiens

<400> 873

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nttgtttagc atcgtttttt acgggtgtat cagcgcggtt agcagcggtt ttagcgggatg
60
catcagcatg ttttgcgtca cgttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggagggtatc aatacgttta gcacgtgttt taacagatgt atcaaacagg ggttcacccg
180
cttttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgttttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaaag
300
acaaagataa tttattttagt ttcatgttcg gagagaagtg tgccaatttc gcgatacagt
360
cag
363

```

<210> 874

<211> 108

<212> PRT

<213> Homo sapiens

<400> 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1             5             10             15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
 20             25             30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
 35             40             45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
 50             55             60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```



```

65          70          75          80
Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
          85          90          95
Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
          100          105

```

<210> 875

<211> 355

<212> DNA

<213> Homo sapiens

<400> 875

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acgcgtgaag gggaccctaa ctgctctggg ctgtaggatg cgggcgaggc ttccacaaac
60
tcactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa
120
ccgcaccaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
180
gcgctcagaa tccttgagcc ggaggccccc cgggattcag accgccagat cccaggaggag
240
tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttccagg
300
cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggctcccc cggen
355

```

<210> 876

<211> 106

<212> PRT

<213> Homo sapiens

<400> 876

```

Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
1          5          10          15
Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
20          25          30
Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
35          40          45
Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
50          55          60
Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
65          70          75          80
Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
85          90          95
Pro Ala Cys His Pro Ala Ala Pro Pro Ala
100          105

```

<210> 877

<211> 487

<212> DNA

<213> Homo sapiens

<400> 877

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acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac
60

```

caatccacct atgctaaacg tggtcagcaa ggttatctca cacgagaatt ctttggtttg
 120
 ttggccaata ccatgggaga tcaaatcctt ttagtacagg cgtacagaga aggcgaagcg
 180
 atgcgcgcgt cgtggtgttt ctttgatgat cttcactat atgggcgtta ttggggctgt
 240
 atggaagaag tggattgect gcattttgaa gcttggtatt accaaggaat cgagttttgt
 300
 ctcgaaaaag ggttacagca ttctgatccg ggtacacaag gggaacacaa gattgcgcgc
 360
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcacaaagg ttttcgtgaa
 420
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc
 480
 cacgcgt
 487

<210> 878
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 878
 Thr Arg Thr Leu Gly Asn Glu Leu Thr Thr Ala Glu Ile Asp Cys Leu
 1 5 10 15
 Tyr Leu Cys Tyr Gln Ser Thr Tyr Ala Lys Arg Gly Gln Gln Gly Tyr
 20 25 30
 Leu Thr Arg Glu Phe Phe Gly Leu Leu Ala Asn Thr Met Gly Asp Gln
 35 40 45
 Ile Leu Leu Val Gln Ala Tyr Arg Glu Gly Glu Ala Ile Ala Ala Ser
 50 55 60
 Trp Cys Phe Phe Asp Asp His Ser Leu Tyr Gly Arg Tyr Trp Gly Cys
 65 70 75 80
 Met Glu Glu Val Asp Cys Leu His Phe Glu Ala Cys Tyr Tyr Gln Gly
 85 90 95
 Ile Glu Phe Cys Leu Glu Lys Gly Leu Gln His Phe Asp Pro Gly Thr
 100 105 110
 Gln Gly Glu His Lys Ile Ala Arg Gly Phe Glu Pro Val Phe Ser His
 115 120 125
 Ser Val His Tyr Ile Ala His Gln Gly Phe Arg Glu Ala Ile Gly Asn
 130 135 140
 Phe Cys Glu Glu Glu Ala Gln Ala Val Arg Glu Tyr His Gln Asp Thr
 145 150 155 160
 His Ala

<210> 879
 <211> 993
 <212> DNA
 <213> Homo sapiens

<400> 879
 nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc
 60

agccagtccta gtagggctct gacccctcct tcctacagta ctgctaaaaa ttcattggga
 120
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcattggggac
 180
 gagcacaggc agctcctctc tcaccaaatg caaggccctg gactccgtgc agctacctca
 240
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta
 300
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggctctgac
 360
 ctggtgaagg ctgtcattaa agaggagggt ttatggccag tgttgaggtc agacgcgttc
 420
 agtggactga cggccttacc tcggagcatc cttttatttg gacctggggg gacaggcaaa
 480
 acattattgg gcagatgcat cgctagttag ctggggggcca catttttcaa aattgctggg
 540
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt
 600
 gtggccagggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc
 660
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccaat tctgatgcaa
 720
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa
 780
 ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccaact
 840
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt
 900
 ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat
 960
 gtggctcatt tgtgtcagga agcagtgggt ggc
 993

<210> 880

<211> 331

<212> PRT

<213> Homo sapiens

<400> 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1			5						10				15		
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
		20					25					30			
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
		35				40					45				
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
		50				55					60				
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65				70					75					80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
			85					90					95		
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
		100					105					110			
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

```

      115              120              125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr
  130              135              140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys
  145              150              155
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe
      165              170              175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu
      180              185              190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser
      195              200              205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn
      210              215              220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln
      225              230              235
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys
      240              245              250
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe
      255              260              265
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln
      270              275              280
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys
      285              290              295
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp
      300              305              310
Val Ala His Leu Cys Gln Glu Ala Val Val Gly
      315              320              325

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<210> 881

<211> 313

<212> DNA

<213> Homo sapiens

<400> 881

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cgctgtgagcg tcgacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggg
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cgtggttttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcctgtggggc
120
gactcgagctg attatgaagg cgggtttcaac gtcacggttg agattccaac atgagcggcc
180
aaaggatgaa catggacacg acgcgcccca atcacggtcg gggcttgccg acgatcagcc
240
ggctggggtgc gcaccggttt tgccatgggt ctggattcgc aggacgacat caccgtgggc
300
tggaagccg acn
313

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<210> 882

<211> 57

<212> PRT

<213> Homo sapiens

<400> 882

```

Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

```

```

      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

```

<210> 883

<211> 576

<212> DNA

<213> Homo sapiens

<400> 883

```

naattaagat ctggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
tcctcactga ccaaggcaag ccatgctctt gagtgcttga ggccaccgaa atgaacaaat
120
ggaaaaact cccatctttt tcaagcctac cttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcagggtca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctctctg tccccagtga agacttggat ggcagccatc agggaaggct ggggcccgag
360
tgggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgcct
420
gtgaaagagg cccaagccac catcgcgatg gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttctctg tgaacgcctt agctaagcag gtcgatg
576

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<210> 884

<211> 105

<212> PRT

<213> Homo sapiens

<400> 884

```

Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
      1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
      65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

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100

105

<210> 885
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 885
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 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc
 120
 aggggggtgt cgcgcctcgg tgcgatcgag ttgtcgtcga ccccggtccg cccagatccg
 180
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc
 240
 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt
 300
 gatccctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac
 360
 ctgcagcgct
 370

<210> 886
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 886
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 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr
 20 25 30
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala
 35 40 45
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg
 50 55 60
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser
 65 70 75 80
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His
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 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu
 100 105 110
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala
 115 120

<210> 887
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 887
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 120
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt
 180
 aaagcggacg tgaccacccat tgcctccggc gcgttgctgg ccgtgctgct ttacatgggt
 240
 ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatgtt gtttgtggcg
 300
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<210> 888

<211> 149

<212> PRT

<213> Homo sapiens

<400> 888

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Leu	Thr	Ala	Ile	Ile	Ile	Ser	Gly	Cys	Leu	Asn	Gln	Leu	Gly	Lys	Arg
			20				25					30			
Tyr	Pro	His	Leu	Thr	Gly	Glu	Gly	Gln	Leu	Met	Pro	Asn	Arg	Ala	Asn
		35					40					45			
Ala	Asp	Thr	Thr	Ala	Ser	Gln	Pro	Ala	Phe	Ser	Gly	Lys	Ala	Asp	Val
	50				55						60				
Thr	Thr	Ile	Ala	Ser	Gly	Ala	Leu	Leu	Ala	Val	Leu	Leu	Tyr	Met	Val
65				70					75				80		
Gly	Arg	Leu	Val	His	Lys	Leu	Ile	Gly	Leu	Pro	Ala	Pro	Val	Gly	Met
			85					90					95		
Leu	Phe	Val	Ala	Val	Leu	Val	Lys	Leu	Cys	Asn	Gly	Ala	Ser	Pro	Arg
			100				105					110			
Leu	Leu	Glu	Gly	Ser	Gln	Val	Val	Tyr	Lys	Phe	Phe	Gln	Thr	Ser	Val
		115				120					125				
Thr	Tyr	Pro	Ile	Leu	Phe	Ala	Val	Gly	Val	Ala	Ile	Thr	Pro	Trp	Gln
	130				135						140				
Glu	Leu	Val	Asn	Ala											
145															

<210> 889

<211> 450

<212> DNA

<213> Homo sapiens

<400> 889

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 atctcccctc agtaaaattc aggatgccca gtgaagtgtt aatgtcagat aaacaatttg
 120
 ttagtataag gatgtacctt gcattgaaat gatgccttgt aatttactaa atctgcaact
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg
 240
 gtgctgggga gatcctgagg tcaggaaccc gtacacctct gcttctgccc tctcttccct
 300
 gtgccggcca caaggcaatg actcctgtgt gggcgcagag gcagaaatgg gtctggaagg
 360
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 420
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<210> 890

<211> 100

<212> PRT

<213> Homo sapiens

<400> 890

Met	Met	Pro	Cys	Asn	Leu	Leu	Asn	Leu	Gln	Leu	Cys	Ser	Leu	Ile	Ser
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Trp	Arg	Ala	Val	Ala	Val	Ile	Pro	Gly	Phe	Arg	Gly	Gly	Glu	Gly	Cys
			20					25					30		
Trp	Gly	Asp	Pro	Glu	Val	Arg	Asn	Pro	Tyr	Thr	Ser	Ala	Ser	Ala	Leu
		35					40				45				
Ser	Ser	Leu	Cys	Arg	Pro	Gln	Gly	Asn	Asp	Ser	Cys	Val	Gly	Ala	Glu
		50				55					60				
Ala	Glu	Met	Gly	Leu	Glu	Gly	Asp	Ser	Gln	Cys	Leu	Ala	Ser	Ser	Gly
65					70				75					80	
Lys	Phe	Cys	Ile	Gly	Gly	Ser	Leu	Cys	Ser	Lys	Gly	Ser	Trp	Pro	Gly
				85					90					95	
Arg	Pro	Ser	Arg												
															100

<210> 891

<211> 318

<212> DNA

<213> Homo sapiens

<400> 891

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 120
 actaacggcc cggtgatag cgggactggc acccactctg agcagggaaa ctccgacata
 180
 tctagccccg tcagctctag tgacgtctgt aacaccaccg acagactgct tggcaatacc
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 318

<210> 892

<211> 106

<212> PRT

<213> Homo sapiens

<400> 892

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His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
 20           25           30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
 35           40           45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
 50           55           60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
 65           70           75           80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
 85           90           95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
100           105

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<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

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120
gcaatcacga aagccaagag tacagcaaat ataaagacag aacaggaagg tgaggcatctt
180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctggggaaaaa gcgctatgaa
420
tgtgatgact gtggaggagac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

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<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

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Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
 20           25           30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

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35										40										45										
Ala	Asn	Ile	Lys	Thr	Glu	Gln	Glu	Gly	Glu	Ala	Ser	Glu	Lys	Ser	Leu															
	50						55				60																			
His	Leu	Ser	Pro	Gln	His	Ile	Thr	His	Gln	Thr	Met	Pro	Ile	Gly	Gln															
65					70				75					80																
Arg	Gly	Ser	Glu	Gln	Gly	Lys	Arg	Val	Glu	Asn	Ile	Asn	Gly	Thr	Ser															
			85						90					95																
Tyr	Pro	Ser	Leu	Gln	Gln	Lys	Thr	Asn	Ala	Val	Lys	Lys	Leu	His	Lys															
			100				105						110																	
Cys	Asp	Glu	Cys	Gly	Lys	Ser	Phe	Lys	Tyr	Asn	Ser	Arg	Leu	Val	Gln															
			115				120					125																		
His	Lys	Ile	Met	His	Thr	Gly	Glu	Lys	Arg	Tyr	Glu	Cys	Asp	Asp	Cys															
			130			135					140																			
Gly	Gly	Thr	Phe	Arg	Ser	Ser	Ser	Ser	Leu	Arg	Val	His	Lys	Arg	Ile															
145					150					155					160															
His	Thr	Gly	Tyr	Gly	Glu	Lys	Thr	Thr	Arg																					
				165					170																					

<210> 895

<211> 1119

<212> DNA

<213> Homo sapiens

<400> 895

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 120
 ccgcaccgga atcgggcttt tcttggggct gccttcctaa atgcgggtgtc ctcttctgtc
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 420
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 480
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 540
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 600
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 660
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 720
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 780
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<210> 896

<211> 147

<212> PRT

<213> Homo sapiens

<400> 896

Val	Arg	Leu	Leu	Phe	Ala	Gly	Thr	Pro	Asp	Val	Ala	Val	Pro	Thr	Leu
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Thr	Ala	Leu	Val	Ala	Asp	Pro	Arg	His	Glu	Val	Ala	Ala	Val	Leu	Thr
	20						25						30		
Arg	Pro	Asp	Ala	Ala	Val	Gly	Arg	His	Arg	Thr	Pro	Arg	Pro	Cys	Pro
	35					40					45				
Val	Ala	Lys	Ala	Ala	Glu	Glu	Leu	Gly	Ile	Pro	Ala	Ile	Lys	Ala	Thr
	50				55						60				
Ser	Val	Lys	Ser	Gly	Glu	Gly	His	Asp	Ala	Val	Thr	Ser	Leu	Asp	Val
	65				70				75				80		
Asp	Val	Ala	Val	Val	Val	Ala	Tyr	Gly	Gly	Leu	Ile	Pro	Ala	Asp	Leu
			85						90				95		
Leu	Ala	Val	Pro	Arg	His	Gly	Trp	Ile	Asn	Leu	His	Phe	Ser	Leu	Leu
	100						105						110		
Pro	Arg	Trp	Arg	Gly	Ala	Ala	Pro	Ile	Gln	Arg	Ala	Ile	Met	Ala	Gly
	115						120					125			
Asp	Glu	Glu	Thr	Gly	Ala	Cys	Val	Phe	Gln	Leu	Val	Glu	Ser	Leu	Asp
	130					135					140				
Ala	Gly	Pro													
145															

<210> 897

<211> 384

<212> DNA

<213> Homo sapiens

<400> 897

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 120
 ccggtcgaag cccgcgcgga cgcgcgcgcg gacacactact acaagcgct cgaattcgag
 180
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 ctggctcgct atgcgctcgg cattaccgat ctogaagtac tgcgctacga cctgctgttc
 360

gagcgcttcc tgaacccgga acgc
384

<210> 898

<211> 128

<212> PRT

<213> Homo sapiens

<400> 898

Glu	Leu	Glu	Ala	Gly	Lys	Pro	Glu	Val	Pro	Leu	Phe	Pro	Thr	Pro	Asp
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Gly	Met	Ser	Leu	Asp	Asp	Tyr	Leu	Val	Gln	Leu	Ser	Lys	Glu	Gly	Leu
			20					25					30		
Glu	Thr	Arg	Leu	Ala	Gln	Leu	Tyr	Pro	Val	Glu	Ala	Arg	Asp	Ala	
			35				40					45			
Gln	Arg	Asp	Thr	Tyr	Tyr	Lys	Arg	Leu	Glu	Phe	Glu	Cys	Gly	Thr	Ile
			50			55				60					
Thr	Lys	Met	Gly	Phe	Pro	Gly	Tyr	Phe	Leu	Ile	Val	Ala	Asp	Phe	Ile
65					70					75				80	
Asn	Trp	Ala	Lys	Asn	Asn	Gly	Val	Pro	Val	Gly	Pro	Gly	Arg	Gly	Ser
				85				90					95		
Gly	Ala	Gly	Ser	Leu	Val	Ala	Tyr	Ala	Leu	Gly	Ile	Thr	Asp	Leu	Glu
			100				105					110			
Val	Leu	Arg	Tyr	Asp	Leu	Leu	Phe	Glu	Arg	Phe	Leu	Asn	Pro	Glu	Arg
			115				120					125			

<210> 899

<211> 6171

<212> DNA

<213> Homo sapiens

<400> 899

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 5700
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 5760
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 5940
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 6060
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 6171

<210> 900

<211> 734

<212> PRT

<213> Homo sapiens

<400> 900

Phe Ser Lys Ala Leu Asn Leu Arg Tyr Leu Asn Ala Ser Ala Asn Ser
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 Leu Glu Ser Leu Pro Ser Ala Cys Thr Gly Glu Glu Ser Leu Ser Met
 20 25 30
 Leu Gln Leu Leu Tyr Leu Thr Asn Asn Leu Leu Thr Asp Gln Cys Ile
 35 40 45
 Pro Val Leu Val Gly His Leu His Leu Arg Ile Leu His Leu Ala Asn
 50 55 60
 Asn Gln Leu Gln Thr Phe Pro Ala Ser Lys Leu Asn Lys Leu Glu Gln
 65 70 75 80
 Leu Glu Glu Leu Asn Leu Ser Gly Asn Lys Leu Lys Thr Ile Pro Thr
 85 90 95
 Thr Ile Ala Asn Cys Lys Arg Leu His Thr Leu Val Ala His Ser Asn
 100 105 110
 Asn Ile Ser Ile Phe Pro Glu Ile Leu Gln Leu Pro Gln Ile Gln Phe
 115 120 125
 Val Asp Leu Ser Cys Asn Asp Leu Thr Glu Ile Leu Ile Pro Glu Ala
 130 135 140
 Leu Pro Ala Thr Leu Gln Asp Leu Asp Leu Thr Gly Asn Thr Asn Leu
 145 150 155 160
 Val Leu Glu His Lys Thr Leu Asp Ile Phe Ser His Ile Thr Thr Leu
 165 170 175
 Lys Ile Asp Gln Lys Pro Leu Pro Thr Thr Asp Ser Thr Val Thr Ser
 180 185 190
 Thr Phe Trp Ser His Gly Leu Ala Glu Met Ala Gly Gln Arg Asn Lys

[illegible]

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625          630          635          640
Pro Ser Thr Ser Cys Leu Tyr Gly Lys Lys Leu Ser Asn Gly Ser Ile
          645          650          655
Val Pro Leu Glu Asp Ser Leu Asn Leu Ile Glu Val Ala Thr Glu Val
          660          665          670
Pro Lys Arg Lys Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro
          675          680          685
Glu Asp Gln Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu
          690          695          700
Gln Met Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu
705          710          715          720
Glu Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
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<210> 901

<211> 309

<212> DNA

<213> Homo sapiens

<400> 901

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atttcctttt tctcttaatg caacaaggtc atcccaagat caggcttcct tcagtttctg
120
tggtaagtag tgatggacac ttatggagtt ttcagagact tatgcattgg gtaacaaggc
180
actgcaagag accccagata gcacagcatc atctcacatt tacaccacat cacatcaaca
240
tcgatgctag gaggtctaaa gctgatgccca ccttcagagc tgcaagtatc caaaagactc
300
cactcatga
309

```

<210> 902

<211> 102

<212> PRT

<213> Homo sapiens

<400> 902

```

Met Ile His Leu Pro Arg Pro Pro Lys Val Leu Gly Leu His Thr Asp
1          5          10          15
Gly Lys Leu His Phe Leu Phe Leu Leu Met Gln Gln Gly His Pro Lys
          20          25          30
Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
          35          40          45
Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
          50          55          60
Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
          65          70          75          80
Asp Ala Arg Arg Ser Lys Ala Asp Ala Thr Phe Arg Ala Ala Ser Ile
          85          90          95
Gln Lys Thr Pro Leu Met
100

```

<210> 903

<211> 349

<212> DNA

<213> Homo sapiens

<400> 903

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 taagggcttt gatggcctca tgggttgaca ggaacagaag acaagacta gggcccaccc
 120
 aaggtgtgaa gtctaataagg aaaccttttc tccataaggc tacaatgggt ctacaaaaaa
 180
 taaaaccatg ccaccccagg gactgcagcc caattttata tcaccatgag gtccaaaaaa
 240
 ttccaagctg tgaatttagt ttcaaatggc cttggtctcc agtatcccta gccatgtggc
 300
 aaaaacaaac aattctcttt ggaggatata tctttatctt aagacttgn
 349

<210> 904

<211> 102

<212> PRT

<213> Homo sapiens

<400> 904

Met	Glu	Ala	Thr	Leu	Ala	Leu	Arg	Ala	Leu	Met	Ala	Ser	Trp	Val	Asp
1				5					10					15	
Arg	Asn	Arg	Arg	Gln	Arg	Leu	Gly	Pro	Thr	Gln	Gly	Val	Lys	Ser	Asn
				20				25					30		
Arg	Lys	Pro	Phe	Leu	His	Lys	Ala	Thr	Met	Gly	Leu	Pro	Lys	Ile	Lys
				35				40				45			
Pro	Cys	His	Pro	Arg	Asp	Cys	Ser	Pro	Ile	Leu	Tyr	His	His	Glu	Val
				50				55				60			
Gln	Lys	Ile	Pro	Ser	Cys	Glu	Phe	Ser	Phe	Lys	Trp	Pro	Trp	Ser	Pro
				65				70				75			80
Val	Ser	Leu	Ala	Met	Trp	Gln	Lys	Gln	Thr	Ile	Leu	Phe	Gly	Gly	Tyr
				85					90					95	
Ile	Phe	Ile	Leu	Arg	Leu										
															100

<210> 905

<211> 377

<212> DNA

<213> Homo sapiens

<400> 905

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 ctcaacgaag acatcattat cgcggtgtgac cgggcagacg cggtgattag cgtatcccg
 120
 gggctctgcy acaggctggc tggacatggc gtgacctcaa cgggtgttcc caacatcggt
 180
 gacgtcgagc tggttgaccg tctctgatcga cgacatgagg ggacgatcgt cgtcagcgct
 240

gccaccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc
 300
 gaggttcagt tgagaatcat cggagatgga ccgcagcggc accaactgga ggccattgcc
 360
 gctgataatc caccgct
 377

<210> 906
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 906
 Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His
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 Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ala Gly Asp Arg Ala
 20 25 30
 Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly
 35 40 45
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu
 50 55 60
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val
 65 70 75 80
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val
 85 90 95
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln
 100 105 110
 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg
 115 120 125

<210> 907
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 907
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 gaccagtctt tcaacggcga ggttcaactg aaccttgtgc cgcagggtac attcgccgag
 120
 cgcattcgtg ccggcgctgc tggatttgca gcattcttca cgcctactgg ctatggtaca
 180
 gccgtgcaga agggtagact tggtcttaag tatgaaaaga aggcaggtaa ggctgtgcca
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 gtcatgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa
 300
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 332

<210> 908
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 908

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Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
 1           5           10           15
Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
           20           25           30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
           35           40           45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
           50           55           60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65           70           75           80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
           85           90           95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
           100           105

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<210> 909

<211> 318

<212> DNA

<213> Homo sapiens

<400> 909

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acgcgctcggg catggcagct gtacagatct atcgcgctcag cagggcctac gcacacatga
60
tgccgcaggg gcaccgacgc tgtcgccatc aaaagagccg cctcgcgccc gcagcgccctc
120
ccaggggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
180
cccttttttt cccaccccaa caccgaacgg gcggggccatg gctgaggatt cgcaccccat
240
tcgctccggc ttgcgcatgc tcaagcgctc ctggagctcg aatgagaatg taccgcccgc
300
acaaagctcg ccgcccggc
318

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<210> 910

<211> 102

<212> PRT

<213> Homo sapiens

<400> 910

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Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
 1           5           10           15
Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
           20           25           30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
           35           40           45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
           50           55           60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65           70           75           80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
           85           90           95
His Lys Ala Arg Arg Arg

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100

<210> 911

<211> 506

<212> DNA

<213> Homo sapiens

<400> 911

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 caaccttatg aggctggcct tgggggaacc ctgttttagg gatgagctga acttaccggg
 120
 aggctgcatg cgaggttggt gtgaaatgca tatctggcct ttagctggtt cggtcacct
 180
 ctgggggttg cacaggggag ggggttctgc catggctaga atgcgctaag ggggtgaaac
 240
 gaagcctgct gggcccgga accacagagc agcctggcct ttgaaggaga ccctgtggca
 300
 cccctgccc accccaagt ccagccattt cacttccctg gagatgggtg aaagcaagaa
 360
 aaaaaaaaa atccagtgtt ctgaggtcag ccttcacca gccaggattc atcgtctgat
 420
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 480
 actcgagtt cacctgaac attttg
 506

<210> 912

<211> 129

<212> PRT

<213> Homo sapiens

<400> 912

Met	Phe	Gln	Val	Asn	Cys	Glu	Leu	Ile	Arg	Lys	His	Trp	Gly	Pro	Thr
1				5					10					15	
His	Leu	His	His	Ser	Met	Leu	Ser	Pro	Gln	Thr	Asp	Gln	Thr	Met	Asn
			20					25					30		
Pro	Gly	Trp	Trp	Lys	Ala	Asp	Leu	Arg	Thr	Leu	Asp	Phe	Phe	Phe	
		35					40				45				
Leu	Ala	Leu	His	His	Leu	Gln	Gly	Ser	Glu	Met	Ala	Gly	Leu	Gly	Gly
		50				55					60				
Gly	Gln	Gly	Val	Pro	Gln	Gly	Leu	Leu	Gln	Arg	Pro	Gly	Cys	Ser	Val
65				70					75					80	
Val	Pro	Gly	Pro	Ser	Arg	Leu	Arg	Phe	His	Pro	Leu	Ala	His	Ser	Ser
			85					90					95		
His	Gly	Arg	Thr	Pro	Ala	Pro	Val	Pro	Thr	Pro	Glu	Val	Ser	Arg	Pro
			100				105						110		
Ala	Thr	Lys	Pro	Asp	Met	His	Phe	Thr	Pro	Thr	Ser	His	Ala	Ala	Ser
		115					120						125		

Arg

<210> 913

<211> 339

<212> DNA

<213> Homo sapiens

<400> 913

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 tttttcgttc gcgagaacgg taaaaccttc gcaacctcga tgttcacgtt ttgtgtcgcc
 120
 ctggcgccca cggacctgct ttctgccttc gactcgattc cggcgctcta tggtttcacc
 180
 aacgaggggt accttatcct taccgctaac gtctttgttc tcatgggctt gcgtcagttg
 240
 tatttcctta ttggaagcct gttggaacgt ctgggtgact tgctcgctgg actggtcgtg
 300
 attttgggct ttatcgccct caagctcatt ggccacgag
 339

<210> 914

<211> 113

<212> PRT

<213> Homo sapiens

<400> 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
1			5						10					15	
Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
			20					25					30		
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
		35					40					45			
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50					55					60				
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65				70					75					80	
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85					90					95		
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
		100						105					110		

Ala

<210> 915

<211> 663

<212> DNA

<213> Homo sapiens

<400> 915

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 gacagtgaag atcctgttgt ggacattgtt gctgctaccc ctgtcatcaa tggacagtca
 120
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatgggtctg
 180
 gaggagaatg gaaaatcggg acacactttg actgggtgatg gtctcaatgg accatcagat
 240

gcaagtgcgc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgcact
 300
 atccctttga ttaagggccc taaaggggtt ggggttgcga ttgctgacac ccctactgga
 360
 cagaagggtga aaatgatact ggatagtcag tgggtgcaag gccttcagaa aggagatata
 420
 attaagggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagagggtg
 480
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tettaagagg aggtccccct
 540
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag
 600
 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga
 660
 tcc
 663

<210> 916

<211> 221

<212> PRT

<213> Homo sapiens

<400> 916

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1				5					10					15	
Pro	Leu	Pro	Asp	Asp	Ser	Glu	Asp	Pro	Val	Val	Asp	Ile	Val	Ala	Ala
			20					25					30		
Thr	Pro	Val	Ile	Asn	Gly	Gln	Ser	Leu	Thr	Lys	Gly	Glu	Thr	Cys	Met
		35					40					45			
Asn	Pro	Gln	Asp	Phe	Lys	Pro	Gly	Ala	Met	Val	Leu	Glu	Gln	Asn	Gly
	50				55					60					
Lys	Ser	Gly	His	Thr	Leu	Thr	Gly	Asp	Gly	Leu	Asn	Gly	Pro	Ser	Asp
65				70					75					80	
Ala	Ser	Glu	Gln	Arg	Val	Ser	Met	Ala	Ser	Ser	Gly	Ser	Ser	Gln	Pro
			85					90						95	
Glu	Leu	Val	Thr	Ile	Pro	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Phe	Gly	Phe
	100						105						110		
Ala	Ile	Ala	Asp	Ser	Pro	Thr	Gly	Gln	Lys	Val	Lys	Met	Ile	Leu	Asp
	115					120					125				
Ser	Gln	Trp	Cys	Gln	Gly	Leu	Gln	Lys	Gly	Asp	Ile	Ile	Lys	Glu	Ile
	130				135					140					
Tyr	His	Gln	Asn	Val	Gln	Asn	Leu	Thr	His	Leu	Gln	Val	Val	Glu	Val
145				150					155					160	
Leu	Lys	Gln	Phe	Pro	Val	Gly	Ala	Asp	Val	Pro	Leu	Leu	Ile	Leu	Arg
			165					170						175	
Gly	Gly	Pro	Pro	Ser	Pro	Thr	Lys	Ser	Ala	Lys	Met	Lys	Thr	Asp	Lys
		180					185						190		
Lys	Glu	Asn	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Asn	Glu	Pro	Ile	Pro	Gln
	195					200						205			
Pro	Met	Pro	Phe	Pro	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Ser			
	210					215					220				

<210> 917

<211> 615

<212> DNA

<213> Homo sapiens

<400> 917

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 120
 caggaggggc acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggaattccag
 180
 atccgccgcg acgcccctcac ggtgcactcc tatcgggcgc ctgcctcttg tgatcactgc
 240
 ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac
 300
 taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggcccg caaacggcgc
 360
 ctgtcatcca cgtctctggc cagtggccac tcggtgccgc tcggcacctc cgagtccctg
 420
 ccttgccacg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca
 480
 tctcttctct cctcttctgc ctcatcgat acggggccgc ccattgagct ggacaagatg
 540
 ctgctctcca aggtcaaggt gccgcacacc ttcctcatcc acagctatac acggcccacc
 600
 gtttgccagg ctgtgc
 615

<210> 918

<211> 148

<212> PRT

<213> Homo sapiens

<400> 918

Ile	Val	Asp	Gln	Lys	Phe	Pro	Glu	Cys	Gly	Phe	Tyr	Gly	Leu	Tyr	Asp
1				5					10					15	
Lys	Ile	Leu	Leu	Phe	Lys	His	Asp	Pro	Thr	Ser	Ala	Asn	Leu	Leu	Gln
		20					25						30		
Leu	Val	Arg	Ser	Ser	Gly	Asp	Ile	Gln	Glu	Gly	Asp	Leu	Val	Glu	Val
		35				40					45				
Val	Leu	Ser	Ala	Ser	Ala	Thr	Phe	Glu	Asp	Phe	Gln	Ile	Arg	Pro	His
		50			55						60				
Ala	Leu	Thr	Val	His	Ser	Tyr	Arg	Ala	Pro	Ala	Phe	Cys	Asp	His	Cys
65				70				75					80		
Gly	Glu	Met	Leu	Phe	Gly	Leu	Val	Arg	Gln	Gly	Leu	Lys	Cys	Asp	Gly
			85					90					95		
Cys	Gly	Leu	Asn	Tyr	His	Lys	Arg	Cys	Ala	Phe	Ser	Ile	Pro	Asn	Asn
		100					105						110		
Cys	Ser	Gly	Ala	Arg	Lys	Arg	Arg	Leu	Ser	Ser	Thr	Ser	Leu	Ala	Ser
		115				120					125				
Gly	His	Ser	Val	Arg	Leu	Gly	Thr	Ser	Glu	Ser	Leu	Pro	Cys	Thr	Ala
	130					135					140				
Glu	Glu	Glu	Pro												
145															

<210> 919
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 919
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 acaaatgcga tcttctcgca tagcgcagcg ggtgagtacc tcgccaagat gggcccgccg
 120
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc
 180
 accttcgccca acccgacctt gctcaacgag atggccgtag tcgatgggtga agtgaagaaa
 240
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc
 294

<210> 920
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 920
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp
 1 5 10 15
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu
 20 25 30
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala
 35 40 45
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn
 50 55 60
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys
 65 70 75 80
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp
 85 90 95
 Glu Ala

<210> 921
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 921
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 aaccaggacg tgctgttggt catcgacaac atcttcgggt tctcccaggc tggttctgag
 120
 gtttcaaccc tgctaggtcg tatgccctcg gcgggtgggct accagcccaa cttggccgac
 180
 gagatgggcc aattgcagga gcgaatcacc tcgaccctgt gtcactccat cacctcgatg
 240
 caggccgtct acgtcccccgc tgacgattac accgaccggt ctccggcgac gaccttcgcc
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctctggcct gtacccggcc
 360
 gtggatccgc tggcgctcg
 378

<210> 922
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 922
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe
 1 5 10 15
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe
 20 25 30
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met
 35 40 45
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln
 50 55 60
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met
 65 70 75 80
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala
 85 90 95
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile
 100 105 110
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser
 115 120 125

<210> 923
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 923
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 ctggacaccc cgctggagca cgtgcgcgga gaaatccgca ttacctgga gcatgcacgc
 120
 caacgcaaga atgtcaaga agaagacatc ttgcgcgcc accttgcgct attggaagac
 180
 cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcgc
 240
 tggcgcgatg caatccaggc gcaatgcgcc gtgttgctgg ccttgggcaa accgctgttt
 300
 gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttgggg
 360
 gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggcat taacttacc
 420
 ccttcgcct tgttgcaact gactgcccc aacgcctggg gtatttgc atggccaaggc
 480
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 540
 ctggcgccgc aagtgcctga cgtgccccaa g
 571

<210> 924
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 924
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu
 1 5 10 15
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile
 20 25 30
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu
 35 40 45
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu
 50 55 60
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala
 65 70 75 80
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly
 85 90 95
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln
 100 105 110
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro
 115 120 125
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu
 130 135 140
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly
 145 150 155 160
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro
 165 170 175
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln
 180 185 190

<210> 925
 <211> 620
 <212> DNA
 <213> Homo sapiens

<400> 925
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 120
 gtggtgtgtg tgcattggtg tgcacgtgtg gactgtgtgt tgtgtgtatg catgtgtgtg
 180
 cactgtgtgc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg
 240
 tgtgtgcacg tgtgcactgt gtatgcatag tgtgtgcacg tgtgcactgt gtgtggatgc
 300
 atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tgggtgtgtgc acgtgtgcac
 360
 ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg
 420
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctgttc ccatctccag
 480

tgcccagcag catcacacgc accttgggtgc ttataaatg catggtcagt gaggctgcc
 540
 gcaccaagct gtccctttac cataaacacct ggaatagtca cctgtgataa gctatcacat
 600
 aggaaacatt tttaaaattt
 620

<210> 926

<211> 89

<212> PRT

<213> Homo sapiens

<400> 926

Thr	Arg	Ala	Leu	Cys	Val	Cys	Met	Val	Thr	Tyr	Thr	Cys	Ala	Leu	Cys
1				5					10					15	
Val	Val	Cys	Met	Xaa	Trp	Cys	Val	His	Val	Cys	Xaa	Cys	Val	Cys	Met
			20					25					30		
Val	Met	Cys	Thr	Cys	Ala	Leu	Cys	Val	Val	Cys	Met	His	Gly	Val	Cys
		35					40					45			
Thr	Cys	Ala	Leu	Cys	Val	Cys	Val	Cys	Met	Cys	Val	His	Val	Cys	Leu
		50				55					60				
Cys	Val	Cys	Met	Val	Met	Cys	Val	Cys	Thr	Val	Trp	Cys	Val	Cys	Met
65					70					75				80	
Cys	Val	His	Val	Cys	Thr	Val	Tyr	Ala							
					85										

<210> 927

<211> 360

<212> DNA

<213> Homo sapiens

<400> 927

gtgcacactc tggaagccac aggatggagc tcctagagat agtgaggcat gaccagaggg
 60
 aagaggcatt tggggctctg ttcagatcat tccaacagca aaccggggcat ggagaccccc
 120
 tctcaggtct gtgcttctct gggggccacc cagccatcct gccaccacgc tcagaggcag
 180
 ggacaaagcc ctcccaagag gcagcaggca gcaagggtca gccagcgcag tggggacagc
 240
 caggtataac ctggaaaacc caaaggaccc cagatggcaa tgtgacacgc cccatccacc
 300
 aagcacctgt aatgccggct tcccacagag gcgagccaga tcttgccact attctttaag
 360

<210> 928

<211> 111

<212> PRT

<213> Homo sapiens

<400> 928

Met	Glu	Leu	Leu	Glu	Ile	Val	Arg	His	Asp	Gln	Arg	Glu	Glu	Ala	Phe
1				5					10					15	
Gly	Val	Leu	Phe	Arg	Ser	Phe	Gln	Gln	Gln	Thr	Gly	His	Gly	Asp	Pro

			20					25				30				
Ile	Ser	Gly	Leu	Cys	Phe	Ser	Gly	Gly	His	Pro	Ala	Ile	Leu	Pro	Thr	
			35				40					45				
Ser	Ser	Glu	Ala	Gly	Thr	Lys	Pro	Ser	Gln	Glu	Ala	Ala	Gly	Ser	Lys	
			50			55					60					
Gly	Gln	Pro	Ala	Gln	Trp	Gly	Gln	Ala	Gly	Thr	Thr	Trp	Lys	Pro	Gln	
65					70					75					80	
Arg	Thr	Pro	Asp	Gly	Asn	Val	Thr	Arg	Pro	Ile	His	Gln	Ala	Pro	Val	
				85					90						95	
Met	Pro	Ala	Ser	His	Arg	Gly	Glu	Pro	Asp	Pro	Gly	Thr	Ile	Leu		
			100					105					110			

<210> 929

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 929

ntccccag	ggccgagtct	tccggagtca	gcagagagcc	tggatggatc	acaggaggat
60	aagcctcggg	gctcatgtgc	ggagcccaat	tttactgata	cggaatgggt
120	aacaacagcc	ggctcaaggc	caagggcgctg	ggccagcagc	acaacgcca
180	aaccagagct	ttgaggagct	gcgagcagcc	tgcttaagaa	agggggagct
240	cccttattcc	ctgtctgaac	cagctcactg	ggcttcaagg	acctggggcc
300	aatgtgcaga	acatctcctg	gcagcggccc	aaggatatca	taaacacccc
360	atggatggga	ttctctcaac	agacatctgc	caggggatcc	tcggggactg
420	gctgccatcg	gtctccttac	cacctgcccc	aaactgctat	accgcgtggg
480	cagagcttca	agaaaaacta	tgctggcatc	ttccattttc	agatttgcca
540	tgggtgaacg	tggtggtaga	tgaccggctg	cccacaaaga	atgacaagct
600	cactcaacgg	aacgcagtga	gttctggagt	gccttgctgg	agaaggcgta
660	agtgggtcct	atgaagcatt	gtcagggggc	agtaccatgg	agggccttga
720	ggaggcgtgg	cccagagctt	ccaactccag	agggcccttc	agaacctgct
780	aggaagggcg	tggaagcgtc	ctccctcatg	ggttgctcca	ttgaagtca
840	gaactggaat	ccatgactga	caagatgctg	gtgagagggc	acgcttactc
900	cttcaggatg	tccactacag	aggcaaaatg	gaaacactga	ttcgggtccg
960	ggccggattg	agtggaatgg	agcttggagt	gacagtgcca	gggagtggga
1020	tcagacatcc	agatgcagct	gctgcacaag	acggaggagc	gggagtgtgt
1080					gatgtcctac

caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc
 1140
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 1200
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 1260
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 1320
 acctgcctg tggccctaata gcagaagaac tggcgcatg cacggcagca gggagccag
 1380
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 1440
 gtccacttga agaaggaatt cttcacgaag tatcaggacc acggcttctc agagatcttc
 1500
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 1560
 cctccacct ttgagccaca cagagatgct gacttcctgc ttcgggtctt caccgagaag
 1620
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 1680
 gtctctgagg atgacatgga ccaggacttc ctacatttgt ttaagatagt ggcaggagag
 1740
 ggcaaggaga taggggtgta tgagctccag aggctgctca acaggatggc catcaaattc
 1800
 aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg
 1860
 gataaagatg gctctggcaa gctggggctt ctagagttca agatcctgtg gaaaaaactc
 1920
 aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc
 1980
 tatgagatgc gcctggttat tgagaaagca ggcatacaag tgaacaacaa ggtaatgcag
 2040
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 2100
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 2160
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 2220
 ttagaggacc tggtcatctc taccagcagc agcagcagc aggttctagc ccaggagggt
 2280
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 2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met Val Ala His Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly
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 Gln His Asp Asn Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu
 20 25 30
 Arg Ala Ala Cys Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe

35					40					45					
Pro	Asn	Glu	Pro	Ser	Ser	Leu	Gly	Phe	Lys	Asp	Leu	Gly	Pro	Asn	Ser
50						55				60					
Lys	Asn	Val	Gln	Asn	Ile	Ser	Trp	Gln	Arg	Pro	Lys	Asp	Ile	Ile	Asn
65				70						75					80
Asn	Pro	Leu	Phe	Ile	Met	Asp	Gly	Ile	Ser	Pro	Thr	Asp	Ile	Cys	Gln
				85					90					95	
Gly	Ile	Leu	Gly	Asp	Cys	Trp	Leu	Leu	Ala	Ala	Ile	Gly	Ser	Leu	Thr
			100					105					110		
Thr	Cys	Pro	Lys	Leu	Leu	Tyr	Arg	Val	Val	Pro	Arg	Gly	Gln	Ser	Phe
		115					120					125			
Lys	Lys	Asn	Tyr	Ala	Gly	Ile	Phe	His	Phe	Gln	Ile	Trp	Gln	Phe	Gly
	130					135					140				
Gln	Trp	Val	Asn	Val	Val	Val	Asp	Asp	Arg	Leu	Pro	Thr	Lys	Asn	Asp
145				150						155				160	
Lys	Leu	Val	Phe	Val	His	Ser	Thr	Glu	Arg	Ser	Glu	Phe	Trp	Ser	Ala
			165						170					175	
Leu	Leu	Glu	Lys	Ala	Tyr	Ala	Lys	Leu	Ser	Gly	Ser	Tyr	Glu	Ala	Leu
		180						185					190		
Ser	Gly	Gly	Ser	Thr	Met	Glu	Gly	Leu	Glu	Asp	Phe	Thr	Gly	Gly	Val
	195					200						205			
Ala	Gln	Ser	Phe	Gln	Leu	Gln	Arg	Pro	Pro	Gln	Asn	Leu	Leu	Arg	Leu
	210					215				220					
Leu	Arg	Lys	Ala	Val	Glu	Arg	Ser	Ser	Leu	Met	Gly	Cys	Ser	Ile	Glu
225				230						235				240	
Val	Thr	Ser	Asp	Ser	Glu	Leu	Glu	Ser	Met	Thr	Asp	Lys	Met	Leu	Val
			245						250					255	
Arg	Gly	His	Ala	Tyr	Ser	Val	Thr	Gly	Leu	Gln	Asp	Val	His	Tyr	Arg
		260						265					270		
Gly	Lys	Met	Glu	Thr	Leu	Ile	Arg	Val	Arg	Asn	Pro	Trp	Gly	Arg	Ile
	275					280						285			
Glu	Trp	Asn	Gly	Ala	Trp	Ser	Asp	Ser	Ala	Arg	Glu	Trp	Glu	Glu	Val
	290					295					300				
Ala	Ser	Asp	Ile	Gln	Met	Gln	Leu	Leu	His	Lys	Thr	Glu	Asp	Gly	Glu
305				310						315				320	
Phe	Trp	Met	Ser	Tyr	Gln	Asp	Phe	Leu	Asn	Asn	Phe	Thr	Leu	Leu	Glu
			325						330					335	
Ile	Cys	Asn	Leu	Thr	Pro	Asp	Thr	Leu	Ser	Gly	Asp	Tyr	Lys	Ser	Tyr
		340						345					350		
Trp	His	Thr	Thr	Phe	Tyr	Glu	Gly	Ser	Trp	Arg	Arg	Gly	Ser	Ser	Ala
		355				360						365			
Gly	Gly	Cys	Arg	Asn	His	Pro	Gly	Thr	Phe	Trp	Thr	Asn	Pro	Gln	Phe
	370					375						380			
Lys	Ile	Ser	Leu	Pro	Glu	Gly	Asp	Asp	Pro	Glu	Asp	Asp	Ala	Glu	Gly
385				390						395				4	


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465              470              475              480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
              485              490              495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
              500              505              510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
              515              520              525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
              530              535              540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545              550              555              560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
              565              570              575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
              580              585              590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Trp
595              600              605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
610              615              620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625              630              635              640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
              645              650              655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
660              665              670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
675              680              685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
690              695              700

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<210> 931

<211> 297

<212> DNA

<213> Homo sapiens

<400> 931

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tcgcgaaggaggcctgacat gggccagaaa atcaatcccc atggtttccg tctcggtgtg
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acgaccgacac acaagaccgc ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttccttt accgcgctcg cccgggcacg
240
gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt
297

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<210> 932

<211> 93

<212> PRT

<213> Homo sapiens

<400> 932

Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

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      1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
      20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
      35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
      50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
      65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
      85           90

<210> 933
<211> 305
<212> DNA
<213> Homo sapiens

<400> 933
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120
gcgctggcca tcctgccgac cgaccgggat cagctggttt cggcgatcca gcagggtcaag
180
gacgaacgcca agttcgtggc gctggtcgac cgtgcgcctt ccgtcaacga caacacgatc
240
cgcgatctct acgtggccgg caacaacccg gcgctcggcg aagtggcggg caaattcatg
300
ggcga
305

<210> 934
<211> 101
<212> PRT
<213> Homo sapiens

<400> 934
Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
      1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
      20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
      35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
      50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
      65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
      85           90           95
Gly Lys Phe Met Gly
      100

<210> 935
<211> 333

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<212> DNA

<213> Homo sapiens

<400> 935

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 120
 gggtaacggga taaatgttcc tggatgaagga aacagcaggg gcaaggcccc tgcagcagaa
 180
 aggagcaggg ccctttggag taacagaaa accatggtga caggagctca gaaagaccac
 240
 tgggtgttaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt
 300
 gaagaccatg gtgaggctct cttggtcttt act
 333

<210> 936

<211> 103

<212> PRT

<213> Homo sapiens

<400> 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
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Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
		35					40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
		50				55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70				75					80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
			85						90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
															100

<210> 937

<211> 464

<212> DNA

<213> Homo sapiens

<400> 937

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 120
 gaccgtgccc tggcaggggt cgtgcccagt cactgcatcg acgaagctcg cgccgaggtg
 180
 cagcggcgctg ccgatctcgc ccgtggccat ctcgccatcc ttcccgcagg cgatgcccgt
 240
 acggcggttg agaccctgtg cgacgaggtg ggttcccggg cggcctgaac cccgaccctg
 300

ccagntcgcg tcccatctcc tggccgggac cgetccagcg tctgctctct gacagctcat
 360
 cgttcttccg acaccaagga gtttctcgtg gcccgctcgc tgcgtctcat cggcattggg
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 cccggcaacc cggactggat caccctggct gccgtcaagg ccan
 464

<210> 938

<211> 95

<212> PRT

<213> Homo sapiens

<400> 938

Xaa	Leu	Ser	Ala	Glu	Gly	Val	Ala	Thr	Leu	Pro	Thr	Leu	Met	Leu	Gln
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Ala	Ser	Thr	Asp	Pro	Ala	Asp	Asp	Glu	Leu	Lys	Asp	Leu	Leu	Thr	Ala
			20				25					30			
Asp	Leu	Met	Asp	Gln	His	Asn	Leu	Asp	Arg	Ala	Leu	Ala	Gly	Leu	Arg
		35					40				45				
Ala	Ser	His	Val	Ile	Asp	Glu	Ala	Arg	Ala	Glu	Val	Gln	Arg	Arg	Ala
		50				55				60					
Asp	Leu	Ala	Arg	Gly	His	Leu	Ala	Ile	Leu	Pro	Ala	Gly	Asp	Ala	Arg
65					70				75				80		
Thr	Ala	Leu	Glu	Thr	Leu	Cys	Asp	Glu	Val	Gly	Ser	Arg	Ala	Ala	
				85				90					95		

<210> 939

<211> 385

<212> DNA

<213> Homo sapiens

<400> 939

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 ggactgtgctc cggctcgaggt ggacttcgcc gccacgaaga cccttgccctt gtcgcacggg
 120
 acatggcggg ggatcgaggt tgggtggctat gaaatccatc acgggctgtct gtcgttcgct
 180
 gaggacgctg aagccttcct cgacggcgta cagctcggtc cggtatgggg gacgatgtgg
 240
 caccggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac
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 360
 atgatcgaaa ccctcgccga cgcgt
 385

<210> 940

<211> 128

<212> PRT

<213> Homo sapiens

<400> 940

Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

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      1           5           10           15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20           25           30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35           40           45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50           55           60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
      65           70           75           80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85           90           95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100          105          110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115          120          125

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<210> 941

<211> 348

<212> DNA

<213> Homo sapiens

<400> 941

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gaagccatgc aaaccatggt cgtgctggcc gggctgccgt tctcggtggt gctgattttc
120
ttcatgttgc gtttcacaa ggcatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggtg aacgtggtcg ccgtggtttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgcgtga tcaagggtg gaagtgcaga ccctgctt
348

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<210> 942

<211> 116

<212> PRT

<213> Homo sapiens

<400> 942

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Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
      1           5           10           15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20           25           30
Pro Phe Ser Val Val Leu Ile Phe Phe Met Phe Gly Leu His Lys Ala
      35           40           45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
      50           55           60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
      65           70           75           80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85           90           95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

```

```

                100                105                110
Gln Thr Leu Leu
115

<210> 943
<211> 439
<212> DNA
<213> Homo sapiens

<400> 943
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120
ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgccccacc agtcaatccc
180
ccttggttct gggatgctat ttcctgggcc gcctccctct aggagtgttt agaaccctca
240
ctgtgggcag aaggagggga agatggctga ggtacctgga aaggagacgt tggatccccg
300
ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaata gttccctaag
360
gaacctggct tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc
420
tgaggaaaga ggctgttcc
439

<210> 944
<211> 118
<212> PRT
<213> Homo sapiens

<400> 944
Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu
1 5 10 15
His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp
20 25 30
Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu
35 40 45
Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly
50 55 60
Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr
65 70 75 80
Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val
85 90 95
Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly
100 105 110
Met Arg Ser Asn Val Pro
115

<210> 945
<211> 339
<212> DNA
<213> Homo sapiens

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<400> 945
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 60
 gagatgggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta
 120
 tatatatata gcggtgtcaa caaaacatgc actgtttact cagcaccgcc tgtttgtctc
 180
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggctcgtga
 240
 cagagtattg tgcaagtga aagtctctgg atggggctat gtatatccta ccagccaatt
 300
 tgggtgtcaaa ttggattga aggcctgcct ctgtccacn
 339

<210> 946
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 946
 Xaa Ile Arg Glu Ala Phe His Ile Phe Phe Leu Leu Ile Ile Ser Ile
 1 5 10 15
 Ala Leu Tyr Val Glu Met Val Ile Tyr Ile Tyr Thr His Thr His Ile
 20 25 30
 Tyr Val Cys Val Cys Ile Tyr Val Tyr Ile Tyr Ser Val Tyr Asn Lys
 35 40 45
 Thr Cys Thr Val Tyr Ser Ala Pro Arg Val Cys Leu Ser Asn Ser Phe
 50 55 60
 Ser Lys Glu Leu Leu Leu Phe Glu Met Glu Gly Glu Gly Gly Pro Gly
 65 70 75 80
 Gln Ser Ile Val Gln Val Glu Ser Leu Trp Met Gly Leu Cys Ile Ser
 85 90 95
 Tyr Gln Pro Ile Trp Val Gln Ile Gly Phe Glu Gly Leu Pro Leu Ser
 100 105 110
 Thr

<210> 947
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 947
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 60
 ctctgtggcat cacacctgtg caccgggggtg gggaaggagt ggacaggagt ggacaagtca
 120
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgctga gctttgcaga
 180
 ggagatgatg cttcaaagt gtccctgttg gggatgagca gccaggcctt tatacactgg
 240
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc
 300

ctggatacca tgcccttctt aggcctggagt tgctgccctt gtccatttac cataaaaaatt
 360
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca
 420
 cgtacatccc caatgtgtac agccctactt ttttctgctg atcaagtcca attacttctg
 480
 ctaagatggt gactattctt gcctgctggt ccttggatgc aaggacccca atgttcaggc
 540
 agcctttggt gccttctagc atacgaatca gagcattatc tttagggtgtg gaataagctg
 600
 ccccaaaacc tgttgaagcc agccaggcac tgtgctccct tcacgcgt
 648

<210> 948

<211> 154

<212> PRT

<213> Homo sapiens

<400> 948

Met	Glu	Met	Ser	Gly	Gln	Gln	Val	Tyr	Gly	Val	Leu	Val	Ala	Ser	His
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Leu	Cys	Thr	Gly	Val	Gly	Lys	Glu	Trp	Thr	Gly	Val	Asp	Lys	Ser	Ser
			20					25				30			
Ser	Ala	Ala	Gly	Ser	Ser	Asp	Ala	Ser	Ala	Phe	Leu	Leu	Cys	Ala	Lys
			35				40				45				
Leu	Cys	Arg	Gly	Asp	Asp	Ala	Ser	Lys	Leu	Ser	Leu	Leu	Gly	Met	Ser
			50			55					60				
Ser	Gln	Ala	Phe	Ile	His	Trp	Asp	Ser	Gln	Ser	Trp	Ile	Arg	Gly	Tyr
65					70					75				80	
Ser	Gly	Asn	Pro	His	Pro	Trp	Arg	Ser	Glu	Pro	Leu	Asp	Thr	Met	Pro
				85					90					95	
Phe	Leu	Gly	Trp	Ser	Cys	Cys	Pro	Cys	Pro	Phe	Thr	Ile	Lys	Ile	Gly
			100					105					110		
Gln	Glu	Asn	Thr	Arg	Thr	His	Leu	Ser	Phe	Ser	Ser	Tyr	Ala	Lys	Pro
			115				120					125			
Val	Leu	Pro	Arg	Thr	Ser	Pro	Met	Cys	Thr	Ala	Leu	Leu	Phe	Ser	Ala
			130			135						140			
Asp	Gln	Val	Gln	Leu	Leu	Leu	Leu	Arg	Trp						
145					150										

<210> 949

<211> 661

<212> DNA

<213> Homo sapiens

<400> 949

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 120
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatatctg
 180
 aggcgtgtgt tttcaccatg gcttctctcc agcaattgggt gtatttggga cagatggatt
 240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa
 300
 tgccaaccga gtccgagggga atttgattgc actttcgggt tggccaggaa cctatcagaa
 360
 cagaaaaagat ttaagttcaa ctctctggga tgcagcaatt gagataaata gagggaccaa
 420
 tacagtttta cagaataatg tagtggctgg atttggaaga gcaggatacc gcattgatgg
 480
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg
 540
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg
 600
 atttaccatt tggacatgct gggattatgg aatttatttt cagaccacag agagtgtgca
 660
 c
 661

<210> 950

<211> 210

<212> PRT

<213> Homo sapiens

<400> 950

Met	Met	Thr	Phe	Lys	Gly	Asn	Ala	Arg	Ile	Ser	Asn	Val	Glu	Phe	Tyr
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His	Ser	Gly	Gln	Glu	Gly	Phe	Arg	Asp	Ser	Thr	Asp	Pro	Arg	Tyr	Ala
			20					25					30		
Val	Thr	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Gln	Glu	His	Gly	Ser	Ser	Tyr
		35					40					45			
Ile	Arg	Gly	Cys	Ala	Phe	His	His	Gly	Phe	Ser	Pro	Ala	Ile	Gly	Val
	50					55					60				
Phe	Gly	Thr	Asp	Gly	Leu	Asp	Ile	Asp	Asp	Asn	Ile	Ile	His	Phe	Thr
65					70					75				80	
Val	Gly	Glu	Gly	Ile	Arg	Ile	Trp	Gly	Asn	Ala	Asn	Arg	Val	Arg	Gly
			85					90						95	
Asn	Leu	Ile	Ala	Leu	Ser	Val	Trp	Pro	Gly	Thr	Tyr	Gln	Asn	Arg	Lys
			100					105					110		
Asp	Leu	Ser	Ser	Thr	Leu	Trp	His	Ala	Ala	Ile	Glu	Ile	Asn	Arg	Gly
		115					120					125			
Thr	Asn	Thr	Val	Leu	Gln	Asn	Asn	Val	Val	Ala	Gly	Phe	Gly	Arg	Ala
		130				135					140				
Gly	Tyr	Arg	Ile	Asp	Gly	Glu	Pro	Cys	Pro	Gly	Gln	Phe	Asn	Pro	Val
145				150						155				160	
Glu	Lys	Trp	Phe	Asp	Asn	Glu	Ala	His	Gly	Gly	Leu	Tyr	Gly	Ile	Tyr
				165						170				175	
Met	Asn	Gln	Asp	Gly	Leu	Pro	Gly	Cys	Ser	Leu	Ile	Gln	Gly	Phe	Thr
			180					185					190		
Ile	Trp	Thr	Cys	Trp	Asp	Tyr	Gly	Ile	Tyr	Phe	Gln	Thr	Thr	Glu	Ser
			195				200					205			
Val	His														
	210														

<210> 951

<211> 2615

<212> DNA

<213> Homo sapiens

<400> 951

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120
agcttcagcc tgactcgggt ggattgtagc ggcctggggc cccacatcat gccggtgccc
180
atccctctgg acacagccca cttggacctg tcctccaacc ggctggagat ggtgaatgag
240
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300
ctcaccagca tctcaccacc tgccttctcc cgccttcgct acctggagtc gcttgacctc
360
agccacaatg gcctgacagc cctgccagcc gagagcttca ccagctcacc cctgagcgac
420
gtgaacctta gccacaacca gctccgggag gtctcagtg ctgccttcac gacgcacagt
480
caggggccggg cactacacgt ggacctctcc cacaacctct caccgctcgg tgcgccacc
540
cacgaggggc ggcttcgctg cggccaccat tcagagcctg aaactggcct ggaaccggct
600
ccatgccgtg cccaacctcg agacttgccc ctgcgtacc tgagcctgga tgggaacctt
660
ctagctgtca ttggtccggg tgccttcgcg gggctgggag gccttacaca cctgtctctg
720
gccagcctgc agaggtctcc tgagctggcg cccagtggct tcctgagct accgggcttg
780
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840
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900
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960
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1020
ctgcactcgc tagacaccgg ggaatctgct gccagggggc ccaccatctt gtgacaaaatg
1080
gtgtggccca gggccacata acagactgct gtccctgggt gcctcaggtc ccgagtaact
1140
tatgttcaat gtgccaacac cagtggggag cccgcaggcc tatgtggcag cgtcaccaca
1200
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1320
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1380
ggccggcctg acccgcaatg ggcagagggt ggggtgggacc cctgctgca gggcagagtt
1440
caggtccact gggctgagtg tccccttggg cccatggccc agtcactcag gggcgagttt
1500

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cttttctaac atagcccttt ctttgccatg aggccatgag gcccgcttca tccttttcta
 1560
 ttccctaga accttaatgg tagaaggaat tgcaaagaat caagtccacc cttctcatgt
 1620
 gacagatggg gaaactgagg ccttgagaag gaaaaaggct aatctaagtt cctgcgggca
 1680
 gtggcatgac tggagcacag cctctgcct cccagcccgg acccaatgca cttctctgtc
 1740
 tcctetaata agccccaccc tccccgcctg ggtccccctt gctgccttg cctgttcccc
 1800
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 1860
 tctgaccagc tgtgcggcat gggctaagtc actctgcctt cggagcctc tggaagctta
 1920
 gggcacattg gttccagcct agccagtctc tcaccctggg ttggggctcc ccagcatcca
 1980
 gactggaaac ctacccattt tcccctgagc atcctctaga tgctgcccc aggagtgtgt
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 2100
 tggccctgag caagacagcc cttcttacc tcccaggaat gccgtgaaag gagacaaggt
 2160
 ctgcccagcc catgtctatg ctctaccccc agggtagcat ctcagcttcc gaaccctggg
 2220
 ctgtttcctt agtcttcatt ttataaaagt tgttgccctt ttaacggagt gtcactttca
 2280
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 2340
 aaggttgcat ttgttcactt ttgtaatat gtctggggc tgtgttgggg tgttggggga
 2400
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 2460
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 2520
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 2580
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 2615

<210> 952

<211> 357

<212> PRT

<213> Homo sapiens

<400> 952

Xaa	Pro	Ala	Pro	Thr	Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val
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Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys
			20				25					30		Glu
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val
			35			40					45			Asp
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu
			50			55					60			Asp
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn
														Glu

```

65          70          75          80
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu
85          90          95
Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu
100
Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu
110
115          120          125
Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser
130
135          140
His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser
145
150          155          160
Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro
165
170          175
Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu
180
185          190
Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp
195
200          205
Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
210
215          220
Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
225
230          235          240
Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
245
250          255
Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
260
265          270
Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
275
280          285
Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
290
295          300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
305
310          315          320
Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
325
330          335
Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
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345          350
Gly Pro Thr Ile Leu
355

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<210> 953

<211> 347

<212> DNA

<213> Homo sapiens

<400> 953

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120
tgttgtacct ggcggctctg cggagtaacc gctcgggaca cacagtagga cgggagggag
180
aagccattgc gtttcaccct ttcattggccc ttcctttccc ctccaagtg agctctttga
240
ggtgagtcac ggagggcagt gtccctctgc atcctgtctg ggggtgtcaa atatggccaa
300

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gtgggctcca tcggggcagc ggggtgggtg ggggggtgtct gtcagag
347

<210> 954

<211> 103

<212> PRT

<213> Homo sapiens

<400> 954

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Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg
 1           5           10          15
Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu
      20          25          30
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser
      35          40          45
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln
      50          55          60
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly
 65           70           75           80
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu
      85           90           95
Arg Thr Gly Met Ala Ser Arg
      100
```

<210> 955

<211> 634

<212> DNA

<213> Homo sapiens

<400> 955

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acgcgtgaag ggctctgcag gtgagcggct ctgcagggtga agggttctgc aggtgagcgg
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ctctgcagggt gaatggttct gcagggtgaag ggctctgcag gtgaacgggt ctgcagggtga
120
agggctctgc aggtgaacgg ttctgcagggt gagcggctct gcagggtgagc ggctctgcac
180
gtgagtgcct ctgtgactgg ctgcgaagca gcatttgtgc acacttgact ggccacaaca
240
gaatgttctt ctctgttgtc agcactgagg aggaagctcc tgcctaagcg accacagcca
300
ggcaccgcgt ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga
360
gctcctggaa tgcaggctga ggcagctccc acacaaaagc tatctactct ggcagttatc
420
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca
480
ggacccgcct ctgagaacac acgggtgcta gtccaagttc acagcagggc tcaagtcact
540
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt
600
caccatctca cacctggaac aagggttacg gccg
634
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<210> 956

<211> 113

<212> PRT

<213> Homo sapiens

<400> 956

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Met Glu Ser Gly Glu Ser Asn Val Ser Met Glu Arg Val Pro Gly Cys
 1           5           10           15
Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu
          20           25           30
His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro
      35           40           45
Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser
      50           55           60
Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser
65           70           75           80
Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser
          85           90           95
Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser
      100           105           110

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Arg

<210> 957

<211> 823

<212> DNA

<213> Homo sapiens

<400> 957

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120
gtacctctg gccacccagc actgcgcagc cgtgggtgtcc agcctcctgg gcagccctt
180
gcccttgga caggtaccag ctcagactcc aggccttaggg gtccctctgg aatgatgtc
240
cccctggaat gatgtcccc gagccctcca cccggctctg caccgcgact ttctgcatga
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gttcccatgg ctgtaggcca cgtgggacag aaagtgcacat ggagccaggc cccagtcct
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420
gcctgcaca gcacccccc agggaaagctg ctgtttctgc ctctcttaa ggtcccaaaa
480
ctgctggct gctctgttg cccagggtc cagcacacac tggaggctgc cctcacct
540
gtgtcttggt tccggctact ccaagccttg tcctctgcag ggcatccact gctgctctg
600
agcagacccc tgggaactgc ctgatctgag cccctcagg agcccaagga caacctgtc
660
tgtaccatac atcactatgt cttcccaagc tcacacctcc cagctccag caaagggcag
720
ggcgtgtcta ccaccacca gcccaactggg gtcccccctc tcgcgcagg cctccggagc
780

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823

<210> 958

<211> 105

<212> PRT

<213> Homo sapiens

<400> 958

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Met Ala Val Gly His Val Gly Gln Lys Val Thr Trp Ser Gln Ala Pro
 1           5           10          15
Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp
 20          25          30
Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu
 35          40          45
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val
 50          55          60
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser
 65          70          75          80
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu
 85          90          95
Pro Val Ser Arg Pro Leu Gly Thr Ala
100          105
```

<210> 959

<211> 586

<212> DNA

<213> Homo sapiens

<400> 959

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ngtcatgact gcatggccaa gcatgactcc aacaccatca ttaagtttgc cgacgacaca
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acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtcagagac
120
ctggcagtggt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg
180
atcgtggact acaggaaaag gagggctcgag cgcgccccca ttctcattga tggggctgta
240
tgaggagccag ttgagagctt caagttcctt ggtgtccaca tcaccatcga actatcatgg
300
tcctaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga
360
caaaaaaagt ttggaatgga tctctcagacc ctcaaaaagt ttgacatcta caccatcgag
420
agcatcatga ctggttgcat caccgcctgg tatggcaact gctcggcctc cgaccgcaag
480
gcactacaga gggtagtgcg tacggccccag tacatcactg gggctaagct tcttgccatc
540
caggacctct ataccaggcg gtgtcagcgg aagaccctga caattg
586
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<210> 960

<211> 195

<212> PRT

<213> Homo sapiens

<400> 960

```

Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe
 1           5           10          15
Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
 20          25          30
Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
 35          40          45
Asn Leu Ser Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
 50          55          60
Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
 65          70          75          80
Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
 85          90          95
Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
100          105          110
Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
115          120          125
Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
130          135          140
Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
145          150          155          160
Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
165          170          175
Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
180          185          190
Leu Thr Ile
195

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<210> 961

<211> 502

<212> DNA

<213> Homo sapiens

<400> 961

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acgcgttggtc gtctctccgt agaccattca gtttggcaaa acttccactg gagtctgtgc
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atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc
120
taaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa
180
atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga
240
gtctacaccc gtgcttcacc agaagaccct gcaggccatg aagagccact cagaaaaggc
300
ccatggccat ggagcttcaa ggaaagaaac ccctcagttt tttccgtcta gtccgccacc
360
tcattcccca ataagtcatg ggcataatcc cagtgcattt gttcttccaa atgctaccca
420
tgactaacac acgtctttct caaactccaa tgetcacaaa gctgaaaaga agcttcaaaa
480
cattgatcac cccttcacgc gt
502

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<210> 962
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 962
 Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro
 1 5 10 15
 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met
 20 25 30
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu
 35 40 45
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser
 50 55 60
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp
 65 70 75 80
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys
 85 90 95
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg
 100 105

<210> 963
 <211> 1298
 <212> DNA
 <213> Homo sapiens

<400> 963
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 60
 gcgctctaga ggagatgaat tatggatccg ccctcccgga atcttggtc ggccctcccc
 120
 acgccaccaca gggccagtcg ggtctgctca cagcccagg aggcgcgctg tccagccgag
 180
 ggcaagagac agagcaggtc cctgtgtatc caagtccctg agcccgtgac accggcccca
 240
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaagacca
 300
 agaaaggga gaaggggaag aaggcaccgg acccgagaa gcccaaacgg agcctgaagg
 360
 ggacgtcgcg ggtgttcctg ggcttccgag accgaacacc caagatctac aagaagggcc
 420
 agttccgcag cgctcgggcc ttcttctggg gcctccacac cgccccccac aagaccaagc
 480
 gcacgaggaa ggcccgacac gtgctcgggt acacgtcaga gcttatgacg cacatgcgca
 540
 tgggcaagaa gaagcgggag atgaagggca agaagccgtc cttcatgggt atccgcttcc
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 660
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 720
 aacaggccac agtggacgcc tggctgcagc gctcgagctc ccgcatgggc tcccgcaaac
 780

tccctctccc gtcgggtgcc gagatcctgc ggctctggggg ccggctccgg aggttcccc
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 900
 ccccattcca tcaactcgggc tcccgcaagt cgtgtacgg gcttgagggc ttccaggacc
 960
 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtcactcc
 1020
 accgctacga ggagcaggaa ccctacctgg cgggcctcgg cccctacagc ccggcctggc
 1080
 caccctacgg cgaccactac tacgggtacc cggccgagga tccctacgac tactaccacc
 1140
 cggactatta cgggtggcccc gtgatccgg ggtacaccta cggctacggc tacgacgatt
 1200
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 1260
 acgaggggcga ggcgcaccct tatggtact acctggat
 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

Ser Ala Ser Gln Ala Ala Val Ala Thr Ala Ala Cys Gly Arg Ala Pro
 1 5 10 15
 Gly His Ser Ala Lys Arg Pro Arg Pro Ser Thr Gly Ser Gln Lys Ser
 20 25 30
 Ser Ser Ser Arg Arg Pro Arg Ser Arg Ala Ala Asn Arg Pro Gln Trp
 35 40 45
 Thr Pro Gly Cys Ser Ala Arg Ala Pro Ala Trp Ala Pro Ala Asn Ser
 50 55 60
 Pro Ser Arg Arg Val Pro Arg Ser Cys Gly Leu Gly Ala Gly Ser Gly
 65 70 75 80
 Gly Ser Pro Ala Ala Ala Ala Ser Thr Arg Gln Ala Ser Pro Trp Ala
 85 90 95
 Ser Cys Pro Ser Arg Thr Arg Pro His Ser Ile Thr Arg Ala Pro Ala
 100 105 110
 Ser Arg Cys Thr Gly Leu Arg Ala Ser Arg Thr Trp Ala Ser Ile Met
 115 120 125
 Thr Ile Thr Ala Thr Ala Thr Thr Thr Thr Gly Ser His Ser Thr
 130 135 140
 Ala Thr Arg Ser Arg Asn Pro Thr Trp Arg Ala Ser Ala Pro Thr Ala
 145 150 155 160
 Arg Pro Gly His Pro Thr Ala Thr Thr Thr Thr Gly Thr Arg Pro Arg
 165 170 175
 Ile Pro Thr Thr Thr Thr Thr Pro Thr Ile Thr Val Ala Pro Leu Ile
 180 185 190
 Arg Gly Thr Pro Thr Ala Thr Ala Thr Thr Ile Thr Asn Pro His Met
 195 200 205
 Arg Pro Arg Arg Gly Thr Arg Leu Leu Thr Ala Thr Thr Met Gly Thr
 210 215 220
 Arg Ala Arg Arg Thr Leu Met Ala Thr Thr Trp

225

230

235

<210> 965
 <211> 336
 <212> DNA
 <213> Homo sapiens

<400> 965
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 cgggtcagcg atgccgaaaa ggcgtgaaatc ctgggccgcg ccgatgtgta tgtcgcccc
 120
 aataccgcggt gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc
 180
 gttgttgctt cagacttgga ggccttccgc gcagtgtgca acgcccattc cgatgatgtt
 240
 gccggcgcg cttatcgcaa tgaggatagt aatgaccttgc ctctgtact caacgaggtg
 300
 ctccaggatc ctgagtatcg tgcccgctta gtgcac
 336

<210> 966
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 966
 Xaa Val Thr Ile Met Gly Gly Ala Arg Thr Arg Glu Val Glu Gly Val
 1 5 10 15
 Asp Phe Val Gly Arg Val Ser Asp Ala Glu Lys Ala Glu Ile Leu Gly
 20 25 30
 Arg Ala Asp Val Tyr Val Ala Pro Asn Thr Gly Gly Glu Ser Phe Gly
 35 40 45
 Ile Val Leu Val Glu Ala Met Ala Ala Gly Ala Val Val Ala Ser
 50 55 60
 Asp Leu Glu Ala Phe Arg Ala Val Cys Asn Ala Asp Ser Asp Asp Val
 65 70 75 80
 Ala Gly Ala Leu Tyr Arg Asn Glu Asp Ser Asn Asp Leu Ala Arg Val
 85 90 95
 Leu Asn Glu Val Leu Glu Asp Pro Glu Tyr Arg Ala Arg Leu Val His
 100 105 110

<210> 967
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 967
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 ggccgaggagg cgtcgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg
 120
 tcggcctccg cttcggccgc agcctgggct gcgcccagact ctgcgggagg caccttctcc
 180

cggttcgcc agccaaatgg cggtgcaggc tccagcatcc agtccgggtgc cttcggcacc
 240
 cccgcactgc gcagagaggc ccgcagaaac gatggcaccg gcggcgcgagg aggtgataca
 300
 ggcgcttcgg ccggagcgct caccgactcc ggcactacag gtgcagcttg cgcttcctgc
 360
 ggcgagacaa cagggtcact tcgaggcgagg gat
 393

<210> 968
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 968
 Pro Ala Arg Ser Asp Thr Glu Leu Val Val Ser Thr Asp Ser Gly Ala
 1 5 10 15
 Glu Ala Ser Gly Ser Ser Ser Ala Ser Ala Pro Val Gly Thr Glu Glu
 20 25 30
 Ser Pro Ser Ala Ser Ala Ser Ala Ala Trp Ala Ala Pro Asp Ser
 35 40 45
 Ala Gly Gly Thr Phe Ser Arg Val Arg Gln Pro Asn Gly Val Ala Gly
 50 55 60
 Ser Ser Ile Gln Ser Gly Ala Phe Gly Thr Pro Ala Leu Arg Arg Glu
 65 70 75 80
 Ala Ala Arg Asn Asp Gly Thr Gly Gly Ala Gly Gly Asp Thr Gly Ala
 85 90 95
 Ser Ala Gly Ala Leu Thr Asp Ser Gly Thr Thr Gly Ala Ala Cys Ala
 100 105 110
 Ser Cys Gly Gly Ala Thr Gly Ser Leu Arg Gly Gly Asp
 115 120 125

<210> 969
 <211> 880
 <212> DNA
 <213> Homo sapiens

<400> 969
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 ttatccttac atgtattgca gaggatcaat atgacctgc atttttgcat gatgatcaac
 120
 atgaattttc gagtaaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac
 180
 aagaatctta ccttgcggtc tttagtattg gaagtactgg acctgatggg agagttttat
 240
 gtaacacaca tgatgaagga gtttcctatg gatctctata tacgctgcat ccaggtagta
 300
 cacaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcgaggag
 360
 ctctgggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg
 420
 gccaaacaca acattttttac attagccctt atgattgtga acctattttaa tatgttttat
 480

acatatggcg acacatttct gccaaccccc agcagctatg atgaacttta ctatgagatt
 540
 atccgcatgc accagagctt tgacaacctc tactccatgg tcctgagggt ttctaccaat
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 660
 atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa
 720
 ctgtcagagg agcagggtgct ggagggtggtg agagccaaat atgacacgct cacgctgaag
 780
 ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc
 840
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 880

<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn
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Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn
			20						25					30	
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu
			35					40					45		
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile
	50					55					60				
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys
	65					70				75				80	
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile
			85						90					95	
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys
			100					105						110	
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met
		115					120							125	
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp
	130					135					140				
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu
	145				150					155				160	
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu
			165						170					175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile
			180					185						190	
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile
			195				200					205			
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr
	210					215					220				
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg
	225				230					235				240	
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg
			245					250						255	
Ser	Ile	Ser	Thr	Asn	Val	Arg									

260

<210> 971
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 971
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 120
 aatccaaccc ccaaatacct ggttgtaaac ggagacgaat ccgaacccgg cacgtgcaag
 180
 gacatgccgc tcattatggc aagcccgac acgcttgctg aaggtgctct tatctccgc
 240
 tacgctttcg gatccgagca ggctttcatc tacctccgtg gagaagttgt tcaggtagcc
 300
 cggcgcccttg aagaaaaaaa aaaaatgcga nnnnnnn
 337

<210> 972
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 972
 Ser Arg Gly Leu Thr Met Glu Pro Ser Glu Val Leu Asn Leu Ile Lys
 1 5 10 15
 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val
 20 25 30
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val
 35 40 45
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu
 50 55 60
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg
 65 70 75 80
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val
 85 90 95
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Met Arg Xaa Xaa
 100 105 110

<210> 973
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 973
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 120
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc
 180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag
 240
 tggctgtgta actttgagga ccactggcaa agtggctctg gggctagaga tccgagttca
 300
 tattctgggt ctgcctctga ctgactgcaa cggtgggcaa gtcacttgcc gtgcccagcc
 360

<210> 974

<211> 91

<212> PRT

<213> Homo sapiens

<400> 974

Met	Ala	Trp	Ser	Cys	Cys	Met	Val	Leu	Ser	Gly	Val	Arg	Asp	Leu	Leu
1				5					10					15	
Tyr	Arg	His	His	Leu	Gly	Thr	Ser	Gln	Thr	Ile	Arg	Phe	Ser	Gly	Pro
			20					25					30		
Thr	Gly	Ser	Thr	Glu	Ser	Gly	Thr	Gln	Gly	Phe	Gln	His	Ile	Leu	Arg
			35				40					45			
Gly	Asp	Ser	Ser	Gly	Cys	Val	Thr	Leu	Arg	Thr	Thr	Gly	Lys	Val	Ala
	50				55					60					
Leu	Gly	Ser	Glu	Ile	Arg	Val	His	Ile	Leu	Gly	Leu	Pro	Leu	Thr	Asp
65					70				75					80	
Cys	Asn	Gly	Gly	Gln	Val	Thr	Cys	Arg	Ala	Gln					
				85					90						

<210> 975

<211> 2604

<212> DNA

<213> Homo sapiens

<400> 975

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 120
 ccttgataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat
 180
 ttggcattag cctggaagag gtccctggtga acgagtttac ccgcccgaag catcttgaac
 240
 tgaccagcca cgatgcaggt tgaagaagcc accggtcagg ctgcggggccg tcgtcggggg
 300
 aacgtgtgtc gaagggtgtt tggccgcctc cggcgctttt tcagtcgcag gcggaatgag
 360
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 420
 ctggctgagc tggaagacgg agccctgctg ctgcagaccc tgcagctttc aaaaatttcc
 480
 tttccaattg gccaacgact tctgggattc aaaaggaaga tgagtctcaa tccgattgag
 540
 aaacaaatcc cccaggttgt tgaggcttgc tgccaattca ttgaaaaaca tggcttaagc
 600
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 660

ttgtgatcaag gtctggatgt agtgctggat gacaatcaga atgtgcatga tgtggctgca
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 780
 tcattctctc tgacagcaac tttaaagccc caggatcagc tttctgcccct gcagttgctg
 840
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 900
 aaaatcactg agaactcgga ggactcaatt ggcatgtatg gacagttggt ccagggcaac
 960
 cgtatgactt cactaactt ggccttggtg tttggatctg ctctcctgaa aaaaggaaa
 1020
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 1080
 aatgtggctc gtgccatgat tgataactgg gatgtcctct tcagggtgcc tccccatatt
 1140
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 1200
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 1260
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 1380
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 1440
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 ctataaggtg ccagacaggg gaaaagggtg ggggtacatc tgggatgtca caggaaacat
 1560
 taaggagaga gttgaaggta aagatctgaa ggtaagaagg agttccacct gatgctcggg
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 1860
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 1920
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 1980
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<210> 976

<211> 411

<212> PRT

<213> Homo sapiens

<400> 976

Met	Gln	Val	Glu	Glu	Ala	Thr	Gly	Gln	Ala	Ala	Gly	Arg	Arg	Arg	Gly
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Asn	Val	Val	Arg	Arg	Val	Phe	Gly	Arg	Ile	Arg	Arg	Phe	Phe	Ser	Arg
		20						25					30		
Arg	Arg	Asn	Glu	Pro	Thr	Leu	Pro	Arg	Glu	Phe	Thr	Arg	Arg	Gly	Arg
		35					40					45			
Arg	Gly	Ala	Val	Ser	Val	Asp	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Gly	Ala
	50					55					60				
Leu	Leu	Leu	Gln	Thr	Leu	Gln	Leu	Ser	Lys	Ile	Ser	Phe	Pro	Ile	Gly
65				70						75				80	
Gln	Arg	Leu	Leu	Gly	Ser	Lys	Arg	Lys	Met	Ser	Leu	Asn	Pro	Ile	Ala
			85						90					95	
Lys	Gln	Ile	Pro	Gln	Val	Val	Glu	Ala	Cys	Cys	Gln	Phe	Ile	Glu	Lys
			100					105					110		
His	Gly	Leu	Ser	Ala	Val	Gly	Ile	Phe	Thr	Leu	Glu	Tyr	Ser	Val	Gln
		115					120					125			
Arg	Val	Arg	Gln	Leu	Arg	Glu	Glu	Phe	Asp	Gln	Gly	Leu	Asp	Val	Val
	130					135					140				
Leu	Asp	Asp	Asn	Gln	Asn	Val	His	Asp	Val	Ala	Ala	Leu	Leu	Lys	Glu
145				150						155				160	
Phe	Phe	Arg	Asp	Met	Lys	Asp	Ser	Leu	Leu	Pro	Asp	Asp	Leu	Tyr	Met
			165						170				175		
Ser	Phe	Leu	Leu	Thr	Ala	Thr	Leu	Lys	Pro	Gln	Asp	Gln	Leu	Ser	Ala
		180						185					190		
Leu	Gln	Leu	Leu	Val	Tyr	Leu	Thr	Pro	Pro	Cys	His	Ser	Asp	Thr	Leu
		195					200					205			
Glu	Arg	Leu	Leu	Lys	Ala	Leu	His	Lys	Ile	Thr	Glu	Asn	Cys	Glu	Asp
	210					215						220			
Ser	Ile	Gly	Ile	Asp	Gly	Gln	Leu	Val	Pro	Gly	Asn	Arg	Met	Thr	Ser
225				230						235				240	
Thr	Asn	Leu	Ala	Leu	Val	Phe	Gly	Ser	Ala	Leu	Leu	Lys	Lys	Gly	Lys
			245						250					255	
Phe	Gly	Lys	Arg	Glu	Ser	Arg	Lys	Thr	Lys	Leu	Gly	Ile	Asp	His	Tyr
		260						265					270		
Val	Ala	Ser	Val	Asn	Val	Val	Arg	Ala	Met	Ile	Asp	Asn	Trp	Asp	Val

275		280		285
Leu Phe Gln Val Pro Pro His Ile Gln Arg Gln Val Ala Lys Arg Val				
290		295		300
Trp Lys Ser Ser Pro Glu Ala Leu Asp Phe Ile Arg Arg Arg Asn Leu				
305		310		315
Arg Lys Ile Gln Ser Ala Arg Ile Lys Met Glu Glu Asp Ala Leu Leu				
		325		330
Ser Asp Pro Val Glu Thr Ser Ala Glu Ala Arg Ala Val Leu Ala				
		340		345
Gln Ser Lys Pro Ser Asp Glu Gly Ser Ser Glu Glu Pro Ala Val Pro				
		355		360
Ser Gly Thr Ala Arg Ser His Asp Asp Glu Glu Gly Ala Gly Asn Pro				
		370		375
Pro Ile Pro Glu Gln Asp Arg Pro Leu Leu Arg Val Pro Arg Glu Lys				
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Glu Ala Lys Thr Gly Val Ser Tyr Phe Phe Pro				400
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<210> 977

<211> 378

<212> DNA

<213> Homo sapiens

<400> 977

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240
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378

<210> 978

<211> 126

<212> PRT

<213> Homo sapiens

<400> 978

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	20
Asp Ser Met Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly	
	35
Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met	
	50
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met	

65		70		75		80									
Gly	Asp	Val	Glu	Ile	Gly	Leu	Gln	Glu	Arg	Asn	Gly	Gln	Leu	Glu	Val
			85						90					95	
Asp	Ile	Ile	Gln	Ala	Arg	Gly	Leu	Thr	Ala	Lys	Pro	Gly	Ser	Lys	Thr
			100					105					110		
Leu	Pro	Ala	Ala	Tyr	Ile	Lys	Ala	Tyr	Leu	Leu	Glu	Met	Ala		
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<210> 979

<211> 3500

<212> DNA

<213> Homo sapiens

<400> 979

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<210> 980

<211> 73

<212> PRT

<213> Homo sapiens

<400> 980

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Leu	Ala	Gln	Gly	Arg	Gly	Cys	Arg	Gln	Gly	Lys	Gly	His	Trp	Pro	Pro
		20						25				30			
Cys	Phe	Gln	Val	Leu	Thr	Ala	Ser	Gly	Trp	Ser	Leu	Glu	Ala	Thr	Glu
		35						40				45			
Glu	Arg	Asn	Ala	Trp	Leu	Arg	Ala	Ala	Glu	His	Ser	Glu	Ala	Ser	Arg
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Glu	Asp	Ser	Arg	Pro	Ala	Arg	Ala	Pro							
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<210> 981

<211> 404

<212> DNA

<213> Homo sapiens

<400> 981

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 120
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 180

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 240
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<210> 982

<211> 134

<212> PRT

<213> Homo sapiens

<400> 982

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 20 25 30
 Thr Ala Pro Val Gly Trp Glu Leu Val Arg Val Glu His Val Glu Leu
 35 40 45
 Asp Asp Glu Asp Val Asp Asp Glu Asn Thr Asp Ile Thr Ala Leu Ala
 50 55 60
 Glu Ala Gly Ala Arg Gly Gly Ala Gly Asn His Arg Phe Gly Gly Asp
 65 70 75 80
 Arg Pro Gly Ser Asp Arg Val Leu Gly Arg Gln Arg Leu Gln Gln Pro
 85 90 95
 Arg His Leu Gln Pro Ser Gly Ala Pro Asp Gln Ala Cys Gly Gly Thr
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 Ala Ser Gly Ala Gln Gly Gly Ala Pro Leu Pro Pro Ala His Cys Pro
 115 120 125
 Gly Ser Glu Pro Gly Arg
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<210> 983

<211> 579

<212> DNA

<213> Homo sapiens

<400> 983

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<210> 984

<211> 103

<212> PRT

<213> Homo sapiens

<400> 984

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Lys	Thr	Leu	His	Asn	Leu	Gly	Pro	Phe	Thr	Ser	Leu	Thr	Leu	Ser	Pro
		20					25						30		
Ile	Thr	Leu	Asn	Ile	Thr	His	Ser	Ser	Pro	Ala	Thr	Leu	Ala	Ser	Leu
		35				40						45			
Leu	Phe	Pro	Lys	Arg	Ala	Arg	Tyr	Pro	Ser	Phe	Ser	Gly	Pro	Leu	Tyr
		50				55					60				
Leu	Phe	Phe	Ser	Leu	Pro	Glu	Thr	Pro	Phe	Leu	Leu	Asn	Asn	Leu	Met
65					70				75					80	
Ser	Cys	Pro	Ser	Thr	Ser	Ser	Val	Leu	Lys	Cys	His	Leu	Pro	Arg	Glu
			85						90					95	
Val	Phe	Pro	Asp	Gln	His	Ile									
						100									

<210> 985

<211> 313

<212> DNA

<213> Homo sapiens

<400> 985

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<210> 986

<211> 98

<212> PRT

<213> Homo sapiens

<400> 986

Met Asn Gly Leu Ala Val Thr Val His Thr Lys Leu Asp Lys Lys Gln

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	20	25	30
Ala Asn Phe Lys Ala His Asp Leu Lys Leu Val Thr Glu Ile Asn His			
	35	40	45
Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser			
	50	55	60
Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Leu Asn Asn Met			
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Gln Ser Ile Ile Asp Gly Lys Pro Glu Leu Asn Ile Thr Glu Leu Ser			
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<210> 987

<211> 4224

<212> DNA

<213> Homo sapiens

<400> 987

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4224

<210> 988

<211> 873

<212> PRT

<213> Homo sapiens

<400> 988

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 Met Leu Leu Arg Gly Leu Thr Gln Ile Gln Ser Arg Ile Leu Gly Pro
 35 40 45
 Gly Arg Lys Cys Cys Ala Leu Ala Asn Leu Ala Asp Met Leu Thr Val
 50 55 60
 Phe Ala Leu Thr Glu Asp Asp Pro Gln Glu Val Ser Ala Thr Val Tyr
 65 70 75 80
 Leu Asp Lys Leu Ala Thr Val Ile Ser Val Trp Asn Ser Asp Thr Gln
 85 90 95
 Asn Pro Tyr His Gln Gln Ala Leu Ala Glu Lys Val Lys Glu Ala Glu
 100 105 110
 Arg Asp Val Ser Leu Thr Ser Leu Ala Lys Leu Pro Ser Glu Thr Ile
 115 120 125
 Phe Val Gly Cys Glu Phe Leu His His Leu Leu Arg Glu Trp Gly Glu
 130 135 140
 Glu Leu Gln Ala Val Leu Arg Ser Ser Gln Gly Thr Ser Tyr Asp Ser
 145 150 155 160
 Tyr Arg Leu Cys Asp Ser Leu Thr Ser Phe Ser Gln Asn Ala Thr Leu
 165 170 175
 Tyr Leu Asn Arg Thr Ser Leu Ser Lys Glu Asp Arg Gln Val Val Ser
 180 185 190
 Glu Leu Ala Glu Cys Val Arg Asp Phe Leu Arg Lys Thr Ser Thr Val
 195 200 205
 Leu Lys Asn Arg Ala Leu Glu Asp Ile Thr Ala Ser Ile Ala Met Ala
 210 215 220
 Val Ile Gln Gln Lys Met Asp Arg His Met Glu Val Cys Tyr Ile Phe
 225 230 235 240
 Ala Ser Glu Lys Lys Trp Ala Phe Ser Asp Glu Trp Val Ala Cys Leu
 245 250 255
 Gly Ser Asn Arg Ala Leu Phe Arg Glu Pro Asp Leu Val Leu Arg Leu
 260 265 270
 Leu Glu Thr Val Ile Asp Val Ser Thr Ala Asp Arg Ala Ile Pro Glu
 275 280 285
 Ser Gln Ile Arg Gln Val Ile His Leu Ile Leu Glu Cys Tyr Ala Asp
 290 295 300
 Leu Ser Leu Pro Gly Lys Asn Lys Val Leu Ala Gly Ile Leu Arg Ser
 305 310 315 320
 Trp Gly Arg Lys Gly Leu Ser Glu Lys Leu Leu Ala Tyr Val Glu Gly
 325 330 335
 Phe Gln Glu Asp Leu Asn Thr Thr Phe Asn Gln Leu Thr Gln Ser Ala
 340 345 350
 Ser Glu Gln Gly Leu Ala Lys Ala Val Ala Ser Val Ala Arg Leu Val
 355 360 365
 Ile Val His Pro Glu Val Thr Val Lys Lys Met Cys Ser Leu Ala Val

370					375					380				
Val Asn	Leu Gly	Thr His	Lys Phe	Leu Ala	Gln Ile	Leu Thr	Ala Phe							
385			390		395		400							
Pro Ala	Leu Arg	Phe Val	Glu Val	Gln Gly	Pro Asn	Ser Ser	Ala Thr							
		405		410			415							
Phe Met	Val Ser	Cys Leu	Lys Glu	Thr Val	Trp Met	Lys Phe	Ser Thr							
		420		425		430								
Pro Lys	Glu Glu	Lys Gln	Phe Leu	Glu Leu	Leu Asn	Cys Leu	Met Ser							
		435		440		445								
Pro Val	Lys Pro	Gln Gly	Ile Pro	Val Ala	Ala Leu	Leu Glu	Pro Asp							
		450		455		460								
Glu Val	Leu Lys	Glu Phe	Val Leu	Pro Phe	Leu Arg	Leu Asp	Val Glu							
465			470		475		480							
Glu Val	Asp Leu	Ser Leu	Arg Ile	Phe Ile	Gln Thr	Leu Glu	Ala Asn							
		485		490		495								
Ala Cys	Arg Glu	Glu Tyr	Trp Leu	Gln Thr	Cys Ser	Pro Phe	Pro Leu							
		500		505		510								
Leu Phe	Ser Leu	Cys Gln	Leu Leu	Asp Arg	Phe Ser	Lys Tyr	Trp Gln							
		515		520		525								
Leu Pro	Lys Glu	Lys Arg	Cys Leu	Ser Leu	Asp Arg	Lys Asp	Leu Ala							
		530		535		540								
Ile His	Ile Leu	Glu Leu	Leu Cys	Glu Ile	Val Ser	Ala Asn	Ala Glu							
545			550		555		560							
Thr Phe	Ser Pro	Asp Val	Trp Ile	Lys Ser	Leu Ser	Trp Leu	His Arg							
		565		570		575								
Lys Leu	Glu Gln	Leu Asp	Trp Thr	Val Gly	Leu Arg	Leu Lys	Ser Phe							
		580		585		590								
Phe Glu	Gly His	Phe Lys	Cys Glu	Val Pro	Ala Thr	Leu Phe	Glu Ile							
		595		600		605								
Cys Lys	Leu Ser	Glu Asp	Glu Trp	Thr Ser	Gln Ala	His Pro	Gly Tyr							
		610		615		620								
Gly Ala	Gly Thr	Gly Leu	Leu Ala	Trp Met	Glu Cys	Cys Cys	Val Ser							
625			630		635		640							
Ser Gly	Ile Ser	Glu Arg	Met Leu	Ser Leu	Leu Val	Val Asp	Val Gly							
		645		650		655								
Asn Pro	Glu Glu	Val Arg	Leu Phe	Ser Lys	Gly Phe	Leu Val	Ala Leu							
		660		665		670								
Val Gln	Val Met	Pro Trp	Cys Ser	Pro Gln	Glu Trp	Gln Arg	Leu His							
		675		680		685								
Gln Leu	Thr Arg	Arg Leu	Leu Glu	Lys Gln	Leu Leu	His Val	Pro Tyr							
		690		695		700								
Ser Leu	Glu Tyr	Ile Gln	Phe Val	Pro Leu	Leu Asn	Leu Lys	Pro Phe							
705			710		715		720							
Ala Gln	Glu Leu	Gln Leu	Ser Val	Leu Phe	Leu Arg	Thr Phe	Gln Phe							
		725		730		735								
Leu Cys	Ser His	Ser Cys	Arg Asn	Trp Leu	Pro Leu	Glu Gly	Trp Asn							
		740		745		750								
His Val	Val Lys	Leu Leu	Cys Gly	Ser Leu	Thr Arg	Leu Leu	Asp Ser							
		755		760		765								
Val Arg	Ala Ile	Gln Ala	Ala Gly	Pro Trp	Val Gln	Gly Pro	Glu Gln							
		770		775		780								
Asp Leu	Thr Gln	Glu Ala	Leu Phe	Val Tyr	Thr Gln	Val Phe	Cys His							
785			790		795		800							
Ala Leu	His Ile	Met Ala	Met Leu	His Pro	Glu Val	Cys Glu	Pro Leu							

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      805              810              815
Tyr Val Leu Ala Leu Glu Thr Leu Thr Cys Tyr Glu Thr Leu Ser Lys
      820              825              830
Thr Asn Pro Ser Val Ser Ser Leu Leu Gln Arg Ala His Glu Gln Cys
      835              840              845
Phe Leu Lys Ser Ile Ala Glu Gly Ile Gly Pro Glu Glu Arg Arg Gln
      850              855              860
Thr Leu Leu Gln Lys Met Ser Ser Phe
865              870

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<210> 989
 <211> 402
 <212> DNA
 <213> Homo sapiens

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<400> 989
gcgtgggata tcgatacccg tcttgagcag gccatggacg ccttgcaagtg cccccaggc
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gacacccctg ttgacgtctt gtcaggcgggt gagcggcgctc gtgtcgcgct atgcaagctg
120
ttgatcgagc agcctgacct gctgcttctc gatgagccca ccaaccacct ggatgctgag
180
tctgtcaact gggtggaggg acacctcaag tcctatccgg gagctgtgct agccgtcaact
240
cacgaccgct atttccttga tcacgtcgcc gagtggatct gtgaggtoga tcgcgggccag
300
ttgcacccct acgagggcaa ctactcgacg tacctggaca ccaagcgcaa gcgtctccag
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402

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<210> 990
 <211> 134
 <212> PRT
 <213> Homo sapiens

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<400> 990
Ala Trp Asp Ile Asp Thr Arg Leu Glu Gln Ala Met Asp Ala Leu Gln
1      5      10      15
Cys Pro Pro Gly Asp Thr Pro Val Asp Val Leu Ser Gly Gly Glu Arg
      20      25      30
Arg Arg Val Ala Leu Cys Lys Leu Leu Ile Glu Gln Pro Asp Leu Leu
      35      40      45
Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ala Glu Ser Val Asn Trp
      50      55      60
Leu Glu Gly His Leu Lys Ser Tyr Pro Gly Ala Val Leu Ala Val Thr
      65      70      75      80
His Asp Arg Tyr Phe Leu Asp His Val Ala Glu Trp Ile Cys Glu Val
      85      90      95
Asp Arg Gly Gln Leu His Pro Tyr Glu Gly Asn Tyr Ser Thr Tyr Leu
      100      105      110
Asp Thr Lys Arg Lys Arg Leu Gln Ile Glu Gly Lys Lys Asp Ala Lys
      115      120      125
Arg Ala Lys Ile Leu Glu

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130

<210> 991
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 991
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 120
 gcccaatttt taggagtaga tgggtattgg ttaacgacgg ggaatactga agattctttt
 180
 agagaaagtg atgtatttag ccgactgta gtgagtgcag aatctactga tcagtatggt
 240
 tggattgaag ttgtagaagc taacttttct tgcgggacag gtgaatctat tgaatttcac
 300
 ttgatgcta ttaatggaaa aattccattc cctgcttcat tctttaaga aaaacgcgt
 359

<210> 992
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 992
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 1 5 10 15
 Lys Met Ser Gln Pro Ala Tyr Gln Ala Leu Glu Ser Gly Lys Asn Leu
 20 25 30
 Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly
 35 40 45
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp
 50 55 60
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val
 65 70 75 80
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser
 85 90 95
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala
 100 105 110
 Ser Phe Phe Lys Glu Lys Arg
 115

<210> 993
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 993
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 120

atgcgctcgct ttggcgcacg aggtttacgc cgtggggagc tcataagggg aataaccagca
 180
 cagggtcgga ccagttgtta cgcgcgctgc atgatctact tgcgcagga ttatatcggt
 240
 gagctaccca agcaacatat ctgcgtggga aagtttgatc ccgacaatat tctgcggac
 300
 ccgaacgaac tgtttgccac gtggtttaa gaagccgttg agaacgaagt cggcgaccct
 360
 actgcggtca ccgtggccac ggtggacgac aacggtcage ccgatgcgcg agtcgtcgac
 420
 cttctgtacc tcaactccga cggcttcac
 450

<210> 994

<211> 110

<212> PRT

<213> Homo sapiens

<400> 994

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Glu	Ile	Pro	Ala	Gln	Gly	Arg	Thr	Ser	Cys	Tyr	Asp	Arg	Cys	Met	Ile
		20					25					30			
Tyr	Leu	Ser	Gln	Asp	Tyr	Ile	Gly	Glu	Leu	Pro	Lys	Gln	His	Ile	Ser
	35					40					45				
Leu	Gly	Lys	Phe	Asp	Pro	Asp	Asn	Ile	Pro	Ala	Asp	Pro	Asn	Glu	Leu
	50				55					60					
Phe	Ala	Thr	Trp	Phe	Lys	Glu	Ala	Val	Glu	Asn	Glu	Val	Gly	Asp	Pro
65				70				75					80		
Thr	Ala	Val	Thr	Val	Ala	Thr	Val	Asp	Asp	Asn	Gly	Gln	Pro	Asp	Ala
			85					90					95		
Arg	Val	Val	Asp	Leu	Leu	Tyr	Leu	Asn	Ser	Asp	Gly	Phe	His		
		100					105						110		

<210> 995

<211> 924

<212> DNA

<213> Homo sapiens

<400> 995

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 120
 aactacgaca tgctcatcgg cgtcaaccag ggagagggcc tcaagtctgt ggaggactct
 180
 gcagagagcg aggacggtgt gtctgccagc gcttttgact tcaactgtctc caactttgtg
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 300
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 420

cagtctcccg tctacttttta cacctttctac caccactgcc aggcggaggg cgggcctgag
 480
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 540
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 600
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 720
 agcaaggaga agcagtatct gcacataggg ctgaagccac gcgtgcgtga caactaccgc
 780
 gccacaacgg tggccttctg gctggagctc gtgccccacc tgcacaacct gcacacggag
 840
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 900
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 924

<210> 996

<211> 308

<212> PRT

<213> Homo sapiens

<400> 996

Arg Glu Leu Val Asp Gln Asp Val Gln Pro Ala Arg Tyr His Ile Ala
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 Phe Gly Pro Val Val Asp Gly Asp Val Val Pro Asp Asp Pro Glu Ile
 20 25 30
 Leu Met Gln Gln Gly Glu Phe Leu Asn Tyr Asp Met Leu Ile Gly Val
 35 40 45
 Asn Gln Gly Glu Gly Leu Lys Phe Val Glu Asp Ser Ala Glu Ser Glu
 50 55 60
 Asp Gly Val Ser Ala Ser Ala Phe Asp Phe Thr Val Ser Asn Phe Val
 65 70 75 80
 Asp Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Val Leu Arg Glu Thr
 85 90 95
 Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Arg Asp Asn Gly Glu Met
 100 105 110
 Arg Arg Lys Thr Leu Leu Ala Leu Phe Thr Asp His Gln Trp Val Ala
 115 120 125
 Pro Ala Val Ala Thr Ala Lys Leu His Ala Asp Tyr Gln Ser Pro Val
 130 135 140
 Tyr Phe Tyr Thr Phe Tyr His His Cys Gln Ala Glu Gly Arg Pro Glu
 145 150 155 160
 Trp Ala Asp Ala Ala His Gly Asp Glu Leu Pro Tyr Val Phe Gly Val
 165 170 175
 Pro Met Val Gly Ala Thr Asp Leu Phe Pro Cys Asn Phe Ser Lys Asn
 180 185 190
 Asp Val Met Leu Ser Ala Val Val Met Thr Tyr Trp Thr Asn Phe Ala
 195 200 205
 Lys Thr Gly Asp Pro Asn Gln Pro Val Pro Gln Asp Thr Lys Phe Ile
 210 215 220
 His Thr Lys Pro Asn Arg Phe Glu Glu Val Val Trp Ser Lys Phe Asn


```

225          230          235          240
Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
          245          250          255
Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
          260          265          270
His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
          275          280          285
Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
          290          295          300
Gly Thr Arg Arg
305

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<210> 997

<211> 320

<212> DNA

<213> Homo sapiens

<400> 997

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120
gccttgctct tgctcggtgc ctttgccgct attatgtacg gtctcattct acttgattct
180
acctgggttag ccttactcgg tatcgatgta cgaggtggtg ccatcgaata ttgggcgaag
240
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tttgatttgc gcccaacgct
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<210> 998

<211> 106

<212> PRT

<213> Homo sapiens

<400> 998

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Tyr Gly Ile Lys Thr Gly Ile His Leu Gly Val Asp Ile Val Leu Asn
          20          25          30
Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
          35          40          45
Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
          50          55          60
Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
65          70          75          80
Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe
          85          90          95
Met Gln Asp Met Phe Asp Leu Arg Pro Arg
          100          105

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<210> 999

<211> 401

<212> DNA

<213> Homo sapiens

<400> 999

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 acatctgagc aagagcttca tcggtgttta tctctactca gaaggcaagt ttgtgaccag
 120
 caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
 180
 gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt
 240
 ggatgagtgg gtggctgatg ctaagaacca cattctcaat actgaaaact tcttttagcgg
 300
 gtcaaacggg ctcaacattg acagtttcta cgtcttttgg gaccaagaca tctgctggca
 360
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 401

<210> 1000

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1000

Met	Val	His	Leu	Ser	Lys	Ser	Phe	Ile	Gly	Val	Tyr	Leu	Tyr	Ser	Glu
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Gly	Lys	Phe	Val	Thr	Ser	Asn	Tyr	Leu	Asn	Arg	Gly	Tyr	Lys	Asp	Ile
		20					25					30			
Leu	Ser	Tyr	Ala	Asp	Asp	Ala	Ser	Leu	Leu	Gln	Lys	Pro	Pro	Ala	Val
		35					40					45			
Ala	Ser	Asp	Asp	Leu	Asp	Thr	Gly	Leu	Leu	Lys	Arg	Ala	Leu	Asp	Glu
	50					55				60					
Trp	Val	Ala	Asp	Ala	Lys	Asn	His	Ile	Leu	Asn	Thr	Glu	Asn	Phe	Phe
65				70					75					80	
Ser	Gly	Ser	Thr	Gly	Leu	Asn	Ile	Asp	Ser	Phe	Tyr	Val	Phe	Gly	Asp
				85				90						95	
Gln	Asp	Ile	Cys	Trp	Gln	Leu	Ala	Ala	Ile	Leu	Lys	Gln	Ser	Met	Asn
			100					105					110		
Arg	Glu	Leu													
			115												

<210> 1001

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1001

cgcggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccggtactg
 60
 ttcccttatg cccctaattgc ggtgattgtt ggcttctctg ccactaccgt tggttcaatt
 120
 atcggatatga ttgtcttccc gctgttttgg ctggcgatga tcttccggg tctgctaact
 180

aaattttctg ctggtggtgc cgctggagtc ttgggcaacg cgatgggagg acgtaaaggg
 240
 gcaattattg gcggcgtagt gcacgggctg ttatcaccc tgttaccagc gatgctaata
 300
 cccttactgg aaaccttcgg cttcaaaggc gtcaccttca gtgattccga t
 351

<210> 1002

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1002

Arg	Gly	Ile	Ala	Met	Arg	Leu	Val	Pro	Asn	Ala	Lys	Pro	Ala	Leu	Asp
1				5					10					15	
Cys	Pro	Val	Leu	Phe	Pro	Tyr	Ala	Pro	Asn	Ala	Val	Ile	Val	Gly	Phe
		20						25					30		
Leu	Ala	Thr	Thr	Val	Gly	Ser	Ile	Ile	Gly	Met	Ile	Val	Phe	Pro	Leu
		35				40					45				
Phe	Gly	Leu	Ala	Met	Ile	Leu	Pro	Gly	Leu	Leu	Thr	Asn	Phe	Phe	Ala
	50				55				60						
Gly	Gly	Ala	Ala	Gly	Val	Phe	Gly	Asn	Ala	Met	Gly	Gly	Arg	Lys	Gly
65				70				75					80		
Ala	Ile	Ile	Gly	Gly	Val	Val	His	Gly	Leu	Phe	Ile	Thr	Leu	Leu	Pro
			85					90					95		
Ala	Met	Leu	Ile	Pro	Leu	Leu	Glu	Thr	Phe	Gly	Phe	Lys	Gly	Val	Thr
		100					105						110		
Phe	Ser	Asp	Ser	Ser	Asp										
		115													

<210> 1003

<211> 444

<212> DNA

<213> Homo sapiens

<400> 1003

acgcgtcctc ctttagtcga tcgcgaatat gataggcgaa gcgcgctgat ggtgtgacgc
 60
 acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc
 120
 acccccgcat ggggcacact ctccggccta aagtcggct tcgctgacgc gccacataaa
 180
 ctgcgcgctt tggtcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg
 240
 gatttgacgc tcgattttatc gaagaacctc cttaccgacg agattcgtga cgctctcctc
 300
 gaactggctg cgcagatgcg cgtcaccgag cgtcgtgacg cgatgtatgc cggtagacac
 360
 atcaacgtca ccgaggaccg cggcgtcctc cataccgcgc tgtgtcgctcc ccgcaactgac
 420
 gagctgcatg ttgacggtca ggat
 444

<210> 1004

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1004

```

Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu
 1             5             10             15
Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg
      20             25             30
Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val
      35             40             45
Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile
      50             55             60
Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg
      65             70             75             80
Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg
      85             90             95
Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His
      100            105            110
Val Asp Gly Gln Asp
      115

```

<210> 1005

<211> 299

<212> DNA

<213> Homo sapiens

<400> 1005

```

ccatggccat tcctctggtg actgcatcca gtccgatgga tttaaacacc cccaatgtgc
60
tggtgactcc caagtttaca cctccagcca gggcttctct cctgggtttg cataccccacc
120
tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctctctca
180
tttcttccca tgctgcttc tcccacactc ctccctctca catgagggca acttcatcct
240
cccagttgct caggcccca acctccatca gttttgactc ttctctcgca cactactcg
299

```

<210> 1006

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1006

```

Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr
 1             5             10             15
Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser
      20             25             30
Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys
      35             40             45
Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala
      50             55             60
Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

```

```

65          70          75          80
Gln Leu Leu Arg Pro Gln Thr Ser Ile Ser Phe Asp Ser Ser Leu Ala
          85          90          95
His Tyr Ser

```

<210> 1007

<211> 389

<212> DNA

<213> Homo sapiens

<400> 1007

```

gccggcgcgga agatctaaag agctggaaag gcaaccgcaa gagagcgggg ttcttgcttg
60
atgagcgcgcg tttcatggac tccatcttcg gccccggggc tgggtgtgacg gtctctgaaa
120
tcaacgacgcg caccgaggca cccagagggtg tgacgttgag tgatggccga cgacagggca
180
acgcccggagc aatcgggtgac ttcttcgcat cgaaggacta caagccgtcc gcggcgagcc
240
tccgagggtcc ggcgagggat ccgaaatgga tcgacgttca acgctcattc cagcagaacg
300
aagaaggccc gtacagctgg tacacctggc gcgggcaggc ttttgacacg ggcgctggat
360
ggcgtaaata cgtccatgcc gcgacaacg
389

```

<210> 1008

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1008

```

Met Asp Ser Ile Phe Gly Pro Gly Pro Gly Val Thr Val Ser Glu Ile.
 1          5          10          15
Asn Asp Ala Thr Glu Ala Pro Arg Gly Val Thr Leu Ser Asp Gly Arg
20          25          30
Arg Gln Gly Asn Ala Gly Ala Ile Gly Asp Phe Phe Ala Ser Lys Asp
35          40          45
Tyr Lys Pro Ser Ala Ala Ser Leu Arg Gly Pro Ala Arg Asp Pro Lys
50          55          60
Trp Ile Asp Val Gln Arg Ser Phe His Glu Asn Glu Glu Gly Pro Tyr
65          70          75          80
Ser Trp Tyr Thr Trp Arg Gly Gln Ala Phe Asp Thr Gly Ala Gly Trp
85          90          95
Arg Lys Tyr Val His Ala Ala Thr Thr
100          105

```

<210> 1009

<211> 324

<212> DNA

<213> Homo sapiens

<400> 1009

ngccttcacg gctgntatgc ctggcctcat ccccatccct ggcacccgtg acgatagcca
 60
 cattccactg gtgtttcccc aggaagccca accctacctg catctcagca gagcttccac
 120
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc
 180
 agaaggagga cgtagttggt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt
 240
 ctgccccgag aggaacgtgg gcattaggct gcacccgcag gaagccatgt attttctgag
 300
 aaacttgccc catggtgcag atct
 324

<210> 1010
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1010
 Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro
 1 5 10 15
 Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly
 20 25 30
 Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys
 35 40 45
 Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu
 50 55 60
 Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys
 65 70 75 80
 His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu
 85 90 95
 Ala Arg His Xaa Ser His Glu Gly
 100

<210> 1011
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1011
 ctgcagaaaa ggaggggggt cccatgccaa ggcagaactg tctgggacag acgctgcccg
 60
 gatccctgcg gctgcctgca ctctggacca cgagctctga gacgagcagg ttgaggggcg
 120
 gtggggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cggtgagctg
 180
 actcctgagg aggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac
 240
 ggcaccatca atgccagga gctggggcgcg gcgctgaagg ccacggggcaa gaacctctcg
 300
 gaggcccagc taaagaaact catctccgag
 330

<210> 1012

<211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1012
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
 1 5 10 15
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
 20 25 30
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
 35 40 45
 Leu Lys Lys Leu Ile Ser Glu
 50 55

<210> 1013
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 1013
 naattgcaca tcgtggtggc gtcgctgcgt gcggcactga caatgtgact ggcgcatctcg
 60
 tggcggcgctc tcctcgctgc cgggagcggc gaggaaggat taacgatgac cagcgacgctc
 120
 cccggggattg gctcgaacgc cgccactttg gcgcgttccc agggctcgag tgacaaggtc
 180
 gagggctgatt tggcgggtcca tcccgacaag tggcgcatc tgggggggga cgcgtctact
 240
 ggcagcctgc acatcggtca ctacttcggg tcgctggcga atcgggtacg cgtgcagaac
 300
 aagggcattg agtctttct tgtcgctcgt gactaccagg ttatctatga cgcggggggg
 360
 ggtggtgacc tgcaggccaa tggtatgtcg aatgtcgccg attacctggc aatcggcatt
 420
 gacccaacgc gt
 432

<210> 1014
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1014
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala
 1 5 10 15
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His
 20 25 30
 Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu
 35 40 45
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln
 50 55 60
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile
 65 70 75 80
 Tyr Asp Arg Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95
Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg
100 105

<210> 1015
<211> 467
<212> DNA
<213> Homo sapiens

<400> 1015
nngaattcga tggctgtgaa aggtcgagct cttaagtgtt ttcatatccc ctgtgtggtt
60
gaaaacttcc cgatgaaagc gcgcacgggt gaagagctga aagaattgga aagagtttta
120
cagcaaaaga agattgaagc agagtgtctt aaactacgga aggaaattgt agaggctcag
180
tctggagtta agttgattaa acacggtcat gaagaggatg atgaagaaga ggaagaggaa
240
gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gactactgat
300
tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa
360
atcaacaaaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat
420
gagtttgacg ctgcatataa acaaaaagag tttgaaattg caccgct
467

<210> 1016
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1016
Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile
1 5 10 15
Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu
20 25 30
Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu
35 40 45
Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys
50 55 60
Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu
65 70 75 80
Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser
85 90 95
Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu
100 105 110
Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys
115 120 125
Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala
130 135 140
Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg
145 150 155

<210> 1017
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 1017
 acgctgggct gggtgggtat gtggaacat gtgcgcgcta atgagaagga tgcgaagggg
 60
 aacattaaag tgggtcgccc cggtactttt gcggagggtca tggatttcta tgcgcattat
 120
 ctgaaggggtg cgggttaccog tttccgtccg aattttattg tgcaggataa tacggggccgt
 180
 tggcgtgttc agtcgtcgtg gccgcagccg aatcgactg ttacttttgc gggaccccg
 240
 ggcattgtcc gctacggtac gacgttggcg gcccgacgc atgggaatgg tcaggctatt
 300
 ccgcagggcg atgcacagtc tcttaaccgc gagaa
 335

<210> 1018
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1018
 Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile
 1 5 10 15
 Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala
 20 25 30
 His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val
 35 40 45
 Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro
 50 55 60
 Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly
 65 70 75 80
 Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln
 85 90 95
 Ala Asp Ala Gln Ser Leu Asn Arg Glu
 100 105

<210> 1019
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 1019
 acgcgtgaag gggtagtcgt agtagaagtc gtccacaac acggggcccg gcagggtccag
 60
 ctctggagcc tctctctcaa tggcgttgcc catgggtgct ggcttgggtg atgaggcggt
 120
 tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtggct
 180
 ggaggagccg ctgectgagc cttcagggcc cagtgtgcc agggggccacc gacagagtgg
 240

cagagagcag gtgacttcct ggcactgcgg agcgaggacc cggagaagta cttcctcaat
 300
 ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac
 360
 gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtctgg
 420
 atccagctgc tgttccagga gagcaaccct gggg
 454

<210> 1020

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1020

Met	Ala	Leu	Pro	Met	Val	Pro	Gly	Leu	Gly	Asp	Glu	Ala	Gly	Glu	Gly
1				5					10					15	
Arg	Gly	Ala	Arg	Trp	Cys	Gly	Met	Lys	Ser	Ala	Ser	Leu	Lys	Ser	Ser
			20					25					30		
Trp	Leu	Glu	Glu	Pro	Leu	Pro	Glu	Pro	Ser	Gly	Pro	Ser	Val	Pro	Arg
		35					40				45				
Gly	His	Arg	Gln	Ser	Gly	Arg	Glu	Gln	Val	Thr	Ser	Trp	His	Cys	Gly
50					55					60					
Ala	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Ser	Met	Val	Ala	Gly	Pro	Ser	Ser
65					70					75				80	
Gly	Thr	Gly	Thr	Thr	Arg	Trp	Gln	Gly	Pro	Pro	Ser	His	Thr	His	Ala
			85					90						95	
Gly	Ala	Thr	Gly	Arg	Thr	Ser	Arg	Pro	Arg	Val	Pro	Pro	Arg	Ser	Leu
			100					105						110	
Ser	Gly	Ser	Ser	Cys	Cys	Ser	Arg	Arg	Ala	Thr	Leu	Gly			
		115					120					125			

<210> 1021

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1021

cagctgtgtc gtgacctcct gtagaccaga gagaggtaga gcatgaaaaa tgctcattga
 60
 gccgagatta tetgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc
 120
 tggttgaggg tcaagtgtct gggcagcagc aacaacaac caaaaaaaag ccctttgaac
 180
 tcccttaaat ttgccccaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt
 240
 taaagggcac tcttgagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa
 300
 atgcagagct ctttttagca tcttcatatt caaggcggaa aaactgagct tggcagaggaa
 360
 ccctgt
 366

<210> 1022

<211> 109

<212> PRT

<213> Homo sapiens

<400> 1022

```

Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
 1           5           10           15
Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
          20           25           30
Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
          35           40           45
Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala
          50           55           60
Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
          65           70           75           80
Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
          85           90           95
Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Gln Leu
          100          105

```

<210> 1023

<211> 426

<212> DNA

<213> Homo sapiens

<400> 1023

```

gccggggcttc gggctctctga agcgatcaac ctggccgact cggatgcaga tctggacggc
60
ggcatcctga ccatacagca gaccaagttt ggcaagtcct gcattggtgcc gctacacccc
120
agcgtgatcg gtccgatggc agcctaccgg gccttgcgcc gccagtacgt gcctgcgaag
180
ccgcagatga cattcttcgt gggctcgcgt ggcggtgcacc ggggtgaacc gctgggagat
240
agggcagggtc atcgagtgtt ctgtcagctg cgcgagcaat tgggttgatg cgatcgcggc
300
ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgcccgtgag acggatgatc
360
ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
420
ggccac
426

```

<210> 1024

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1024

```

Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
 1           5           10           15
Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
          20           25           30
Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

```

```

          35              40              45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
   50              55              60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
65              70              75              80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
   85              90              95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
   100              105              110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
   115              120              125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
   130              135              140

```

<210> 1025

<211> 518

<212> DNA

<213> Homo sapiens

<400> 1025

```

nagcgctggt gcgcgcagggt ggccgccgcgg tccctttgct cctcgcgcaa gccggagggg
60
tgcccagaag gctaccacta gctccagcga aggggtgcgcc ctgagagccg ggtagcctcg
120
gatagcggcg ctgcgtacgc gatgatggat gagccgtggt gggaaaggcg cgctgcctcg
180
gacgtccact gcacctcgcg cgagaaggaa ctgaagctgc ccaccttcgc agccactcc
240
ccactctga agagccgcgc gttcttcgtg gacatcctga cctcgctgag cagccactgc
300
cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
360
tacaacgtca ccacctccaa gcagctctac accgtggccg tctcctgcct cctgcttgca
420
agtaagtctg aggatcgga agaccacgtc cccaagttgg agcaaataaa cagcacgagg
480
atcctgagca gccagaactt caccctcacc aagaagga
518

```

<210> 1026

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1026

```

Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
   1              5              10              15
Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
   20              25              30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
   35              40              45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
   50              55              60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

```

```

65          70          75          80
Gln Leu Tyr Thr Val Ala Val Ser Cys Leu Leu Ala Ser Lys Phe
      85          90          95
Glu Asp Arg Glu Asp His Val Pro Lys Leu Glu Gln Ile Asn Ser Thr
      100        105        110
Arg Ile Leu Ser Ser Gln Asn Phe Thr Leu Thr Lys Lys
      115        120        125

```

<210> 1027

<211> 465

<212> DNA

<213> Homo sapiens

<400> 1027

```

ggcccaaaag tcatacaaga aaagctgaca caggagctga aggaccacaa cgccaccagg
60
atccctgcagc agctgccgct gctcaaggcc atgcgggaaa agccagccgg aggcacccct
120
gtgctgggga gcctgggtgaa caccngtctc gaagcacatc atnctggctg gaaggtcatc
180
acagctaaca tcctccagct gcagggtgaag ccctcggccca atgaccagga gctgctagtc
240
aagatcccc tggacatggg ggctggattc aacacgcccc tggtaagac catcgtggag
300
ttccacatga cgactgaggc ccaagccacc atccgcatgg acaccagtgc aagtggcccc
360
acccgcctgg tcctcagtga ctgtgccacc agccatggga gcctgcgcat ccaactgctg
420
cataagctct ccttcaagct gaacgcctca gctaagcagg tcatg
465

```

<210> 1028

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1028

```

Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys Asp His
1      5      10      15
Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Lys Ala Met Arg
      20      25      30
Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser Leu Val Asn Thr
      35      40      45
Xaa Pro Glu Ala His His Xaa Trp Leu Lys Val Ile Thr Ala Asn Ile
      50      55      60
Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp Gln Glu Leu Leu Val
      65      70      75      80
Lys Ile Pro Leu Asp Met Val Ala Gly Phe Asn Thr Pro Leu Val Lys
      85      90      95
Thr Ile Val Glu Phe His Met Thr Thr Glu Ala Gln Ala Thr Ile Arg
      100     105     110
Met Asp Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys
      115     120     125
Ala Thr Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser

```

```

      130                135                140
Phe Lys Leu Asn Ala Ser Ala Lys Gln Val Met
145                150                155

<210> 1029
<211> 479
<212> DNA
<213> Homo sapiens

<400> 1029
acgcgtgaag ggaaactgtc ctcacagatg agtgtgaggg ttcaaaaaga tactgcctgc
60
caagcactgg ccacaaatgc ctggcagaac aactgctcat aagtgtgtag ttgtgtgtat
120
tattactaac caagtgagga aaattatccc tagcaggtcc agatgaccgt gtgcatgaat
180
cacagggaga ccctaaagga ttctctcctg taaagctctt tccccacctt tttgctactg
240
cctgaaattg ctttagcagg aaacagaatc tctcatgcc aagtgaagca taaagttaa
300
aatgtaaatg ctctaggaaa aggcaactca tctcttaaat tctctcaag gttcaaatcc
360
tttccaaaga ggaggtcttt gtataagtca gaaggcccag tcctgaagg tcatggaaaa
420
ggtcatgaca cacggagggg gtgtcaaagg gagactggga aactgaagat gaagctagc
479

<210> 1030
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1030
Met Ser Cys Leu Phe Leu Glu His Leu His Phe Lys Leu Tyr Ala His
1      5      10      15
Leu Trp His Glu Arg Phe Cys Phe Leu Leu Lys Gln Phe Gln Ala Val
20      25      30
Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser
35      40      45
Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe
50      55      60
Pro His Leu Val Ser Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser
65      70      75      80
Cys Ser Ala Arg His Leu Trp Pro Val Leu Gly Arg Gln Tyr Leu Phe
85      90      95
Glu Pro Ser His Ser Ser Val Arg Thr Val Ser Leu His Ala
100     105     110

<210> 1031
<211> 322
<212> DNA
<213> Homo sapiens

<400> 1031

```

nacgcgtttt atgtcagcgt tgaattggaa gacggcaagt ctatcgccat gctgccccag
 60
 gcagatggct ggtttgaagt ggaggtgaag tgccccggcg gcactacta cgcctataac
 120
 atcgacggcg aaaccgatgt acccgacccg gcatccaggc cgcaagccaa cgaatgtgcat
 180
 ggggtggagcg tcgtcgtcga cccgctcgcc tatcaatggc gacaccctaa ctggcaaggc
 240
 cgccccctggc atgaggcggt gatttacgag ctgcacgttg cgcactctgg cggtacggc
 300
 gctgttgaac agcaactgcc gc
 322

<210> 1032

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1032

Xaa	Ala	Phe	Tyr	Val	Ser	Val	Glu	Leu	Glu	Asp	Gly	Lys	Ser	Ile	Ala
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Ala	Gly	Thr	His	Tyr	Arg	Tyr	Asn	Ile	Asp	Gly	Glu	Thr	Asp	Val	Pro
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Asp	Pro	Ala	Ser	Arg	Ala	Gln	Ala	Asn	Asp	Val	His	Gly	Trp	Ser	Val
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Arg	Pro	Trp	His	Glu	Ala	Val	Ile	Tyr	Glu	Leu	His	Val	Gly	Val	Leu
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<210> 1033

<211> 579

<212> DNA

<213> Homo sapiens

<400> 1033

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 420

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 <213> Homo sapiens

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 Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg
 35 40 45
 Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg
 50 55 60
 Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn
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 Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val
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<213> Homo sapiens

<400> 1036

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 Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr
 50 55 60
 Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser
 65 70 75 80
 Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa
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<210> 1037

<211> 5832

<212> DNA

<213> Homo sapiens

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<210> 1038

<211> 1485

<212> PRT

<213> Homo sapiens

<400> 1038

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Gln	Gly	Asn	Tyr	Ser	Arg	Pro	Pro	Ala	Tyr	Ser	Gly	Val	Pro	Ser	Ala
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Ser	Tyr	Ser	Gly	Pro	Gly	Pro	Gly	Met	Gly	Ile	Ser	Ala	Asn	Asn	Gln
	50					55					60				
Met	His	Gly	Gln	Gly	Pro	Ser	Gln	Pro	Cys	Gly	Ala	Val	Pro	Leu	Gly
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Arg	Met	Pro	Ser	Ala	Gly	Met	Gln	Asn	Arg	Pro	Phe	Pro	Gly	Asn	Met
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Ser	Ser	Met	Thr	Pro	Ser	Ser	Pro	Gly	Met	Ser	Gln	Gln	Gly	Gly	Pro
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Gly	Met	Gly	Pro	Pro	Met	Pro	Thr	Val	Asn	Arg	Lys	Ala	Gln	Glu	Ala
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Ala	Ala	Ala	Val	Met	Gln	Ala	Ala	Ala	Asn	Ser	Ala	Gln	Ser	Arg	Gln
		130				135						140			
Gly	Ser	Phe	Pro	Gly	Met	Asn	Gln	Ser	Gly	Leu	Met	Ala	Ser	Ser	Ser
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Pro	Tyr	Ser	Gln	Pro	Met	Asn	Asn	Ser	Ser	Ser	Leu	Met	Asn	Thr	Gln
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Ala	Pro	Pro	Tyr	Ser	Met	Ala	Pro	Ala	Met	Val	Asn	Ser	Ser	Ala	Ala
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Ser	Val	Gly	Leu	Ala	Asp	Met	Met	Ser	Pro	Gly	Glu	Ser	Lys	Leu	Pro
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Ser	Ile	Ser	Ser	Phe	His	Gly	Asp	Glu	Ser	Asp	Ser	Ile	Ser	Ser	Pro
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Pro Ser Pro Ala Asn Ser Gly Ser Leu Gln Gly Pro Gln Thr Pro Gln
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Asp Ser Ser Phe Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr
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Gln Gln Gly Met Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu
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Pro Asn Lys Asp Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser
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Gln	Lys	Val	Met	Pro	Thr	Val	Pro	Thr	Ser	Gln	Val	Thr	Gly	Pro	Pro
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Ser	Gly	Leu	Leu	Ala	Glu	Ser	Thr	Trp	Ala	Leu	Asp	Thr	Ile	Asn	Ile
				885					890					895	
Leu	Leu	Tyr	Asp	Asp	Ser	Thr	Val	Ala	Thr	Phe	Asn	Leu	Ser	Gln	Leu
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Ala	Asp	Asp	Ser	Gly	Lys	Glu	Glu	Glu	Asp	Ala	Glu	Cys	Ile	Asp	Asp
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Asp	Glu	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Asp	Ser	Glu	Lys	Thr	Glu	
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Ala	Gly	Lys	Lys	Lys	Glu	Leu	Ala	Gly	Lys	Gly	Asp	Ser	Glu	Glu	Gln
				1090			1095					1100			
Gln	Glu	Lys	Ser	Ile	Ile	Ala	Thr	Ile	Asp	Asp	Val	Leu	Ser	Ala	Arg
				1105			1110					1115			1120
Pro	Gly	Ala	Leu	Pro	Glu	Asp	Ala	Asn	Pro	Gly	Pro	Gln	Thr	Glu	Ser
				1125					1130					1135	
Ser	Lys	Phe	Pro	Phe	Gly	Ile	Gln	Gln	Ala	Lys	Ser	His	Arg	Asn	Ile
				1140					1145					1150	
Lys	Leu	Leu	Glu	Asp	Glu	Pro	Arg	Ser	Arg	Asp	Glu	Thr	Pro	Leu	Cys
				1155			1160					1165			
Thr	Ile	Ala	His	Trp	Gln	Asp	Ser	Leu	Ala	Lys	Arg	Cys	Ile	Cys	Val
				1170			1175					1180			
Ser	Asn	Ile	Val	Arg	Ser	Leu	Ser	Phe	Val	Pro	Gly	Asn	Asp	Ala	Glu

```

1185          1190          1195          1200
Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly Lys Leu Ile Leu
1205          1210          1215
Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu
1220          1225          1230
Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp
1235          1240          1245
Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu
1250          1255          1260
Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile
1265          1270          1275          1280
Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser
1285          1290          1295
Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro
1300          1305          1310
Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln
1315          1320          1325
Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln
1330          1335          1340
Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn
1345          1350          1355          1360
Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln
1365          1370          1375
Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
1380          1385          1390
Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr
1395          1400          1405
Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu
1410          1415          1420
Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala
1425          1430          1435          1440
Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu Leu His Glu Gly
1445          1450          1455
Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala
1460          1465          1470
Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln Leu
1475          1480          1485

```

<210> 1039

<211> 379

<212> DNA

<213> Homo sapiens

<400> 1039

```

gcaggagcca gggatgctgc tgaacatccc gcagtgccacg agacaggcct ccaccacacg
60
gaattacctt ggcctgaggt gttacgagag cacagagaga aaccagggtac agacgcgggg
120
cagagggggag agaggggagag agtgtgagag ctaaggtttc gggagaagac tttgtggaaa
180
aagtcttttg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca
240
gattttgtat gtattgaagg cctgaatac ttttttgaaa gagaatgaca tgagtacacc
300

```


tggtcagcca cacgtgagag gggttggagg agggaaagtag cagaggcagg gagaccaggt
 360
 agaaagacct cgccatagt
 379

<210> 1040

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1040

Met	Ala	Arg	Ser	Phe	Tyr	Leu	Val	Ser	Leu	Pro	Leu	Val	Leu	Pro	Ser
1			5					10				15			
Ser	Asn	Pro	Ser	His	Val	Trp	Leu	Thr	Arg	Cys	Thr	His	Val	Ile	Leu
			20				25					30			
Phe	Gln	Lys	Ser	Ile	Gln	Gly	Leu	Gln	Tyr	Ile	Gln	Asn	Leu	Glu	Trp
		35				40					45				
Ser	Ser	Pro	Val	Thr	Glu	Ser	Trp	Leu	Cys	Cys	Arg	Thr	Gln	Pro	Lys
	50				55					60					
Thr	Phe	Ser	Thr	Lys	Ser	Ser	Pro	Glu	Thr	Leu	Ala	Leu	Thr	Leu	Ser
65				70					75					80	
Pro	Ser	Leu	Pro	Ser	Ala	Pro	Arg	Leu	Tyr	Leu	Val	Ser	Leu	Cys	Ala
			85					90					95		
Leu	Val	Thr	Pro	Gln	Ala	Lys	Val	Ile	Pro	Cys	Gly	Gly	Gly	Leu	Ser
		100						105					110		
Arg	Ala	Leu	Arg	Asp	Val	Gln	Gln	His	Pro	Trp	Leu	Leu			
		115				120						125			

<210> 1041

<211> 388

<212> DNA

<213> Homo sapiens

<400> 1041

ttagtggccg tggaggccat cggtacatc gcgagtattg acaaggccga tatgtcaatc
 60
 gaaacggcgt acctgccgcg gctgttggtt tccctggccc tgaccatccc ggtgctcgcc
 120
 ttgtcgatga tcccgccctt gcacttcccg cattggccgt tgtgggcgtt ggcgcttacc
 180
 accccggtgg tggtctgggg tgccctggcg ctgcaccacg ccgcgtggac caacctgcgg
 240
 cacggcgccg ccatcatgga caccctgggt tcgctcgagg tcctcacttc gtacctctgg
 300
 tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt
 360
 cacgacgctg atcctggccg gcaaattt
 388

<210> 1042

<211> 129

<212> PRT

<213> Homo sapiens

<400> 1042

```

Leu Val Ala Val Glu Ala Ile Gly Tyr Ile Ala Ser Ile Asp Lys Ala
 1             5             10             15
Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu
           20             25             30
Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His
 35             40             45
Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val
 50             55             60
Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg
 65             70             75             80
His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr
           85             90             95
Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu
          100             105             110
Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln
          115             120             125
Ile

```

<210> 1043

<211> 555

<212> DNA

<213> Homo sapiens

<400> 1043

```

accggtgaaa ccctgatcgg ccaatcgttt tccaccgttc cggcgggcaa gggcgcaaac
60
caggcggtcg cttcggcgcg tcttggggcc gaagtcgcga tggctgggtg cgtgggtacc
120
gatgcctacg gcgcgcaatt acgcgacgca ttgttggtgg aaggcatcga ttgccaggcc
180
gtcagcacccg tcgacgggttc cagcgggtgt gcgctgatcg tgggtggatga cagcagccag
240
aatgcgatcg ttatcgtcgc cggtagcaat ggcgagctga ctccggccaa gttacagacc
300
tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggac
360
actgtcggcc atgcgcctaa gcgcgggtcg gaactgggca agacggtgat cctcaatccg
420
gcgcgggcca gcggcccgct gcctgaggat tggtagccgc ccacgatta cctgattccc
480
aacgaaagcg aagcctcgcc cttgagtggc gtgggtgggt attcactgga cagcgccaag
540
gtcgtgcta cgcgt
555

```

<210> 1044

<211> 185

<212> PRT

<213> Homo sapiens

<400> 1044

```

Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

```

```

1           5           10           15
Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val
20
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg
35
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val
50
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln
65
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala
85
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val
100
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg
115
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser
130
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro
145
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu
165
Asp Ser Ala Lys Val Ala Ala Thr Arg
180
185

```

<210> 1045

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1045

```

ctattgccat actaccgccc cggaaccta caggacatga tcaacgcaa cctcttcaat
60
cactccaaat tccccgagac gcaccttatg aatctatttc tcggcgctctg caaggccctg
120
cgcgccatgc acgattacca cgcaccgccc gcagagcgca tgccaattgg gcaccgaagg
180
cagaccacca cccagggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaacgta
240
cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
300
ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaacagg tacgtgctgc
360
aagctcctcg g
371

```

<210> 1046

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1046

```

Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
1           5           10           15
Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu

```

20										25					30				
Phe	Leu	Gly	Val	Cys	Lys	Ala	Leu	Arg	Ala	Met	His	Asp	Tyr	His	Ala				
35										40					45				
Pro	Pro	Ala	Glu	Arg	Met	Pro	Ile	Gly	His	Arg	Arg	Gln	Thr	Thr	Thr				
50										55					60				
Gln	Val	Gln	Ser	Asn	Ser	Gly	Arg	Ala	Val	Ala	His	Arg	Arg	Asn	Val				
65										70					75				
Arg	Lys	Lys	Thr	Lys	Arg	Arg	Ser	Arg	Lys	Asp	Leu	Leu	Trp	Asn	His				
80										85					90				
Arg	Thr	Thr	Ser	Gly	Arg	Ala	Ala	Ser	Thr	Lys	Pro	Tyr	Ala	His	Arg				
100										105					110				
Asp	Ile	Lys	Pro	Gly	Thr	Cys	Cys	Lys	Leu	Leu									
115										120									

<210> 1047

<211> 754

<212> DNA

<213> Homo sapiens

<400> 1047

1	atgtccca	aggacctgga	cgaggcgttg	ccagcccttg	atgcggctct	ggccagccta
60	gcacacctca	acaagaacga	agtgacccag	gtacgtgcca	tgcagcggcc	acccccgggt
120	gtgaaactgg	tcatagaagc	tgtgtgcatt	atgaaaggca	tcaagcccaa	gaagggtgcct
180	ggagaaaaag	caggcaccaa	ggtggatgac	tactggggagc	ctggcaaggg	gctgtgtcag
240	gacccggggc	acttccttga	gagcctcttc	aagtttgaca	aggacaacat	tggagatgtg
300	gtgatcaaa	ccatccagcc	gtacatcgat	aatgaagagt	tccagccagc	caccatttgc
360	aagggtgtcca	aggggtgccc	cttcatttgg	ccgtgggggg	gggcaatgcc	caagtacccc
420	tttgtggcca	aggccgtgga	gccccagcgg	caagccctgc	tggaggccca	ggatgacctg
480	gggggtgacac	agaggatcct	ggatgaggca	aaacagcgcc	ttcgtgaggt	ggaggacggc
540	atcgccacaa	tgcaggctaa	gtaccgggaa	tgcatatcca	agaaggagga	gctggagagt
600	aagtgtgagc	agtgtgagca	gcggctgggc	cacgctggca	aggtgcgcac	cctcctcctg
660	caaggcctgc	aagcggggcc	ggcccagaca	ggggccagaa	aggaccaggg	cgccgggtgg
720	tctctggggtg	gctgtccaac	cccctccctg	gcaa		
754						

<210> 1048

<211> 251

<212> PRT

<213> Homo sapiens

<400> 1048

Xaa Ala Gln Lys Asp Leu Asp Glu Ala Leu Pro Ala Leu Asp Ala Ala

```

      1           5           10           15
Leu Ala Ser Leu Arg Asn Leu Asn Lys Asn Glu Val Thr Gln Val Arg
      20
Ala Met Gln Arg Pro Pro Pro Gly Val Lys Leu Val Ile Glu Ala Val
      35
Cys Ile Met Lys Gly Ile Lys Pro Lys Lys Val Pro Gly Glu Lys Pro
      50
Gly Thr Lys Val Asp Asp Tyr Trp Glu Pro Gly Lys Gly Leu Leu Gln
      65
Asp Pro Gly His Phe Leu Glu Ser Leu Phe Lys Phe Asp Lys Asp Asn
      85
Ile Gly Asp Val Val Ile Lys Ala Ile Gln Pro Tyr Ile Asp Asn Glu
      100
Glu Phe Gln Pro Ala Thr Ile Ala Lys Val Ser Lys Gly Cys Pro Phe
      115
Ile Trp Pro Trp Gly Gly Ala Met Pro Lys Tyr Pro Phe Val Ala Lys
      130
Ala Val Glu Pro Lys Arg Gln Ala Leu Leu Glu Ala Gln Asp Asp Leu
      145
Gly Val Thr Gln Arg Ile Leu Asp Glu Ala Lys Gln Arg Leu Arg Glu
      165
Val Glu Asp Gly Ile Ala Thr Met Gln Ala Lys Tyr Arg Glu Cys Ile
      180
Thr Lys Lys Glu Glu Leu Glu Leu Lys Cys Glu Gln Cys Glu Gln Arg
      195
Leu Gly His Ala Gly Lys Val Arg Thr Leu Leu Leu Gln Gly Leu Gln
      210
Ala Gly Pro Ala Gln Thr Gly Ala Arg Lys Asp Gln Gly Ala Gly Gly
      225
Ser Trp Gly Gly Cys Pro Thr Pro Ser Leu Ala
      245
      250

```

<210> 1049

<211> 558

<212> DNA

<213> Homo sapiens

<400> 1049

```

cgagcaata gctgcacttg accagactgg gctttgcaat aagcgcatcc cccgggctga
60
atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt
120
gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac
180
tttatggcct acataatcca gagatagatg ggctgggcat gattccattt ttctgttggg
240
gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac
300
ctcatgtctc ccagactccc ggggtcccg gctttttctc ggggcgggccc cattcacatt
360
gcaattcatg gccggggcaa atgctcacc acagagatat taagcactcc aacactccat
420
ccaccagggt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg
480

```

cagctaaaga aagggttttg catgctctgc tttattgttt cacagaagat aagaaaaataa
 540
 actgcaaagt aacttaag
 558

<210> 1050
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 1050
 Met Ile Pro Ile Phe Cys Trp Gly Asn Arg Leu Thr Glu Lys Leu Arg
 1 5 10 15
 Asp Lys Tyr Lys Val Met Lys Leu Cys Thr Glu Pro His Val Ser Gln
 20 25 30
 Thr Pro Gly Ser Pro Gly Phe Phe Ser Gly Arg Pro His Ser His Cys
 35 40 45
 Asn Ser Trp Pro Gly Gln Met Leu Thr His Arg Asp Ile Lys His Ser
 50 55 60
 Asn Thr Pro Ser Thr Arg Leu Gln Pro Lys Asp Ser Glu Asp Asn Asp
 65 70 75 80
 His Ser Ile Ser Met His Tyr Ala Ala Lys Glu Arg Phe Trp His Ala
 85 90 95
 Leu Leu Tyr Cys Phe Thr Glu Asp Lys Lys Ile Asn Cys Lys Val Thr
 100 105 110

<210> 1051
 <211> 317
 <212> DNA
 <213> Homo sapiens

<400> 1051
 gcgttgagtc gggatgtcgc attcatgccc ggcgaaacctt tttttgccga accggagcgt
 60
 aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaaggt
 120
 ctcaagcgcc tggtgctgt catccgtcac gcacaggctg cacaagcggc ttaaggggag
 180
 ggccatgtac aagggtttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat
 240
 gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc
 300
 gagaccccg aattttt
 317

<210> 1052
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1052
 Ala Leu Ser Arg Asp Val Ala Phe Met Pro Gly Glu Pro Phe Phe Ala
 1 5 10 15
 Glu Pro Glu Arg Asn Pro Gly Asn Leu Arg Leu Asn Phe Ser His Ile

```

                20                25                30
Ala Pro Glu Arg Leu Asp Glu Gly Leu Lys Arg Leu Ala Ala Val Ile
                35                40                45
Arg His Ala Gln Ala Ala Gln Ala Ala
                50                55

```

<210> 1053
 <211> 318
 <212> DNA
 <213> Homo sapiens

```

<400> 1053
caattggcta cgcgatccga acgggcgcgt ggggtctctat gactggcaag ccgtcgctcg
60
cggggagtg ggcctcgact atgcctacgc gatgtcgggtg aacctgacca ccgagaaccg
120
gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgcctcgccg aagaggggtg
180
cgccaacccg ccctcggttcg agcaagcgtg gctacgttac cggcaacagc cgttcacagt
240
cgggatcttc tcaactctga ccacggcgcg cggacgcttt caaccggcca tgcaaccggc
300
ggactcnnnn ccccnnc
318

```

<210> 1054
 <211> 96
 <212> PRT
 <213> Homo sapiens

```

<400> 1054
Met Gly Leu Tyr Asp Trp Gln Ala Val Ala Arg Gly Glu Trp Ala Leu
1      5      10      15
Asp Tyr Ala Tyr Ala Met Ser Val Asn Leu Thr Thr Glu Asn Arg Arg
      20      25      30
Ala Trp Glu Arg Asp Leu Leu Glu Arg Tyr Leu Trp Arg Leu Ala Glu
      35      40      45
Glu Gly Val Ala Asn Pro Pro Ser Phe Glu Gln Ala Trp Leu Arg Tyr
      50      55      60
Arg Gln Gln Pro Phe His Val Gly Ile Phe Ser Leu Leu Thr Ile Gly
      65      70      75      80
Ala Gly Arg Phe Gln Pro Ala Met Gln Pro Ala Asp Ser Xaa Pro Xaa
      85      90      95

```

<210> 1055
 <211> 391
 <212> DNA
 <213> Homo sapiens

```

<400> 1055
tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat
60
ctgcagccac tcatttaact ctccctggcta gctccacgtg ggccgtctga actctcttag
120

```

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg
 180
 aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac
 240
 tgccaggggt gaagccaag gatgggaaaa aggcctccgg ggcagagtcc tgaatgtca
 300
 gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg
 360
 ccaagggtgc agtgagtggt tgacaccatg g
 391

<210> 1056

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1056

Met	Val	Ser	Pro	Leu	His	Cys	Ser	Leu	Gly	Asn	Arg	Met	Arg	Pro	Cys
1				5				10					15		
Leu	Ser	Asn	Asn	Val	Met	Leu	Phe	Pro	Leu	Trp	Cys	Thr	Ser	Asp	Ile
		20						25				30			
Ser	Gly	Leu	Cys	Pro	Gly	Gly	Leu	Phe	Pro	Ile	Leu	Gly	Leu	His	Pro
		35				40					45				
Trp	Gln	Phe	Ser	Leu	Pro	Ser	Gln	Val	Ser	Gly	Pro	Arg	Met	Val	Phe
	50					55				60					
Ile	Arg	Pro	Gly	Pro	Leu	Arg	Ser	Ala	Glu	Arg	Gln	Met	Pro	Leu	Ala
65				70					75					80	
Pro	Gly	Ala													

<210> 1057

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1057

gaattccctg cgcgtgtgac gccggtcgcc gagcaactcg cgcgtgcgct gacgctgcat
 60
 ccgatgac cgccgcgtcc gctgttcggg ttgccgcgca ttgcgtccag cgccgaggac
 120
 tatcaggcgc tgttcgatgc ggtaccgtcc aaggcgaacg gcatctgcct gtgcacgggt
 180
 tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cgcccccgct
 240
 atcgcccttg cgcattctgc gcgaccaag cgcgacgccg atggcctgtc gtttcatgaa
 300
 tccgaccatc tcgacggcga tgcgacatg gtcgcgtgct c
 341

<210> 1058

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1058

```

Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser
 1           5           10           15
Leu Thr Leu His Pro Asp Asp Pro Arg Pro Leu Phe Gly Leu Pro
      20           25           30
Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val
      35           40           45
Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val
 50           55           60
Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg
65           70           75           80
Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu
      85           90           95
Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala
      100           105           110
Cys

```

<210> 1059

<211> 372

<212> DNA

<213> Homo sapiens

<400> 1059

```

nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa
60
gtcgagcggtt cgggcctgcg caccacgttc atgaacaagc tggacgtcga tgaggaaagtc
120
gccgacatcc tgatcgacga aggtttcacc ggtatcgagg aaatcgcccta cgtccccatg
180
caggaactgc tggagatcga ggcgttcgac gaagacacca tcaacgagtt gcgcgcccgt
240
gcccccaatg cgctgctgac cgaggccatc gcccaggaag agcgccctga gaccgcgcag
300
gatctgcttt aactcgaagg cgtgacgccg gaactggctg ccaagctggc cgagcgtcaa
360
gtgcgtacgc gt
372

```

<210> 1060

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1060

```

Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val
 1           5           10           15
Asn Arg Arg Glu Val Glu Arg Ser Gly Leu Arg Thr Thr Phe Met Asn
      20           25           30
Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly
      35           40           45
Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu
 50           55           60
Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg

```

```

65              70              75              80
Ala Arg Asn Ala Leu Thr Glu Ala Ile Ala Gln Glu Glu Arg Leu
      85              90              95
Glu Thr Ala Gln Asp Leu Leu Glu Leu Glu Gly Val Thr Pro Glu Leu
      100              105              110
Ala Ala Lys Leu Ala Glu Arg Gln Val Arg Thr Arg
      115              120

```

```

<210> 1061
<211> 456
<212> DNA
<213> Homo sapiens

```

```

<400> 1061
tctagactcc atggcacccg gctgagcggg taagtaagaa agataaaaaa tgccttttgc
60
cccttcgagg aaaccctttt gcaggccaag caagggtgc aagtgtttgg gagctgagag
120
gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtg ggggggggtt
180
gggacacgaa gggctcttcg gaccctctgt cctcttctgc cccaaggcgc agaagacggg
240
cttcgcagcg accctcgggg gtccatggag ccgcctgcct tcgccccctc gctcttccca
300
ggctctgaacc tggatgggga gaagaaattg aagtgccttg gagacggggg ggcttaaaac
360
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420
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456

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<210> 1062
<211> 125
<212> PRT
<213> Homo sapiens

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<400> 1062
Met Arg Leu Pro Ser Val Leu Ser Pro Pro Val Ser Lys Ala Leu Gln
1      5      10      15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
      20      25      30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
      35      40      45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
      50      55      60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65      70      75      80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
      85      90      95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
      100      105      110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
      115      120      125

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<210> 1063
<211> 3760
<212> DNA
<213> Homo sapiens

<400> 1063
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120
taagggtctta taactagtaa atatctgcat taaagaacga gttgaatgaa aattctgata
180
aattcctact taaagtgtat ccaagaaaaa cggaaaaagt ctaggagtta gtgatattag
240
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300
aagtaattga gtaaagtcac aggaatgtgt accatataaa ggaatggctc taaatgtatt
360
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420
gagagagaga gtgacaggga gagagagaca gagcggggaa ggagagaatg agaagggaaa
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540
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600
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660
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1080
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1140
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1200
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1380
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1440

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2160
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2700
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2760
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3060

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 3180
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 3240
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 3300
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 3360
 ctgttttaacc tgttgcttcc ttctggatta atacatttag agccattctc ttatatgggc
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 3540
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 3600
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 3660
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 3760

<210> 1064

<211> 483

<212> PRT

<213> Homo sapiens

<400> 1064

Met	Gln	Gly	His	Val	Ser	Asn	Arg	Ser	Gly	Leu	Leu	Gly	Thr	Ser	Leu
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His	Gly	Ser	Pro	Ser	Cys	Thr	Leu	Arg	Arg	Ser	Ala	Val	Lys	Ser	Arg
			20					25					30		
Leu	Gly	Cys	Ala	Val	Ala	Gly	Ser	Phe	Thr	Ser	Thr	Trp	Asn	Phe	
			35				40					45			
Leu	Lys	Ser	Ser	Leu	Leu	Pro	Gly	Met	Gln	His	Ala	Val	Phe	Ser	Ser
			50				55				60				
Met	Gly	Met	Phe	Ser	Ala	Ser	Ser	Leu	Val	Thr	Ala	Leu	Leu	Leu	Leu
					70					75				80	
Arg	Thr	Pro	Leu	Thr	Pro	Ser	Ser	Arg	Pro	Arg	Ala	Gly	Arg	Trp	His
				85					90					95	
Leu	Ser	Cys	Ser	Ser	Ser	Ala	Ser	Ser	Phe	Arg	Ala	Leu	Leu	Cys	Trp
				100				105						110	
Thr	Ser	Arg	Leu	Leu	Leu	Ser	Arg	Ser	Leu	Cys	Ser	Val	Ala	Arg	Ser
				115				120					125		
Ser	Ala	Ser	Ser	Arg	Leu	Ser	Tyr	Gln	Val	Lys	Leu	Gln	Met	Ala	Leu
				130			135					140			
Glu	Leu	Met	Arg	Lys	Glu	Leu	Glu	Asp	Ala	Leu	Thr	Gln	Glu	Ala	Asn
				145			150				155			160	
Val	Gly	Lys	Lys	Thr	Val	Ile	Trp	Lys	Glu	Lys	Val	Glu	Met	Gln	Arg
				165				170						175	
Gln	Arg	Phe	Arg	Leu	Glu	Phe	Glu	Lys	His	Arg	Gly	Phe	Leu	Ala	Gln

```

      180              185              190
Glu Glu Gln Arg Gln Leu Arg Arg Leu Glu Ala Glu Glu Arg Ala Thr
      195              200              205
Leu Gln Arg Leu Arg Glu Ser Lys Ser Arg Leu Val Gln Gln Ser Lys
      210              215              220
Ala Leu Lys Glu Leu Ala Asp Glu Leu Gln Glu Arg Cys Gln Arg Pro
      225              230              235              240
Ala Leu Gly Leu Leu Glu Gly Val Arg Gly Val Leu Ser Arg Ser Lys
      245              250              255
Ala Val Thr Arg Leu Glu Ala Glu Asn Ile Pro Met Glu Leu Lys Thr
      260              265              270
Ala Cys Cys Ile Pro Gly Arg Arg Glu Leu Leu Arg Lys Phe Gln Val
      275              280              285
Asp Val Lys Leu Asp Pro Ala Thr Ala His Pro Ser Leu Leu Leu Thr
      290              295              300
Ala Asp Leu Arg Ser Val Gln Asp Gly Glu Pro Trp Arg Asp Val Pro
      305              310              315              320
Asn Asn Pro Glu Arg Phe Asp Thr Trp Pro Cys Ile Leu Gly Leu Gln
      325              330              335
Ser Phe Ser Ser Gly Arg His Tyr Trp Glu Val Leu Val Gly Glu Gly
      340              345              350
Ala Glu Trp Gly Leu Gly Val Cys Gln Asp Thr Leu Pro Arg Lys Gly
      355              360              365
Glu Thr Met Pro Ser Pro Glu Asn Gly Val Trp Ala Leu Trp Leu Leu
      370              375              380
Lys Gly Asn Glu Tyr Met Val Leu Ala Ser Pro Ser Val Pro Leu Leu
      385              390              395              400
Gln Leu Glu Ser Pro Arg Cys Ile Gly Ile Phe Leu Asp Tyr Glu Ala
      405              410              415
Gly Glu Ile Ser Phe Tyr Asn Val Thr Asp Gly Ser Tyr Ile Tyr Thr
      420              425              430
Phe Asn Gln Leu Phe Ser Gly Leu Leu Arg Pro Tyr Phe Phe Ile Cys
      435              440              445
Asp Ala Thr Pro Leu Ile Leu Pro Pro Thr Thr Ile Ala Gly Ser Gly
      450              455              460
Asn Trp Ala Ser Arg Asp His Leu Asp Pro Ala Ser Asp Val Arg Asp
      465              470              475              480
Asp His Leu

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<210> 1065

<211> 892

<212> DNA

<213> Homo sapiens

<400> 1065

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naccgtggt gtcattggga ggtgggctgc agtcatgaga aaaggccggg ggctgtgcaa
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taccatgctt cacaaggga gaagatcaaa gtgacctcc cccatggctt tggaaccttc
120
ttgtccagtc tggaaggggg gaagaagaga tgaggggaag gctgtccagg ggggtgcaag
180
gccctagaga cccagcagag aagggaactct ggccactgaa ggggccctcc cattgtggct
240

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ctggttccct agagcagctc cagcttcttg gcctcccccg tctgatgctt agctcatccc
 300
 atccccctgga gtgctgtgga gcttagatga aacagcccag tgctcactct tcaatgagcc
 360
 caccagagc agcatcaaga tgcagttggc ggggtactgg aactggcttg gcaagggtg
 420
 cgacggcaac aggtcccagc aagagtcagc tagcctagct cagccctgca cacctggaga
 480
 cctgggggtg ctccagacac ctccggccctt taggtccctt taattgaatg tgtgtggate
 540
 agtgaaggtt gaggaatcat ttctctatgg cccaagacgt ttctctctgc agttgtcatg
 600
 ttagtacctg ccagcttttc ctctcttaca taaatttcat gccagagcct ggaaatgtgt
 660
 gccctttgta ggaggggcat cacaggctgg ctccacctcag cagtgccagg cagagcccgt
 720
 ccctctcatt gcaggaggcg catgaagcgt gtctgggacc gagctgtgga gttcttgccc
 780
 tcacaacgaat cccgatcca gacggagtcc caccgcgttg caggagagga catgctgggtg
 840
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 892

<210> 1066

<211> 76

<212> PRT

<213> Homo sapiens

<400> 1066

Met	Cys	Ala	Leu	Cys	Arg	Arg	Gly	Ile	Thr	Gly	Trp	Leu	Thr	Ser	Ala
1				5						10				15	
Val	Pro	Gly	Arg	Ala	Arg	Pro	Ser	His	Cys	Arg	Arg	Arg	Met	Lys	Arg
			20					25					30		
Val	Trp	Asp	Arg	Ala	Val	Glu	Phe	Leu	Ala	Ser	Asn	Glu	Ser	Arg	Ile
			35				40					45			
Gln	Thr	Glu	Ser	His	Arg	Val	Ala	Gly	Glu	Asp	Met	Leu	Val	Leu	Arg
		50				55					60				
Trp	Thr	Lys	Pro	Ser	Ser	Phe	Ser	Asp	Ser	Glu	Arg				
65					70					75					

<210> 1067

<211> 418

<212> DNA

<213> Homo sapiens

<400> 1067

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 120
 ggactagaca tctggaaagc ccgagtctcc gctgacatcg aaggcgactg gactatgcac
 180
 gttgaaggct ggtcagacac ctggggcacy tggcatcaca atgccaatgc caagctcgcc
 240

gctgccatcg acgtcgaaact ggtgtgcgcc gaaggccatg ccctcataaa cgaggcggtc
 300
 cggcacgcgcg agcaatccgg ggatactgac gcgatcacgg ctctgcgcga gaccgatgcc
 360
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 418

<210> 1068

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1068

Glu	Phe	Glu	Val	Thr	Ala	Asn	Val	Phe	Arg	Glu	Gly	His	Asp	Ala	Val
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Gly	Ala	Ser	Val	Val	Leu	Thr	Asp	Pro	Glu	Gly	Asn	Arg	His	Leu	Thr
			20				25					30			
Asp	Met	His	Gln	Val	Glu	Pro	Trp	Gly	Leu	Asp	Ile	Trp	Lys	Ala	Arg
		35				40					45				
Val	Ser	Ala	Asp	Ile	Glu	Gly	Asp	Trp	Thr	Met	His	Val	Glu	Gly	Trp
	50				55				60						
Ser	Asp	Thr	Trp	Gly	Thr	Trp	His	His	Asn	Ala	Asn	Ala	Lys	Leu	Ala
65				70				75				80			
Ala	Ala	Ile	Asp	Val	Glu	Leu	Val	Cys	Ala	Glu	Gly	His	Ala	Leu	Ile
			85				90					95			
Asn	Glu	Ala	Val	Arg	His	Ala	Glu	Gln	Ser	Gly	Asp	Thr	Asp	Ala	Ile
		100					105				110				
Thr	Ala	Leu	Arg	Glu	Thr	Asp	Ala	Asn	Leu	Thr	Leu	Asp	Arg	Ala	Pro
		115				120					125				
Asp	Ser	Leu	Gln	Gln	Val	Ile	Asn	Thr	Tyr	Ala					
	130					135									

<210> 1069

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1069

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 120
 ttttctggag ctgaacatct caggtgccat gtaaggcttg gtgccagcca tgggtggagac
 180
 ctgcgttatc acctgcaaca gaacgtccac ttcaaggaag aaacagtga gctcttcac
 240
 tgtgagctgg tcatggccct ggactacctg cagaaccagc gcatacttca cagggatatg
 300
 aagcctgaca atattttact tgacgaacat gggcacgtgc acatcacaga tttaacact
 360
 gctgcgatgc t
 371

<210> 1070

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1070

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Xaa Tyr Asn Phe Leu Ala Gly Ser Thr Gly Ala Asn Met Ile Arg Ser
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Pro Ala Ser Gln Gln Phe Ile Cys Arg His Ser Gln Gly Pro Val
      20             25             30
Asn Ser Lys Gly Ile Ala Cys Ser Phe Ser Gly Ala Glu His Leu Arg
 35             40             45
Cys His Val Arg Leu Gly Ala Ser His Gly Gly Asp Leu Arg Tyr His
 50             55             60
Leu Gln Gln Asn Val His Phe Lys Glu Glu Thr Val Lys Leu Phe Ile
 65             70             75             80
Cys Glu Leu Val Met Ala Leu Asp Tyr Leu Gln Asn Gln Arg Ile Ile
      85             90             95
His Arg Asp Met Lys Pro Asp Asn Ile Leu Leu Asp Glu His Gly His
      100            105            110
Val His Ile Thr Asp Phe Asn Ile Ala Ala Met
      115            120

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<210> 1071

<211> 998

<212> DNA

<213> Homo sapiens

<400> 1071

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120
cccaccgcaa gtacgtggcc ttggagtgcc attcgcactc cacttggccca cgttttgcat
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300
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420
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480
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600
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660
attcgccgct actccaagtg aagaatccag gtacatgtcc atgagtagca gccccaatat
720
cgagattagc cacatacatg accatgtggt ccttgggtca gcacgcgaag aaaatgccaa
780

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gcgtaccctt tgggttggtg cgcttacggt ggtgatgatg gttggcgaaa tcgtcgccgg
 840
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 998

<210> 1072

<211> 72

<212> PRT

<213> Homo sapiens

<400> 1072

Met	Gly	His	Thr	Ala	Ser	Asn	Lys	Asp	Asp	Leu	Leu	Lys	Arg	Val	Lys
1				5				10					15		
Arg	Ile	Ala	Gly	Gln	Ile	Gln	Ala	Val	Glu	Arg	Ala	Leu	Glu	Ser	Asp
			20				25					30			
Ala	Asp	Cys	Ala	Lys	Thr	Leu	His	Leu	Val	Ala	Ala	Thr	Arg	Gly	Ala
		35				40					45				
Ile	Asn	Gly	Leu	Met	Asp	Glu	Ile	Ile	Glu	Asp	His	Ala	Arg	Lys	His
	50				55				60						
Val	Ala	Ser	Pro	Thr	Leu	Ser	Asp								
65					70										

<210> 1073

<211> 468

<212> DNA

<213> Homo sapiens

<400> 1073

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 120
 ttcccccat gataaaatct tgcttctctt caaactccta ggcaaatttc tctacttca
 180
 gaaagtcttg tttctccata tccttcgtaa ccaccacctg gtgcacatgc tgaaggcaga
 240
 attcattgtc tcctctcctt cactctcgaa tagctttgcc cagaccctca ggtactcctt
 300
 catcctctgt ataataattg gttttcacct ctttatgaac tcttttgat tctcattact
 360
 ggctctggaa ccagaacat accacgggtt caaggatgt tttaatgaat tgaatggaat
 420
 aaattttgtt gtgcttatgc agatacagat gccactaaac actgatca
 468

<210> 1074

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1074

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Gly Cys Phe Ser Pro Thr Asp Lys Ile Leu Leu Leu Phe Lys Leu Leu
20        25        30
Gly Lys Phe Leu Leu Leu Gln Lys Val Leu Phe Leu His Ile Leu Arg
35        40        45
Asn His His Leu Val His Met Leu Lys Ala Glu Phe Ile Val Ser Ser
50        55        60
Pro Ser Leu Ser Asn Ser Phe Ala Gln Thr Leu Arg Tyr Ser Phe Ile
65        70        75        80
Leu Cys Ile Ile Phe Gly Phe His Leu Phe Met Asn Ser Phe Val Phe
85        90        95
Ser Leu Leu Ala Leu Glu Pro Arg Thr Tyr His Gly Phe Lys Val Cys
100       105       110
Phe Asn Glu Leu Asn Gly Ile Asn Phe Val Val Leu Met Gln Ile Gln
115       120       125
Met Pro Leu Asn Thr Asp
130

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<210> 1075

<211> 1633

<212> DNA

<213> Homo sapiens

<400> 1075

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120
gcgcctgctg atcctgcccc aggaggagga ctatggcctt gacatcgagg agaagaacaa
180
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240
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300
ggagtccatc ctcaaccagt ccttctgtct ccgcccgcct ctgcgcctcc tgggtggccac
360
gaaggccaaa gagatcatca aaatccccga ccagccggac acactgtgct tccagattcg
420
tggagctgcc ccaccgtacg tctatgtgtg ggggagaggc tctgaggcca tggctgcagg
480
gtctgtgtgt ggtcagtgca ttctgaaggt caatggcagc aacgtgatga acgatgggtg
540
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720
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gactgtggac aacgtgcacc tggaaacagg cgtgggtgtat gagtatgtga gcacggcagg
840

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cgtcagggtgc catgtgctgg agaagatcgt ggagccccgc ggctgcttcg gcctcaccgc
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 1020
 caccaagctg gagagcattg gccagaggat tgcctgctac caggagtttg cagcccaact
 1080
 gaagagcagg gtcagccac ccttcaaaca agccccctg gagccccacc cgctgtgtgg
 1140
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 1200
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 1440
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 1620
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<210> 1076

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1076

His	Gln	Ala	Gly	Glu	His	Trp	Pro	Glu	Asp	Cys	Leu	Leu	Pro	Gly	Val
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Cys	Ser	Pro	Thr	Glu	Glu	Gln	Gly	Gln	Pro	Thr	Leu	Gln	Thr	Ser	Pro
			20					25					30		
Pro	Gly	Ala	Pro	Pro	Ala	Val	Trp	Pro	Thr	Ser	Ala	Pro	Pro	Ile	Ala
		35					40				45				
Thr	Ser	Thr	Ser	Trp	Lys	Cys	Pro	Thr	Pro	Arg	Pro	Pro	Pro	Gln	Trp
	50					55				60					
Ala	Gly	Pro	Ser	Ala	Ser	Ala	Leu	Asp	Ala	Asn	Pro	Pro	Ser	Ser	Ala
65				70					75					80	
Leu	Thr	Arg	Ser	Lys	Ala	Thr									
				85											

<210> 1077

<211> 419

<212> DNA

<213> Homo sapiens

<400> 1077

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 caccagagt ttacatatcc aatttttggga gaggctgagg caatttacgg ctacaacggc
 180
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 300
 gtgctcccg cagatgtcgt tactcctgca gaacttgatg ctatcgttgc acgcgacggc
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 419

<210> 1078

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1078

Xaa	Arg	Val	Thr	Arg	Leu	Ala	Thr	Arg	Leu	His	Ser	Met	Ser	Thr	Lys
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Trp	Thr	Cys	Asn	Ala	Asn	Glu	Ala	Thr	Cys	Leu	Arg	Leu	Ala	Gly	Ala
			20					25					30		
Pro	Ser	Pro	Ser	Asp	Ala	Leu	Phe	His	Pro	Glu	Phe	Thr	Tyr	Pro	Ile
			35				40					45			
Phe	Gly	Glu	Ala	Glu	Ala	Ile	Tyr	Gly	Tyr	Asn	Gly	Leu	His	Met	Asn
	50					55				60					
Leu	Ala	Phe	Ala	Ser	Gly	Ser	Leu	Val	Pro	Ser	Leu	Glu	Ile	Thr	Tyr
65				70					75					80	
Arg	Ala	Lys	Asn	Thr	Thr	Thr	Ser	Ala	Lys	Val	Asp	Asp	Val	Glu	Gln
			85					90						95	
Ala	Leu	Arg	Gly	Val	Leu	Pro	Pro	Asp	Val	Val	Thr	Pro	Ala	Glu	Leu
			100					105					110		
Asp	Ala	Ile	Val	Ala	Arg	Asp	Ala	Arg	Ala	Val	Arg	Ala	His	Leu	Arg
	115					120						125			
Arg	Arg	Ala	Pro	Arg	Leu	Arg	Arg	Thr	Leu	Ala					
	130					135									

<210> 1079

<211> 584

<212> DNA

<213> Homo sapiens

<400> 1079

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 120
 gctcaaaactg cttcccaagc cagcaggagg ggggaaccatg ctgcctgctg acctgggtag
 180
 ttctatttag gtcttgtgac acaacagtgg gcaagggtgat gccctctgtg accaaaagta
 240

tttaccacca gttccccag gccctccctt tegtctgcaa agacacacat ctgtttcact
 300
 gtgtcttctg caaagacaca catctgtttc actgggggtt tctgcaaaga caccattttg
 360
 ttccccctt taagggtttt cccctccatc ttgtctattt ttaaaaaaat aaaccgggtt
 420
 cccaggtatg cttccccccc cagatcaaga gcccatgtga aatgaggggg ccgacttgac
 480
 cacagcacct tgttctcttc tgtaatctag acacttctgc acaatagagg gcccacccct
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 584

<210> 1080
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1080
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 20 25 30
 Phe Pro Ser Gln Gln Gly Gly Glu Pro Cys Cys Leu Leu Thr Trp Val
 35 40 45
 Val Leu Phe Arg Ser Cys Asp Thr Thr Val Gly Lys Val Met Pro Ser
 50 55 60
 Val Thr Lys Ser Ile Tyr Pro Lys Phe Pro Gln Ala Leu Pro Phe Val
 65 70 75 80
 Cys Lys Asp Thr His Leu Phe His Cys Val Phe Cys Lys Asp Thr His
 85 90 95
 Leu Phe His Trp Gly Phe Leu Gln Arg His Pro Phe Val Ser Pro Phe
 100 105 110
 Lys Gly Phe Pro Leu His Leu Val Tyr Phe
 115 120

<210> 1081
 <211> 3077
 <212> DNA
 <213> Homo sapiens

<400> 1081
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 120
 tatatccaca atgggaagaa atccagggcc ttaagccccc tatctcctgt ggccatagag
 180
 cagacatctc ttaagatgat gcaggcagta ggaggtgcac ctgcacgtcc cactggagaa
 240
 tatatctgta atcaatgtgg tgctaagtac acatccctag acagctttca gactcaccta
 300
 aaaactcatc tcgacactgt gcttccaaaa ttgacctgtc ctacgtgcaa caaggaattc
 360

cccaaccaag aatccttgct gaagcatggt accattcact ttatgatcac ttcaacgtat
420
tacctctgtg agagttgtga caagcaattc acatcagtgg atgaccttca gaaacacctg
480
ctggacatgc acacctttgt cttctttcgc tgcacctctc gccaggaagt ttttgactca
540
aaagtctcca ttccagctcca ctgggctgtg aagcacagta acgaaaagaa agtctatagg
600
tgcacatctt gcaactggga cttccgcaac gaaactgact tgcagctcca tgtgaaacac
660
aaccacctgg aaaaccaagg gaaagtgcac aagtgcattt tctgcgtgta gtcctttggc
720
accgagggtg agctgcaatg ccacatcacc actcacagta agaagtacaa ctgcaagttc
780
tgtagcaaa ccttccatgc gatcattttg ttagaaaaac acttgcgaga aaaacactgt
840
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900 agctgcagac ttgtctgacc aacagccagg agtccacaa cagtcacgat 960
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1020
gcctacacta tggaactttt gctgcagaat caccagctcc gagaccacaa catcagacct
1080
ggagaaagtg ccactcgtga aaagaaagct gagctcatta aagggaatta caagtgcagc
1140
gtgtgctctc gaacctttct cttcgaaaat ggcctccggg aacatatgca gaccaccta
1200
ggcctgtgca aacactacat gtgccctatt tgcggagagc ggtttccctc ctttttaact
1260
cttactgaac acaaagtcac gcatagtaag agtcttgata ctggaaactg ccgattttgc
1320
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1380
aggaattccc tgacaggctt tgcgtgcgtg gtgtgcatgc agacagtgc cttccacctg
1440
gaactcaaaa tccatgggac gttccacatg caaaagacag ggaatgggtc tgcagttcag
1500
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1560
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1620
gccggctgcg tgaatctcag taagagcgcc agcccaggca ttaacgtccc tcccgccagc
1680
aatagaccag gcttgggcca gaatgagaat ctgagtgcc aatggggaaa gcaagggtgg
1740
gggactgaaa cacgtgctc tagctgcaac gtttaagttg agtctgaaa tgaactccag
1800
aaccacatcc aaaccatcca ccgagagctc gtgccagaca gcaacagcac acagttgaaa
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acgcccccaag tatcaccaat gcccagaatc agtccctccc agtcggatga gaagaagacc
1920
tatcaatgca tcaagtgtca gatgggtttc tacaatgaat gggatattca ggttcatggt
1980
gcaaatcaca tgattgatga aggactgaac catgaatgca aactctgcag ccagaccttt
2040

gactctcctg ccaaactcca gtgccacctg atagagcaca gtttcgaagg gatgggaggc
 2100
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 2160
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 2220
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 2280
 tacagtctct caaggagaat tgattttgtg gcacaaaaag ggaacatggt ttactctttg
 2340
 cacgaaactt tcattgttaa tgtatattat tcagaaacat tgtattgtac cataaaactt
 2400
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 2460
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 2520
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 2580
 gcttaagata aagtattttt aaggagaaga gattaaaaac aactgttata catgagacta
 2640
 tgggtggact tccttttctt tacacttaag cctagaattt ctcttttagt atatcagcgc
 2700
 ttaaatccaa gactattttt tattgctgaa gattcttgca aaccatgaag agatgttctc
 2760
 acagaacaga accccacagc tggataaggc ccgtatatat atatttgtaa gccttgcaat
 2820
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 2880
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 2940
 ccaaattctt gaatcagttg aactaacctg tatgttactg ttattaatgt ttactctgca
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 3060
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 3077

<210> 1082

<211> 757

<212> PRT

<213> Homo sapiens

<400> 1082

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 20 25 30
 Lys Asn Ile Pro Leu Ala Leu Asn Tyr Ile His Asn Gly Lys Lys Ser
 35 40 45
 Arg Ala Leu Ser Pro Leu Ser Pro Val Ala Ile Glu Gln Thr Ser Leu
 50 55 60
 Lys Met Met Gln Ala Val Gly Gly Ala Pro Ala Arg Pro Thr Gly Glu
 65 70 75 80
 Tyr Ile Cys Asn Gln Cys Gly Ala Lys Tyr Thr Ser Leu Asp Ser Phe

[illegible]

515 520 525
 Lys Leu Asp Ile Asn Gly Leu Pro Tyr Gly Leu Cys Ala Gly Cys Val
 530 535 540
 Asn Leu Ser Lys Ser Ala Ser Pro Gly Ile Asn Val Pro Pro Gly Thr
 545 550 555 560
 Asn Arg Pro Gly Leu Gly Gln Asn Glu Asn Leu Ser Ala Ile Gly Glu
 565 570 575
 Arg Gln Gly Gly Gly Thr Glu Thr Arg Cys Ser Ser Cys Asn Val Lys
 580 585 590
 Phe Glu Ser Glu Ser Glu Leu Gln Asn His Ile Gln Thr Ile His Arg
 595 600 605
 Glu Leu Val Pro Asp Ser Asn Ser Thr Gln Leu Lys Thr Pro Gln Val
 610 615 620
 Ser Pro Met Pro Arg Ile Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr
 625 630 635 640
 Tyr Gln Cys Ile Lys Cys Gln Met Val Phe Tyr Asn Glu Trp Asp Ile
 645 650 655
 Gln Val His Val Ala Asn His Met Ile Asp Glu Gly Leu Asn His Glu
 660 665 670
 Cys Lys Leu Cys Ser Gln Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys
 675 680 685
 His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr Phe Lys Cys
 690 695 700
 Pro Val Cys Phe Thr Val Phe Val Gln Ala Asn Lys Leu Gln Gln His
 705 710 715 720
 Ile Phe Ser Ala His Gly Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln
 725 730 735
 Cys Pro Gln Lys Phe Phe Phe Gln Thr Glu Leu Gln Asn His Thr Met
 740 745 750
 Thr Gln His Ser Ser
 755

<210> 1083

<211> 516

<212> DNA

<213> Homo sapiens

<400> 1083

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 120
 ccaatgaccc cggttctgtc ggccaattgg gatgaagagc gcagttggaa gctgcttaac
 180
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 240
 gttgtctcgc tgggtaagga cgctaacctg cgtggccgtg gtggcgccgg gttccccacc
 300
 ggcatgaagt ggtccttcgt gcctaaggac aatcccaacc gcacctacct cgttgtcaac
 360
 ggcgacgagt ctgagccggg cacytgcaag gacatgccgc tcatgatggc ctccccgcac
 420
 accctcgtcg agggcgctcat cattgcctcc tacgccatca aggcccaagat ggccttcac
 480

tacatccgcg gtgaggtgct gcacgtcgtc cgacgc
516

<210> 1084
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1084
Ala Arg Gly Arg Gly Glu Glu Val Thr Asp Pro Leu Thr Pro Val Leu
1 5 10 15
Ser Ala Asn Trp Asp Glu Glu Arg Ser Trp Lys Leu Leu Asn Tyr Glu
20 25 30
Arg Gln Gly Gly Tyr Thr Gly Leu Arg Lys Ala Leu Thr Met Pro Pro
35 40 45
Asp Asp Val Val Ser Leu Val Lys Asp Ala Asn Leu Arg Gly Arg Gly
50 55 60
Gly Ala Gly Phe Pro Thr Gly Met Lys Trp Ser Phe Val Pro Lys Asp
65 70 75 80
Asn Pro Asn Pro Thr Tyr Leu Val Val Asn Gly Asp Glu Ser Glu Pro
85 90 95
Gly Thr Cys Lys Asp Met Pro Leu Met Met Ala Ser Pro His Thr Leu
100 105 110
Val Glu Gly Val Ile Ile Ala Ser Tyr Ala Ile Lys Ala Lys Met Ala
115 120 125
Phe Ile Tyr Ile Arg Gly Glu Val Leu His Val Val Arg Arg
130 135 140

<210> 1085
<211> 374
<212> DNA
<213> Homo sapiens

<400> 1085
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aaatcgtaga gtgtctctga gctgcctagg gggctgtttg cgatcttgcg gacagtgtct
120
atatccacaa ggttcagctc cgccaggaga ctgtcgccga tcattttcag gaagttttct
180
ttgctgcgtt cgtagtcttg gtgcaggctg aagctgtagt cgcttttgta gatgtcccg
240
tagaagaact cgggcagggt gcctttcatg gcttccagga tgacgggttt gctcatccg
300
tgcccgtca gaacaccgg gtacaccagg gaagagcgga tcatgtcgtc ctcaaggtag
360
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374

<210> 1086
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1086

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Met Ile Arg Ser Ser Leu Val Tyr Pro Gly Val Leu Ser Gly His Gly
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Met Ser Lys Pro Val Ile Leu Glu Ala Met Lys Gly Thr Leu Pro Glu
           20           25           30
Phe Phe Tyr Arg Asp Ile Tyr Lys Ser Asp Tyr Ser Phe Asp Leu His
           35           40           45
Gln Asp Tyr Glu Arg Ser Lys Glu Asn Phe Leu Lys Met Ile Gly Asp
           50           55           60
Ser Leu Leu Ala Glu Leu Asn Leu Val Asp Ile Asp Thr Val Arg Lys
65           70           75           80
Ile Ala Asn Ser Pro Leu Gly Ser Ser Glu Thr Leu Tyr Asp Phe Glu
           85           90           95
Arg Met Thr His Met Glu Val Trp Leu Arg Glu Asn Tyr Val
           100           105           110

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<210> 1087

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1087

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120
nggcaccact gtgcctggcc catccaccgg agtctagggg tgcaatccac cgcccgtgca
180
tcgtttctact tctacaacac ttccccgaa gtggatgcgt tagcgtcgcc ggtgccccgc
240
gcccgggaat ttttcggagt gcattaggat tggctctgaac gtgaaccttg aatccatgta
300
ccaggaagtc atcctggacc actacaagaa tcccacgcac gcagggttga aggtccctt
360
tgatgccgaa gtgcaccatg tgaacccttc ctgcggtgac ganaccgtct cgggtggaag
420
ctt
423

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<210> 1088

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1088

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Met Thr Ile Val Ala Pro Pro Pro Pro Thr Ala Gly Ala Ala Ile Ser
 1           5           10           15
Phe Leu Val Asp Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp
           20           25           30
Asp His Gly Val Ser Ile Arg Val Xaa His His Cys Ala Trp Pro Ile
           35           40           45
His Arg Ser Leu Gly Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Phe
50           55           60
Tyr Asn Thr Phe Pro Glu Val Asp Ala Leu Ala Ser Ala Val Arg Ala

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65          70          75          80
Ala Arg Glu Phe Phe Gly Val His
      85

<210> 1089
<211> 750
<212> DNA
<213> Homo sapiens

<400> 1089
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120
agagtggtaa gaatggggct cggggaagaa gccttaccctt tttctctctt taatttggcg
180
aaaggacttt tgggccaagg tcaccctagc cttctcttgg gggcctcaat tttccttcct
240
tctgtaaaaa atgggggggt aattcagaag taccctcctt attgtcaggg ttttggggaa
300
gggagtaaaa agaaattggc ttgggaaaaa acttaataca gggcctgggc atgtaacaaa
360
tattcacaaa atgctagcag ttatcaccac agtgggagcc acagggagct ctgaggataa
420
gcagggtagt cgagggatgg gacagaactt gattgaagcc agacagacct ccaaattctt
480
gactcagaca gaatgatcac tgatccagcg agacgtcagg atcgagagga gtgtagcaag
540
gagtcaggag ggtgggctcg cgccagtgtc gccccgactc tgttcagtaa catgaaggca
600
aacacagaag ggcattgtcg gagacacacg tgatcacgct agtgatgcag aggcagaccc
660
agacaaaaa cggagacagg agctaggcag acacacagac agagacagcc ccgcgagatc
720
atgtagacag ggataatgac aggaacgcgt
750

<210> 1090
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1090
Met Val Thr Trp Val Glu Leu Lys Gly Arg Leu Thr Gln Glu Met Ala
1          5          10          15
Cys Glu Asp Lys Thr Lys Gly Gly Arg Val Gly Gln Arg Gln Tyr Ile
20          25          30
Arg Val Val Arg Met Gly Leu Gly Glu Glu Ala Leu Pro Leu Phe Phe
35          40          45
Phe Asn Leu Ala Lys Gly Leu Leu Gly Gln Gly His Pro Ser Leu Leu
50          55          60
Leu Gly Ala Ser Ile Phe Leu His Ser Val Lys Asn Gly Gly Val Ile
65          70          75          80
Gln Lys Tyr Pro Pro Tyr Cys Gln Gly Phe Gly Glu Gly Ser Lys Lys

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85
Lys Leu Ala Trp Glu Asn Thr
100

90

95

<210> 1091
<211> 438
<212> DNA
<213> Homo sapiens

<400> 1091
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gcgattatta cggttatat gaacgaagtg tatttggtc aagtaggtaa tgaggggctt
120
catggctttg ccgaggcgag tcagcacttt ttgggacgac ctttaaaaga acttaatatc
180
gacgagcttg ccttgtagt aggaatgggt aaagggcctt ctattttataa tcctgaacga
240
caccctaaac gtgctttatc acgcagaaat acggtattag caatttttaa aagccaagat
300
cgtttaaccg agtcggatta taatatctta cggaaacaac ccattcgctt ggcagataaa
360
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420
gactttgatc gctgcatg
438

<210> 1092
<211> 146
<212> PRT
<213> Homo sapiens

<400> 1092
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Tyr Ser Lys Ser Ala Ile Ile Thr Ala Tyr Met Asn Glu Val Tyr Leu
20 25 30
Ala Gln Val Gly Asn Glu Gly Leu His Gly Phe Ala Glu Ala Ser Gln
35 40 45
His Phe Phe Gly Arg Pro Leu Lys Glu Leu Asn Ile Asp Glu Phe Ala
50 55 60
Leu Leu Val Gly Met Val Lys Gly Pro Ser Ile Tyr Asn Pro Glu Arg
65 70 75 80
His Pro Lys Arg Ala Leu Ser Arg Arg Asn Thr Val Leu Ala Ile Leu
85 90 95
Lys Ser Gln Asp Arg Leu Thr Glu Ser Asp Tyr Asn Ile Leu Arg Lys
100 105 110
Gln Pro Ile Arg Leu Ala Asp Lys His Gln Glu Arg Ser Val Tyr Gly
115 120 125
Asp Tyr Leu Asp Leu Val Ser Met Gln Leu Ser Arg Asp Phe Asp Arg
130 135 140
Cys Met
145

<210> 1093
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1093
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 ggtcagctgc tgaacgacga gcagtacttc gaagcgctgg aagagttcgg cgacgatttc
 120
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 Gly Arg Lys Gln Pro Pro Val Ser Glu Ser His Trp Arg Thr Leu Leu
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 Ser Glu Asn Pro Pro Ala Gly Ile Ala His Lys Gly Lys Pro His Tyr
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 Thr Lys Leu Leu Gly Leu Ala Glu Leu Leu Arg Val Ala Gly Glu Asn
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<212> DNA

<213> Homo sapiens

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ttgcgcacat agcgccttggg gcggctggca aggatatagg cgagtatcaa tgcacctcgg
180
agggcgagga tcgaggcaat ggtcagccag aagcgcaact tgtccatggc tatgttgagg
240
gcgattatgcc gacgatcttc ttcaccagg aaactgttga tgggttttcc gacgtcatcc
300
atctggcca
309

```

<210> 1100

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1100

```

Met Asp Asp Val Arg Lys Thr Ile Asn Ser Phe Leu Gly Glu Glu Asp
1      5      10      15
Arg Arg Leu Ile Ala Arg Asn Ile Ala Met Asp Lys Leu Arg Phe Trp

```

```

                20                25                30
Leu Thr Ile Ala Ser Ile Leu Ala Leu Ala Gly Ala Leu Ile Leu Ala
   35                40                45
Tyr Ile Leu Ala Ser Arg Thr Lys Arg Tyr Val Arg Lys Leu Thr Glu
   50                55                60
Gly Gln Ser Thr Leu Leu Ser Glu Lys Ser Gln Leu Glu Glu Met Val
   65                70                75                80
Gln Leu Arg Thr Ala Glu Leu Glu Lys Ala Met Leu Ile Ala Lys Arg
                85                90                95
Glu Arg Ala Arg
                100

```

```

<210> 1101
<211> 540
<212> DNA
<213> Homo sapiens

```

```

<400> 1101
gtcgacgtta ccaactacgt catgttggag tctggtcagc cgcttcatgc ctatgatgcc
60
gacaacgtca gctggacgat tgtggtccgt aaggccacg aggggtgagca tctattgacc
120
ctcgacgaca ccgatcgcac cctcgatcct gacgatctag tcacgcgcga cgactcgagg
180
gccattggcc tggctggcgt catgggtggt gcggccaccg aagtgactgc tgagacgacg
240
tcaatcatcc tcgagggcgc tcacttcgac ccgatgacgg gcgctcgtgc ttaccgacgc
300
cacaagctcg gttcggaggc ctcccgcgcg tttagcgagg gcgttatgcc gatttgcgcc
360
cataccgcag ccgttcgcgc agcggaattg ctgcccagt acggcgggtgc caccgtcggg
420
gagccaccgg tcgttggtga ggtccccgag atgccacgtc aaacgatcaa cgctgattta
480
cctaaccgga ttctcggcac gaagggtcca actgaagagg tcacgagat cttgacgcgt
540

```

```

<210> 1102
<211> 180
<212> PRT
<213> Homo sapiens

```

```

<400> 1102
Val Asp Val Thr Asn Tyr Val Met Leu Glu Ser Gly Gln Pro Leu His
   1                5                10                15
Ala Tyr Asp Ala Asp Asn Val Ser Gly Thr Ile Val Val Arg Lys Ala
   20                25                30
His Glu Gly Glu His Leu Leu Thr Leu Asp Asp Thr Asp Arg Thr Leu
   35                40                45
Asp Pro Asp Asp Leu Val Ile Ala Asp Asp Ser Gly Ala Ile Gly Leu
   50                55                60
Ala Gly Val Met Gly Gly Ala Ala Thr Glu Val Thr Ala Glu Thr Thr
   65                70                75                80
Ser Ile Ile Leu Glu Gly Ala His Phe Asp Pro Met Thr Gly Ala Arg

```



```

      85              90              95
Ala Tyr Arg Arg His Lys Leu Gly Ser Glu Ala Ser Arg Arg Phe Glu
      100              105              110
Arg Gly Val Asp Pro Ile Cys Ala His Thr Ala Ala Val Arg Ala Ala
      115              120              125
Glu Leu Leu Ala Gln Tyr Gly Gly Ala Thr Val Gly Glu Pro Thr Val
      130              135              140
Val Gly Glu Val Pro Glu Met Pro Arg Gln Thr Ile Asn Ala Asp Leu
      145              150              155              160
Pro Asn Arg Ile Leu Gly Thr Lys Val Pro Thr Glu Glu Val Ile Glu
      165              170              175
Ile Leu Thr Arg
      180

```

<210> 1103

<211> 537

<212> DNA

<213> Homo sapiens

<400> 1103

```

cctttctctcc aaccaggcgc tgcggcgccg gcacttgccc gacgttataa aacaattcaa
60
cgtcagggttt accatcgctg tactcaacca aatggtagcc gtatccacct tccccaccga
120
tcgcgaccaca ggtgatcttt ccctcgccat agattgacgt ggcattctcg tcggagttaa
180
tcaagcagcg cttaggcagc tgcctggcgc gcggtctgcg ctgctcgccc ggagcacacg
240
aacccttccc gaagataacc gccaaaggcct ggcacaccct ctgctgcacc cattccggct
300
tgacgccgac cgccaccgca ctggtgaaca tagccgcaat aaggagaatt gcgatgtatt
360
cgggcgcggc ggcaccccga tcgtcccttg tccgcatggg tctccccctc actacctacc
420
caatacaggg gagagcataa aaagaaaccc atagccgcac ctgagcccat ggccccaaac
480
cgggggcccaa gccggggcca aaccatggga tcaaccggat gtccgtacat cacgcgt
537

```

<210> 1104

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1104

```

Met Tyr Gly His Pro Val Asp Pro Met Val Trp Ala Arg Leu Gly Pro
1      5      10      15
Arg Phe Gly Ala Met Gly Ser Gly Ala Ala Met Gly Phe Phe Leu Cys
      20      25      30
Ser Pro Leu Tyr Trp Val Gly Ser Gly Gly Glu Thr His Ala Asp Lys
      35      40      45
Gly Arg Ser Gly Cys Arg Arg Ala Gly Ile His Arg Asn Ser Pro Tyr
      50      55      60
Cys Gly Tyr Val His Gln Cys Gly Gly Gly Arg Arg Gln Ala Gly Met

```

```

65              70              75              80
Gly Ala Ala Glu Gly Val Pro Gly Leu Gly Tyr Leu Arg Glu Gly
      85              90              95
Phe Val Cys Ser Gly Glu Leu Gly Glu Ala Ala Gly Pro Ala Ala Ala
      100              105              110

<210> 1105
<211> 448
<212> DNA
<213> Homo sapiens

<400> 1105
agggacctgg ggcagcacgt gcacgtgggt gggaggctcc ttgctaccga cagccagcca
60
tgggggtgggc ccttcagagg ctgcctccag gacctgcgac togatggctg ccacctcccc
120
ttctttcttc tgccactgga taaactcaagc cagcccagcg agctcggcgg caggcagtcc
180
tggaacctca ctgcgggctg cgtctccgag gacatgtgca gtctgaccc ctgtttcaat
240
ggtgggactt gcctcgtcac ctggaatgac ttccactgta cctgccctgc caatttcacg
300
gggcctacat gtgcccaaga gctgtggtgt ccgggccagc cctgtctccc acctgccacg
360
tgtgaggagg tccctgatgg ctttgtgtgt gtggcggagg ccacgttccg cgaggggtccc
420
cccgccgcgt tcagcgggca caacgcgt
448

<210> 1106
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1106
Arg Asp Leu Gly Gln His Val His Val Gly Gly Arg Leu Leu Ala Thr
1      5      10      15
Asp Ser Gln Pro Trp Gly Gly Pro Phe Arg Gly Cys Leu Gln Asp Leu
20     25     30
Arg Leu Asp Gly Cys His Leu Pro Phe Phe Pro Leu Pro Leu Asp Asn
35     40     45
Ser Ser Gln Pro Ser Glu Leu Gly Gly Arg Gln Ser Trp Asn Leu Thr
50     55     60
Ala Gly Cys Val Ser Glu Asp Met Cys Ser Pro Asp Pro Cys Phe Asn
65     70     75     80
Gly Gly Thr Cys Leu Val Thr Trp Asn Asp Phe His Cys Thr Cys Pro
85     90     95
Ala Asn Phe Thr Gly Pro Thr Cys Ala Gln Gln Leu Trp Cys Pro Gly
100    105    110
Gln Pro Cys Leu Pro Pro Ala Thr Cys Glu Glu Val Pro Asp Gly Phe
115    120    125
Val Cys Val Ala Glu Ala Thr Phe Arg Glu Gly Pro Pro Ala Ala Phe
130    135    140
Ser Gly His Asn Ala

```

145

<210> 1107

<211> 618

<212> DNA

<213> Homo sapiens

<400> 1107

acgcgttgat gaagtacctg ccacgcttca gcaatgacgg ctcggtgaac ggcttctata
 60
 tctttgttat cgatgagacc gaacgcaaac tcaccgaaga ggccctgcgc cacctcaacg
 120
 agaacctcga agagcgcgtc gccacgcgca cacaggcgct ggctgaagcc aaccaacgcc
 180
 tggcaaaaaca aaatgttcaa acgcaagcgc gccgaagacg cgctgcgtca cgcgcagaaa
 240
 atggaagccg ggggccgact caccggcggc atcgcccatg atttcaaca catgctgacc
 300
 gggattatcg gcagcctgga cttgatgcag cgctacatcn aggcggggcg cagcgacgaa
 360
 atcgccgcnc ttactgacgc cgccgtatcg tccgcccacg gcgcggcgcg cctcaccat
 420
 cggctgctgg cgttctcgcg ccgccagtcg ctggcccccc gcccgctgga cccaaccag
 480
 ctggtagcgt ccttgaggga tctgttccag cgaaccaaag gcgcgcata cgcgtcaaa
 540
 gtgcaactgg gccgcgatat ctggcccgtg aataccgatg ccagccagtt ggaaaacgcc
 600
 ctgctcaacc tggcgatc
 618

<210> 1108

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1108

Met	Arg	Pro	Asn	Ala	Asn	Ser	Pro	Lys	Arg	Pro	Cys	Ala	Thr	Ser	Thr
1			5					10					15		
Arg	Thr	Ser	Lys	Ser	Ala	Ser	Pro	Ser	Ala	His	Arg	Arg	Trp	Leu	Lys
		20						25				30			
Pro	Thr	Asn	Ala	Trp	Gln	Asn	Lys	Met	Phe	Lys	Arg	Lys	Arg	Ala	Glu
		35				40					45				
Asp	Ala	Leu	Arg	His	Ala	Gln	Lys	Met	Glu	Ala	Gly	Gly	Gln	Leu	Thr
		50				55					60				
Gly	Gly	Ile	Ala	His	Asp	Phe	Asn	Asn	Met	Leu	Thr	Gly	Ile	Ile	Gly
65				70					75				80		
Ser	Leu	Asp	Leu	Met	Gln	Arg	Tyr	Ile	Xaa	Ala	Gly	Arg	Ser	Asp	Glu
		85						90					95		
Ile	Gly	Arg	Leu	Thr	Asp	Ala	Ala	Val	Ser	Ser	Ala	His	Arg	Ala	Ala
		100						105				110			
Ala	Leu	Thr	His	Arg	Leu	Leu	Ala	Phe	Ser	Arg	Arg	Gln	Ser	Leu	Ala
		115				120						125			
Pro	Arg	Pro	Leu	Asp	Pro	Asn	Gln	Leu	Val	Ala	Ser	Leu	Glu	Asp	Leu

```

      130              135              140
Phe Gln Arg Thr Lys Gly Ala His Ile Thr Leu Lys Val Gln Leu Gly
145              150              155              160
Arg Asp Ile Trp Pro Val Asn Thr Asp Ala Ser Gln Leu Glu Asn Ala
      165              170              175
Leu Leu Asn Leu Ala Ile
      180

```

```

<210> 1109
<211> 325
<212> DNA
<213> Homo sapiens

```

```

<400> 1109
accggtgagc atcagggagg caccatgcag acgactctcc catccagtct caagccgtcc
60
agcctcaaga tcgtcgacac gctggggggc atcctcgtgc ccctggatca ggtgcccgat
120
cccgtttttc cccagaagat ggtggggagac gggatctccc tggaccccat ctcaaacgaa
180
ttgctggcgc cggtcgccgg caccgtgacc cagctccaca acgcccacca cgcgctcacg
240
atcacgaccc cggaaggcat cgaggttctg gtccatatcg gactggatac cgtgatgctg
300
cgcggggaca gctatcccc ccccn
325

```

```

<210> 1110
<211> 108
<212> PRT
<213> Homo sapiens

```

```

<400> 1110
Thr Gly Glu His Gln Gly Gly Thr Met Gln Thr Thr Leu Pro Ser Ser
1      5      10      15
Leu Lys Pro Ser Ser Leu Lys Ile Val Ala Pro Leu Gly Gly Ile Leu
20      25      30
Val Pro Leu Asp Gln Val Pro Asp Pro Val Phe Ala Gln Lys Met Val
35      40      45
Gly Asp Gly Ile Ser Leu Asp Pro Ile Ser Asn Glu Leu Leu Ala Pro
50      55      60
Val Ala Gly Thr Val Thr Gln Leu His Asn Ala His His Ala Leu Thr
65      70      75      80
Ile Thr Thr Pro Glu Gly Ile Glu Val Leu Val His Ile Gly Leu Asp
85      90      95
Thr Val Met Leu Arg Gly Asp Ser Tyr Pro Pro Pro
100      105

```

```

<210> 1111
<211> 385
<212> DNA
<213> Homo sapiens

```

```

<400> 1111

```

nnacgcgtcg ccccggtgctg cctggcagtg ggagaagagc atgaccttac cgagctcgcg
 60
 actgaaactcg tcaacgcgcg ctagagccgg gttgacatgg tggaaacgccg tggcgaattc
 120
 gcagtacgtg gcggcatcgt cgacgtcttc ccaccggtgc tagaacaccc ggtagcgtatc
 180
 gattttttttg gtgacgagat cgaggaaatg acctccttcg cggtagccga ccagcgatcc
 240
 accgacgaga ctcaccaaga actgatctgc gctccttgcc gtgagctcat cctcaccgac
 300
 gaggtacgtt cccgagccaa ggctttgctg accgaccatc ccgaattagc tgacatgttg
 360
 gagcggatcg gcaacggtca agctt
 385

<210> 1112

<211> 128

<212> PRT

<213> Homo sapiens

<400> 1112

Xaa	Arg	Val	Ala	Pro	Val	Arg	Leu	Ala	Val	Gly	Glu	Glu	His	Asp	Leu
1				5					10					15	
Thr	Glu	Leu	Ala	Thr	Glu	Leu	Val	Asn	Ala	Ala	Tyr	Ser	Arg	Val	Asp
			20					25					30		
Met	Val	Glu	Arg	Arg	Gly	Glu	Phe	Ala	Val	Arg	Gly	Gly	Ile	Val	Asp
		35					40					45			
Val	Phe	Pro	Pro	Val	Leu	Glu	His	Pro	Val	Arg	Ile	Asp	Phe	Phe	Gly
		50					55				60				
Asp	Glu	Ile	Glu	Glu	Met	Thr	Ser	Phe	Ala	Val	Ala	Asp	Gln	Arg	Ser
65					70					75				80	
Thr	Asp	Glu	Thr	His	Gln	Glu	Leu	Ile	Cys	Ala	Pro	Cys	Arg	Glu	Leu
				85					90					95	
Ile	Leu	Thr	Asp	Glu	Val	Arg	Ser	Arg	Ala	Lys	Ala	Leu	Leu	Thr	Asp
			100					105					110		
His	Pro	Glu	Leu	Ala	Asp	Met	Leu	Glu	Arg	Ile	Gly	Asn	Gly	Gln	Ala
			115					120					125		

<210> 1113

<211> 400

<212> DNA

<213> Homo sapiens

<400> 1113

nnnccgaccga tgagcgatcg cgaacccgctc aacctgggat acccctacgt cgagtctttc
 60
 cactcggact tctcggggac cggcgggagtc gatcagaccg accgtttctac caatatcgac
 120
 gagcacacca tcgaggagat gcatcagatc gctcgcgtt accccgactc ccgttcggcg
 180
 ttgctgccga tctctcacct gggttcagtc gtggacggac gcatctcgcg ggtagctatt
 240
 gagactgcgg ctgaagtgtc cggcattacc accgcccagg tatccggggg ggcgaccttc
 300

tacacatgtg ataagaagca ccctgcgggc cagcatcaca tcggtgtctg caccacggcg
 360
 ctgtgcgcgc tcatgggtgg cgaggaggtg cttgcccgtn
 400

<210> 1114
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 1114
 Xaa Arg Pro Met Ser Asp Arg Glu Pro Val Asn Leu Gly Tyr Pro Tyr
 1 5 10 15
 Val Glu Ser Phe His Ser Asp Phe Ser Gly Thr Gly Gly Val Asp Gln
 20 25 30
 Thr Asp Arg Ser Thr Asn Ile Asp Glu His Thr Ile Glu Glu Met His
 35 40 45
 Gln Ile Ala Ser Arg Tyr Pro Asp Ser Arg Ser Ala Leu Leu Pro Ile
 50 55 60
 Leu His Leu Val Gln Ser Val Asp Gly Arg Ile Ser Pro Val Gly Ile
 65 70 75 80
 Glu Thr Ala Ala Glu Val Leu Gly Ile Thr Thr Ala Gln Val Ser Gly
 85 90 95
 Val Ala Thr Phe Tyr Thr Met Tyr Lys Lys His Pro Ala Gly Gln His
 100 105 110
 His Ile Gly Val Cys Thr Thr Ala Leu Cys Ala Val Met Gly Gly Glu
 115 120 125
 Glu Val Leu Ala Arg
 130

<210> 1115
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 1115
 ttctcgactg cacagattag agaaaggact gcgatgacca ttgcaccac tcatgttggt
 60
 tccttgcccc gcaccccgga gctgacgcag gcgaatcgtg cgcgccgtga ggggttcgct
 120
 ggcgagcgtg acttcacgtc gctgctgcag gatcaggttg acggcggttg gaagcgtcag
 180
 gctgagattg gcctggatat cgtcaatgac ggcgagtacg gtcacgcgat gcttgacacg
 240
 gttgattacg gcgcgtggtg gacgtattcc atctctcgtt tcggcgggct gtcctttgag
 300
 gacgtgcagc gttttgatgt gcgtcccccg gctggccgtg acggctgcct gtctttctcg
 360
 tcgttcgctg agcgcgcgga ctggcagcgt ttccggacgc gt
 402

<210> 1116
 <211> 134
 <212> PRT

<213> Homo sapiens

<400> 1116

```

Ser Pro Thr Ala Gln Ile Arg Glu Arg Thr Ala Met Thr Ile Arg Thr
 1           5           10           15
Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Ile Glu Ala Asn
          20           25           30
Arg Ala Arg Arg Glu Gly Ser Leu Gly Glu Ala Asp Phe Thr Ser Leu
          35           40           45
Leu Gln Asp Gln Val Asp Gly Val Val Lys Arg Gln Ala Glu Ile Gly
          50           55           60
Leu Asp Ile Val Asn Asp Gly Glu Tyr Gly His Ala Met Leu Asp Thr
65           70           75           80
Val Asp Tyr Gly Ala Trp Trp Thr Tyr Ser Ile Ser Arg Phe Gly Gly
          85           90           95
Leu Ser Phe Glu Asp Val Gln Arg Phe Asp Val Arg Pro Pro Ala Gly
          100          105          110
Arg Asp Gly Arg Leu Ser Phe Ser Ser Phe Ala Glu Arg Arg Asp Trp
          115          120          125
Gln Arg Phe Arg Thr Arg
130

```

<210> 1117

<211> 307

<212> DNA

<213> Homo sapiens

<400> 1117

```

ggcgccggtc ttgcctctggc tggaagtggc atgcagacct tgggtgcggaa cccgctggct
60
gacccctacc tgctaggtgt atcggtctggc gcaagtgtgg gagcaaccgc agtcctcgct
120
ttggggatgt tcaattctgt gggaactcac cgactcactc ttggtgcctc tgtagggggc
180
ttggcgcgac ctgcattggt ctatctcatt tccatggcgc aaggaggcat gacgcccgtt
240
cggttggtgc tgcggggcgt ggtgttgtcc tcggcgctct cgcgttggcg agtttcctcg
300
tctttctg
307

```

<210> 1118

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1118

```

Gly Ala Gly Leu Ala Leu Ala Gly Ser Gly Met Gln Thr Leu Val Arg
 1           5           10           15
Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ala Ser
          20           25           30
Val Gly Ala Thr Ala Val Ile Ala Leu Gly Met Phe Thr Ser Trp Gly
          35           40           45
Thr His Arg Leu Thr Leu Gly Ala Leu Val Gly Ala Leu Ala Ala Ala

```

```

      50              55              60
Ala Leu Val Tyr Leu Ile Ser Met Ala Gln Gly Gly Met Thr Pro Leu
65              70              75              80
Arg Leu Val Leu Ser Gly Val Val Leu Ser Ser Ala Phe Ser Arg Trp
      85              90              95
Arg Val Ser Ser Ser Phe
      100

```

```

<210> 1119
<211> 353
<212> DNA
<213> Homo sapiens

```

```

<400> 1119
cgcgtccttg agatgcttga gcaggtcggg attgaggatc cagccagggt gatggattcc
60
tatccgcgac aactgtccgg tggccagcgt caacgggttc tgcttgccat ggcgttggtg
120
aactcgccgg atctgctcat ttgtgacgag ccgacgaccg ccttgagcgt cacgggtgcag
180
tctcaggtac tggcgactat cgtatgaggtg cttgactcgg ttggtgcccg atgcctattt
240
attacccacg atttggcggg tgtctcgcac atctgccggg agcttatcgt gatgacgtcg
300
ggcaaggctg ttgaagccgg atcagcgcgt gatgtgttat ctcaccctga tca
353

```

```

<210> 1120
<211> 117
<212> PRT
<213> Homo sapiens

```

```

<400> 1120
Arg Val Leu Glu Met Leu Glu Gln Val Gly Ile Glu Asp Pro Ala Arg
1              5              10              15
Val Met Asp Ser Tyr Pro His Gln Leu Ser Gly Gly Gln Arg Gln Arg
20              25              30
Val Leu Leu Ala Met Ala Leu Val Asn Ser Pro Asp Leu Leu Ile Cys
35              40              45
Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Val Gln Ser Gln Val Leu
50              55              60
Ala Thr Ile Asp Glu Val Leu Asp Ser Val Gly Ala Ala Cys Leu Phe
65              70              75              80
Ile Thr His Asp Leu Ala Val Val Ser His Ile Cys Arg Glu Leu Ile
85              90              95
Val Met Thr Ser Gly Lys Val Val Glu Ala Gly Ser Ala Arg Asp Val
100             105             110
Leu Ser His Pro Asp
115

```

```

<210> 1121
<211> 406
<212> DNA
<213> Homo sapiens

```


<400> 1121
 tgatcaccca tgctccactc gaccgcgcgc tcgacgatgc gacggctgag acgatgctcg
 60
 cccagggcac ggtgttcac cgcacctga cgatgatgaa aggcgtcgcc gcgaatctca
 120
 ccgcagcggg cgttcccggg gtgagctatg cacacgcccc cgagagcacg cgcgcgatgc
 180
 atgcgcggg cgttccggtc ctggccggca ccgacgccta catcgggtcc ttcacacggg
 240
 catcgccgcc atacggcgag agcatgcacg acgaagacgc ctacatcggg ctcctcgaac
 300
 gggcaatgcc gccatacggc gagagcatgc acgacgaact cgctctgctc gtggacgccg
 360
 gcctgtcaac agccgaagcg ctgcgcgctg ccacctcgac gggcgc
 406

<210> 1122
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1122
 Met Leu Ala Gln Gly Thr Val Phe Ile Pro Thr Leu Thr Met Met Lys
 1 5 10 15
 Gly Val Ala Ala Asn Leu Thr Ala Ala Gly Val Pro Gly Val Ser Tyr
 20 25 30
 Ala His Ala His Glu Ser Thr Arg Ala Met His Ala Ala Gly Val Pro
 35 40 45
 Val Leu Ala Gly Thr Asp Ala Tyr Ile Gly Ser Phe Thr Arg Ala Ser
 50 55 60
 Pro Pro Tyr Gly Glu Ser Met His Asp Glu Asp Ala Tyr Ile Gly Leu
 65 70 75 80
 Leu Glu Arg Ala Met Pro Pro Tyr Gly Glu Ser Met His Asp Glu Leu
 85 90 95
 Ala Leu Leu Val Asp Ala Gly Leu Ser Thr Ala Glu Ala Leu Arg Ala
 100 105 110
 Ala Thr Ser Thr Gly
 115

<210> 1123
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 1123
 gccggcgatg cgttcattaa ggcctaagat gcgcgcacgc ctccccgctt tctcgcctc
 60
 cgcctccacc gcccttgccg cagcggggat ggtgggggtgc tcgtccgagg gggcatcgcc
 120
 aagcgaatgc tccccgttg atattgcgc agtgccgcgag gccctgcgcg attcgctcgc
 180
 taaggcgaag ctgcaccgc actccaccaa cgaggatgaa cactcctttt ccattgctcta
 240

ccgcgcgcaa gataaggagc aggtcagctt gctggggacg aagtatgagg ccgacgggtgc
 300
 acccgctctgc cccgatgacc ccaatgaggc agcgcgcg
 337

<210> 1124
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1124
 Met Arg Ser Leu Arg Pro Lys Met Arg Arg Arg Leu Pro Ala Phe Leu
 1 5 10 15
 Ala Leu Ala Ser Thr Ala Leu Ala Ala Gly Met Val Gly Cys Ser
 20 25 30
 Ser Glu Gly Ala Ser Pro Ser Glu Cys Ser Pro Val Asp Ile Ala Ala
 35 40 45
 Val Arg Glu Ala Leu Pro His Ser Leu Ala Lys Ala Lys Leu Asp Pro
 50 55 60
 His Ser Thr Asn Glu Asp Glu His Ser Phe Ser Met Leu Tyr Arg Ala
 65 70 75 80
 Gln Asp Lys Glu Gln Val Ser Leu Leu Gly Thr Lys Tyr Glu Ala Asp
 85 90 95
 Gly Ala Pro Val Cys Pro Asp Asp Pro Asn Glu Ala Ala Arg
 100 105 110

<210> 1125
 <211> 555
 <212> DNA
 <213> Homo sapiens

<400> 1125
 nncttgaatc gaatcggcat tgcgtctaaa catgacgttg agacactctc tgctaagctc
 60
 gaagagctga cggcattgct agaactgtgc gcgcgtaaac actaaggaga catcgggatg
 120
 gctgttaaaa agactactca gaaagaaggc agctcgtgga tcgggggaagt tgaaaaatat
 180
 tcccgtaaaa tctggcttgc tggtttaggc gtgtactcga aggttagcag tgacggcgcc
 240
 aaatacttcg agacgttggt caaggacggc gagaaggccg agaagttgac caagagccca
 300
 gtcggtaaaa aagtagaggc ggcaaaagcg agcgccggtt ctgcgaaatc gagcatttgc
 360
 gataacctggg gcaagttgga agagacttcc gacaagcgtc tcaacagtgc tatttcgcga
 420
 ttgggcgtgc ccagcaaagc ggaactgaag acgctgcaca gcaaggtcga taccttgacc
 480
 aagcaaatcg aaaaactcac cggtgccaaa gtggcccccg ctaaaacggc agccgctaaa
 540
 cctgctgcca agctt
 555

<210> 1126

<211> 146

<212> PRT

<213> Homo sapiens

<400> 1126

```

Met Ala Val Lys Lys Thr Thr Gln Lys Glu Gly Ser Ser Trp Ile Gly
  1             5             10             15
Glu Val Glu Lys Tyr Ser Arg Lys Ile Trp Leu Ala Gly Leu Gly Val
      20             25             30
Tyr Ser Lys Val Ser Ser Asp Gly Gly Lys Tyr Phe Glu Thr Leu Val
      35             40             45
Lys Asp Gly Glu Lys Ala Glu Lys Leu Thr Lys Ser Pro Val Gly Lys
      50             55             60
Lys Val Glu Ala Ala Lys Ala Ser Ala Gly Ser Ala Lys Ser Ser Ile
      65             70             75             80
Ser Asp Thr Trp Gly Lys Leu Glu Glu Thr Phe Asp Lys Arg Leu Asn
      85             90             95
Ser Ala Ile Ser Arg Leu Gly Val Pro Ser Lys Ala Glu Leu Lys Thr
      100            105            110
Leu His Ser Lys Val Asp Thr Leu Thr Lys Gln Ile Glu Lys Leu Thr
      115            120            125
Gly Ala Lys Val Ala Pro Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala
      130            135            140
Lys Leu
145

```

<210> 1127

<211> 352

<212> DNA

<213> Homo sapiens

<400> 1127

```

ccgaccgcg tactcgtggt cgggtgccga gtgatgggtg cagcacacgc acacgcgctc
  60
cgcggtgccc tccaggcagt cgtgtgcggc gtggtcgacc tgcaggagcg agcagcgcaa
  120
tcactcgctt cggaagtggg cgtaccgggg ttcaccgacc tgggtgaagg gatcgagtcg
  180
accgctccgg acgccgcggt catcgccacg ccggactcgg ctcaccgcca accggctgag
  240
accgccatcg acgcggcct tgccgtcctg gtcgagaaac cgctcgccac gaccgtcgat
  300
gacgccgaag cgatcgtgct ccgcgctgaa cgggccggcg tccgtctcat ga
  352

```

<210> 1128

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1128

```

Pro Asp Arg Val Leu Val Val Gly Ala Gly Val Met Gly Ala Ala His
  1             5             10             15
Ala His Ala Leu Arg Gly Ser Leu Gln Ala Val Val Cys Gly Val Val

```

```

                20                25                30
Asp Leu Gln Glu Arg Ala Ala Gln Ser Leu Ala Ser Glu Val Gly Val
    35                40                45
Pro Gly Phe Thr Asp Leu Val Lys Ala Ile Glu Ser Thr Ala Pro Asp
    50                55                60
Ala Ala Val Ile Ala Thr Pro Asp Ser Ala His Arg Gln Pro Ala Glu
    65                70                75                80
Thr Ala Ile Asp Ala Gly Leu Ala Val Leu Val Glu Lys Pro Leu Ala
    85                90                95
Thr Thr Val Asp Asp Ala Glu Ala Ile Val Leu Arg Ala Glu Arg Ala
    100                105                110
Gly Val Arg Leu Met
    115

```

<210> 1129

<211> 336

<212> DNA

<213> Homo sapiens

<400> 1129

```

ntggcagccc tggaggagccc gatggtggac ctggacggcg agctgccttt cgtgcggccc
60
ctgccccaca ttgccgtgct ccaggacgag ctgccgaac tcttcagga tgacgacgtc
120
ggggccgatg aggaagaggg agagtgcgg ggcgaaacaca cgctcacaga gaagtttgc
180
tgccctggatg actcctttgg ccatgactgc agcttgacct gtgatgactg caggaacgga
240
gggacctgcc tcctgggctt ggatggctgg gattgccccg agggctggac tgggctcatc
300
tgcaatgaga cttgttcctc gggctgcatg gatatt
336

```

<210> 1130

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1130

```

Xaa Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
    1                5                10                15
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
    20                25                30
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu
    35                40                45
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
    50                55                60
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
    65                70                75                80
Gly Thr Cys Leu Leu Gly Leu Asp Gly Trp Asp Cys Pro Glu Gly Trp
    85                90                95
Thr Gly Leu Ile Cys Asn Glu Thr Trp Ser Ser Gly Cys Met Asp Ile
    100                105                110

```

<210> 1131
 <211> 672
 <212> DNA
 <213> Homo sapiens

<400> 1131
 gcgttggtgg tgctcatggc cgggaaaaat ccgctggatc aatacctctt tgagcacecc
 60
 gaattattgt tctcgtcctc ggtggaatcg actgtgttgc acccgataa cccgatgtgtg
 120
 ctcggcccg cagtgggccgc ggccgcccag gaggcatacc tctccccctgc ggacgaagag
 180
 ttttacgggt cggcctttgc cgggatatgc aaaacgctga caggccagaa cgtactgcga
 240
 cgtcgcggaa atcggctgtt ctggactcgt ccggaacggg ctgtcgacgc catcgacctg
 300
 cgatcggcgg caggcaaaag gattgacatt atcgacgtgt ccaccgggag ggtcatcggg
 360
 gtagtgcagc aagccgccgc agaccgtacc gtgcatccag gcgcggtgta cctgcatcag
 420
 ggggatcagt ggctggtcga cgaatacaac ccggtcgagc accacgcctt ggtgcaccag
 480
 gacctgccgc gatattggac tcaaccgcag tcagcgtcga cggtgagaat ccttcgggag
 540
 gagagacgct gcgcttggg tcccgatat gtggcgtgcy ggcagggtgga actgacagag
 600
 caagttgttg ggtatctgcy tcgcgacgaa ttcaccaatg atgtgttgta ctgcgtggcc
 660
 ctcgagatgc cc
 672

<210> 1132
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 1132
 Ala Leu Val Val Leu Met Ala Arg Glu Asn Pro Leu Asp Gln Tyr Leu
 1 5 10 15
 Phe Glu His Pro Glu Leu Leu Phe Ser Ser Ser Val Glu Ser Thr Val
 20 25 30
 Leu His Pro Asp Asn Pro Tyr Val Leu Gly Pro His Val Ala Ala Ala
 35 40 45
 Ala Gln Glu Ala Tyr Leu Ser Pro Ala Asp Glu Glu Phe Tyr Gly Ser
 50 55 60
 Ala Phe Ala Gly Ile Cys Lys Thr Leu Thr Gly Gln Asn Val Leu Arg
 65 70 75 80
 Arg Arg Gly Asn Arg Leu Phe Trp Thr Arg Pro Glu Arg Ala Val Asp
 85 90 95
 Ala Ile Asp Leu Arg Ser Ala Ala Gly Lys Gly Ile Asp Ile Ile Asp
 100 105 110
 Val Ser Thr Gly Arg Val Ile Gly Val Val Asp Glu Ala Ala Ala Asp
 115 120 125
 Arg Thr Val His Pro Gly Ala Val Tyr Leu His Gln Gly Asp Gln Trp

130	135	140
Leu Val Asp Glu Tyr Asn	Pro Val Glu His His	Ala Leu Val His Gln
145	150	155
Asp Leu Pro Gly Tyr Trp	Thr Gln Pro Gln Ser	Ala Ser Thr Val Arg
165	170	175
Ile Leu Arg Glu Glu Arg	Arg Arg Ala Cys Gly	Pro Gly Tyr Val Ala
180	185	190
Cys Gly Gln Val Glu Leu	Thr Glu Gln Val Val	Gly Tyr Leu Arg Arg
195	200	205
Asp Glu Phe Thr Asn Asp	Val Trp Tyr Ser Leu	Ala Leu Glu Met Pro
210	215	220

<210> 1133

<211> 796

<212> DNA

<213> Homo sapiens

<400> 1133

acgcgtgaag ggggggtccag cgggtgtggc actcgatgac aagacagttt gagagcggct
 60
 tgtctccggg gacctggcgt aggtctcttc tgccttaacc cttggctttt gcaactcttc
 120
 tgtctgtcct ccatacaagc ttcttgcccc tagggaggac gggcttctta acagggggag
 180
 ccggttcctg tcctaacccc actggcatct tacactctgg gagatagctt cccccgaga
 240
 ggcgagtgag ccacgtaagg ggaggtgggc gatggcttcc cttctgtctt gggttggggg
 300
 agtcaggtag agtatttttt cttttaaagc atcattgatc acataataag gtttgtcata
 360
 gtccctaata acagacctgt gaaatttgga gaattcacgg cacctaggat gggagtgcgc
 420
 ttctgattgt gagctgattt gggagctaac ctcaaggaaa ctccctctgc aagccccctg
 480
 ctgggtgtgc gggccttcgc cagggaacct ccggggactc tggacgtctt ttgtctgccc
 540
 ttcccttttc ctcacctgcg tcccccgtag gaaagtgggg ctcctgcagc tcagctcagt
 600
 gacagagggt ttattagggg tagctctggg acccatcttt tggtgatttc ttctctctct
 660
 ttctctaagt gaataattgt ttctgtctac acttctttat ttctctctct ctacagctgc
 720
 cttctaaaaa tgtgcttttc tgttctctga gaactgaagc ttgcatggcc ttgtgtgtga
 780
 ctttcccttc acgcgt
 796

<210> 1134

<211> 147

<212> PRT

<213> Homo sapiens

<400> 1134

Met Gly Pro Arg Ala Thr Pro Asn Lys Pro Ser Val Thr Glu Leu Ser

```

1           5           10           15
Cys Met Ser Pro Thr Phe Ser Arg Gly Ser Glu Val Arg Glu Lys Glu
20           25           30
Gly Gln Thr Lys Ser Val Gln Ser Pro Arg Glu Val Pro Gly Glu Gly
35           40           45
Pro Asp Thr Gln Gln Gly Ala Cys Lys Arg Ser Phe Leu Glu Val Ser
50           55           60
Ser Gln Ile Ser Ser Gln Ser Glu Ala His Ser His Pro Arg Cys Arg
65           70           75           80
Glu Phe Ser Lys Phe His Arg Ser Val Ile Lys Asp Tyr Asp Lys Pro
85           90           95
Tyr Tyr Val Ile Asn Asp Ala Leu Lys Glu Lys Ile Leu Tyr Leu Thr
100          105          110
Pro Pro Thr Gln Asp Arg Arg Glu Ala Ile Ala His Leu Pro Leu Arg
115          120          125
Gly Ser Leu Ala Ser Gln Gly Glu Ala Ile Ser Gln Ser Val Arg Cys
130          135          140
Gln Trp Gly
145

```

<210> 1135

<211> 376

<212> DNA

<213> Homo sapiens

<400> 1135

```

gatcaggcca cacaggacaa cttcgagaag ggctccatct tcccaccctt caccagcatc
60
agaaagatct ctgcgcacat cgctgcagcc gtggtctgcaa aagcctacga gctcggctgtg
120
gcgacccgctc tgccctcccc cagcgacctg gtgaaatatg cagagaactg catgtacact
180
cccgctacc gcaactaccg gtagtgctgc ggggatcaat ttgacagtaa taaaaaatct
240
actatcaacg cggatggtac tctgtgtgtt atagtccctg ctgctaacca ccctgtgtgc
300
tggtgctgct ggagaggcat tgtacctgtc catgcatata tgatatatat atgttgtaac
360
gttgtgaaag caaact
376

```

<210> 1136

<211> 67

<212> PRT

<213> Homo sapiens

<400> 1136

```

Asp Gln Ala Thr Gln Asp Asn Phe Glu Lys Gly Ser Ile Phe Pro Pro
1           5           10           15
Phe Thr Ser Ile Arg Lys Ile Ser Ala His Ile Ala Ala Val Ala
20           25           30
Ala Lys Ala Tyr Glu Leu Gly Leu Ala Thr Arg Leu Pro Pro Ser
35           40           45
Asp Leu Val Lys Tyr Ala Glu Asn Cys Met Tyr Thr Pro Val Tyr Arg

```

50
Asn Tyr Arg
65

<210> 1137
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1137
acgcgcgcgt ggaacccgaa gatgaagcgc ttcatcttca ccgagcgcaa cggtatctac
60
atcattgacc tgcaccagtc gctgacctac attgataaagg cgtacgcctt cgtcaaggag
120
actgtcgcca agggcgcgcca gattcttttc gtcggcacga agaagcagggc ccaggaggtcc
180
atcgctgagc agggccactcg cgttggcatg ccctatgtca accagcgttg gcttggggga
240
atgctcacta atttccagac catctcgaag cgcattgccg ggctcaagga gctcgaggcc
300
atggactttg acaaggtttc cggctccggt ctcaccaaga aggagctgct tatgtctc
357

<210> 1138
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1138
Thr Arg Arg Trp Asn Pro Lys Met Lys Arg Phe Ile Phe Thr Glu Arg
1 5 10 15
Asn Gly Ile Trp Ile Ile Asp Leu His Gln Ser Leu Thr Tyr Ile Asp
20 25 30
Lys Ala Tyr Ala Phe Val Lys Glu Thr Val Ala Lys Gly Gly Gln Ile
35 40 45
Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ser Ile Val Glu Gln
50 55 60
Ala Thr Arg Val Gly Met Pro Tyr Val Asn Gln Arg Trp Leu Gly Gly
65 70 75 80
Met Leu Thr Asn Phe Gln Thr Ile Ser Lys Arg Ile Ala Arg Leu Lys
85 90 95
Glu Leu Glu Ala Met Asp Phe Asp Lys Val Ser Gly Ser Gly Leu Thr
100 105 110
Lys Lys Glu Leu Met Leu
115

<210> 1139
<211> 456
<212> DNA
<213> Homo sapiens

<400> 1139
gtgcacaggt cgtctgaggc catgccgagg acgatcgatc cgagtatggc ggcaccttca
60

ccaatcccgt aggaccgctc tcgtccagca tcgaccaagg cgctgttgag gcgttcggct
 120
 tcggtaataga actcgatgcg ctcaatatcc acgggggtag cgaatcgta gatcttggcc
 180
 agactgaggc ctggaggag cgcgccgctc ggggggacgt ggctgcccgc cgggcggtcc
 240
 ttgctctcaa ggacttcgctc gtcgcggtc acaaggaata cgtttgtgtg gtcgctgca
 300
 atgcatgctc gagcgtgggtg accatcgagg tgaaggacgg ttctggcata gaggtcatcg
 360
 tccacatcgg ccacagttag ttgcacgact cctgagtcga ctatgatgacg cgccttctct
 420
 gccgctctt cgctgacgct gcccaggacc gctagc
 456

<210> 1140

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1140

Met	Trp	Thr	Met	Thr	Ser	Met	Pro	Lys	Pro	Ser	Phe	Thr	Ser	Met	Val
1				5					10					15	
Thr	Thr	Leu	Glu	His	Ala	Leu	Gln	Ala	Thr	Thr	Gln	Thr	Tyr	Ser	Leu
		20					25						30		
Ser	Ala	Ala	Thr	Thr	Lys	Ser	Leu	Arg	Ala	Arg	Asn	Ala	Arg	Pro	Gln
		35					40				45				
Ala	Thr	Ser	Pro	Arg	Arg	Pro	Arg	Ser	Ser	Lys	Ala	Ser	Val	Trp	Pro
		50				55				60					
Arg	Ser	Thr	Ile	Ser	Leu	Pro	Pro	Trp	Ile	Leu	Ser	Ala	Ser	Ser	Ser
65			70						75					80	
Leu	Pro	Lys	Pro	Asn	Ala	Ser	Thr	Ala	Pro	Trp	Ser	Met	Leu	Asp	Glu
			85						90					95	
Thr	Gly	Pro	Thr	Gly	Leu	Val	Lys	Val	Pro	Pro	Tyr	Ser	Asp	Arg	Ser
		100					105							110	
Ser	Ala	Ala	Trp	Pro	Gln	Thr	Thr	Cys	Ala						
		115					120								

<210> 1141

<211> 354

<212> DNA

<213> Homo sapiens

<400> 1141

ggcgccatgc tcggcgggct ggtgctgggt gtggccgaag cctttggcgc cgatatcttc
 60
 ggcgaccagt acaaggacgt ggtggcggtt ggctgtgttg ttctgggtgct gttgttccgt
 120
 ccgaccggca ttctggggcg tccggaggtt gagaagatat gagcagatat cttaaatcgg
 180
 cgtttttcag cgccctgttg gtgtggggcg tggcctttcc ggtactcggc ctcaagctga
 240
 gcattgtcgg gatcaaccac gaagtgcatt gcaccgggtc cgtgaccttg accatcatcg
 300

ccctgtgctc ggtgccgatg ttccctgcgcg tgctgtttac ccagcaagtc ggtg
354

<210> 1142

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1142

Gly Ala Met Leu Gly Gly Leu Val Leu Gly Val Ala Glu Ala Phe Gly
1 5 10 15
Ala Asp Ile Phe Gly Asp Gln Tyr Lys Asp Val Val Ala Phe Gly Leu
20 25 30
Leu Val Leu Val Leu Leu Phe Arg Pro Thr Gly Ile Leu Gly Arg Pro
35 40 45
Glu Val Glu Lys Val
50

<210> 1143

<211> 353

<212> DNA

<213> Homo sapiens

<400> 1143

acgcgttgca catccccag gaccatcaac cgcggcattg ccgcatagac ctggagatcc
60
catgcaacgt gaaatgaagt tcgaatcgat caaggcaaag gccaggcgga tgctcatcgg
120
cgcagccgac gacacagcaa gcgcaggcgc gaccaaccga gggtggtctca acagcgccgc
180
attcgaaatc ctggcccacg tggccgtcaa tgcccaacac tacgcgctct ccgagagacc
240
ggcgctggag gagttcgcca agagcttcca gccgcgcaac aaccaggact acgtggccgc
300
gatcgccaag aaggccgcga accacacat gcattccggc aggcagtcga ttt
353

<210> 1144

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1144

Met His Gly Val Val Arg Gly Leu Leu Gly Asp Arg Gly His Val Val
1 5 10 15
Leu Val Val Ala Arg Leu Glu Ala Leu Gly Glu Leu Leu Gln Arg Arg
20 25 30
Ser Leu Gly Glu Arg Val Val Leu Gly Ile Asp Gly His Val Gly Gln
35 40 45
Asp Phe Glu Cys Gly Ala Val Glu Pro Pro Ser Val Gly Arg Ala Cys
50 55 60
Ala Cys Cys Val Val Gly Cys Ala Asp Glu His Arg Leu Gly Leu Cys
65 70 75 80
Leu Asp Arg Phe Glu Leu His Phe Thr Leu His Gly Ile Ser Arg Ser

85
Met Arg Gln Cys Arg Gly
100

90

95

<210> 1145
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1145
gtcttcggcg ggctcggcct gttctattgc gtcattgaccc cgggtgactg gttctcggcc
60
catgaagtgg ccggcacctg ggtactcggg ctgtcggcgg cgatggctct gatgggtgtt
120
ttctacgtcc aggtcatcgc caagaagatc aatcctcgac cctccgacga gaaggacgac
180
gaggtgatcg acggggctgg tccggctcgg ttcttccgc cacaagatg ctggccgttc
240
tggtgcgcgc tcgttgctgc catcatgtgc ctgcggccga tcttcggctg gtggatctct
300
ctgctcgggc tgggcattgt tatctgggac gctcggggtt gggcttttga gtactaccgc
360

<210> 1146
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1146
Val Phe Gly Gly Leu Gly Leu Phe Tyr Cys Val Met Thr Pro Val Tyr
1 5 10 15
Trp Phe Ser Ala His Glu Val Ala Gly Thr Trp Val Leu Gly Leu Ser
20 25 30
Ala Ala Met Ala Leu Met Val Phe Phe Tyr Val Gln Val Ile Ala Lys
35 40 45
Lys Ile Asn Pro Arg Pro Ser Asp Glu Lys Asp Ala Glu Val Ile Asp
50 55 60
Gly Ala Gly Pro Val Gly Phe Phe Pro Pro Gln Ser Ile Trp Pro Phe
65 70 75 80
Trp Cys Ala Leu Val Val Ala Ile Met Cys Leu Gly Pro Ile Phe Gly
85 90 95
Trp Trp Ile Ser Leu Leu Gly Leu Gly Ile Val Ile Trp Ala Ala Ser
100 105 110
Gly Trp Ala Phe Glu Tyr Tyr Arg
115 120

<210> 1147
<211> 409
<212> DNA
<213> Homo sapiens

<400> 1147
tgtacattgg ctatgcagtc tggcctcctg aaggttatga tagtagccaa aaatatagaa
60

gccccaaaagg catccacctt ctcatcaat ccagaattga tcattgctcat gcctgtgggt
 120
 ggatcactat gtgctctcca aattgggagg ggaagtctac tctctctctt cctctctctc
 180
 ccacettccc ctctctcttc tctctttctt attcccaggg cagtgggaaca tgatgaggtt
 240
 cttttccctt catggatata ctctttctgc cctccacata aaggggcatt gatggatctt
 300
 caagaatggg atgcctttcc ctgaaaaggc taaatattca tgaggctgaa tgtgaggatc
 360
 cagagtagac tgaaatataa ctgggtcatca gtacacatag aatctgatn
 409

<210> 1148
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1148
 Met Gln Ser Gly Leu Leu Lys Val Met Ile Val Ala Lys Asn Ile Glu
 1 5 10 15
 Ala Lys Lys Ala Ser Thr Phe Phe Ile Asn Pro Glu Leu Ile Met Leu
 20 25 30
 Met Pro Val Gly Gly Ser Leu Cys Ala Leu Gln Ile Gly Arg Gly Ser
 35 40 45
 Leu Leu Ser Ser Leu Leu Ser Leu Pro Pro Ser Pro Leu Ser Ser Leu
 50 55 60
 Leu Ser Ile Pro Arg Ala Val Glu His Asp Glu Val Leu Phe Pro Ser
 65 70 75 80
 Trp Ile Ser Ser Phe Cys Pro Pro His Lys Gly Ala Leu Met Asp Leu
 85 90 95
 Gln Glu Trp Asp Ala Phe Pro
 100

<210> 1149
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 1149
 gtcgacttct gcatggaaaa acgcatctct gtgattgagc acgttgcgga gatgtacggc
 60
 cgtgaggcgg tatcgcatat cattaccttc ggtaccatgg cggcgaaagc gggtattcgt
 120
 gacgtggggc gtgtactggg taccctgtat ggcttcgtcg atcgcatctc caagctgggt
 180
 ccgcccgatc cgggcatgac gctggaaaaa gcctttgccg ccgaaccgca gttgccggaa
 240
 atctacgagg ccgatgagga agtcaaaagc ctgatcgaca tggcgcgcaa gctgggaagg
 300
 gtgacgcgg
 309

<210> 1150

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1150

```

Val Asp Phe Cys Met Glu Lys Arg Asp Leu Val Ile Glu His Val Ala
 1             5             10             15
Glu Met Tyr Gly Arg Glu Ala Val Ser Gln Ile Ile Thr Phe Gly Thr
          20             25             30
Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val Leu Gly His
          35             40             45
Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Val Pro Pro Asp Pro
          50             55             60
Gly Met Thr Leu Glu Lys Ala Phe Ala Ala Glu Pro Gln Leu Pro Glu
          65             70             75             80
Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp Met Ala Arg
          85             90             95
Lys Leu Gly Arg Val Thr Arg
          100

```

<210> 1151

<211> 360

<212> DNA

<213> Homo sapiens

<400> 1151

```

gcgcgcattt ttgtcaaccc aagcgacgtc attatggccg agtcgccgcg ttatgtcggg
60
gcgctcaata ccttcgcctc gtaccaaact gaggtcattc acgtcgacat ggacgacagc
120
gggttggttc cggaatccct gcgtgagaaa gtgactgcag cgcgtcaaga cggcaagtcg
180
gtgaagtctc ttacacggt tcctaactac tcgaaccggt cggaatctc gcaatccacc
240
gagcgtgcgc ggagatcct agcgtgggct gacgagctgg atctgttggt ggttgaggac
300
aaccgcgtac gggtactcaa cctcgatggt gatccactgc cgagcttgaa gtcgatggat
360

```

<210> 1152

<211> 120

<212> PRT

<213> Homo sapiens

<400> 1152

```

Ala Arg Ile Phe Cys Asn Pro Ser Asp Val Ile Met Ala Glu Ser Pro
 1             5             10             15
Ala Tyr Val Gly Ala Leu Asn Thr Phe Ala Ser Tyr Gln Thr Glu Val
          20             25             30
Ile His Val Asp Met Asp Asp Ser Gly Leu Val Pro Glu Ser Leu Arg
          35             40             45
Glu Lys Val Thr Ala Ala Arg Gln Asp Gly Lys Ser Val Lys Phe Leu
          50             55             60
Tyr Thr Val Pro Asn Tyr Ser Asn Pro Ser Gly Ile Ser Gln Ser Thr

```

```

65          70          75          80
Glu Arg Arg Arg Glu Ile Leu Ala Val Ala Asp Glu Leu Asp Leu Leu
      85          90          95
Val Val Glu Asp Asn Pro Tyr Gly Leu Leu Asn Leu Asp Gly Asp Pro
      100          105          110
Leu Pro Thr Leu Lys Ser Met Asp
      115          120

```

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<210> 1153
<211> 416
<212> DNA
<213> Homo sapiens

```

```

<400> 1153
gcgtggattc gtctggcgg cgctcgtacc gacctgccg agaccgggct cgaccagttg
60
cgtgacctca tcaagcggat ggaagaagtag ctccccgaga tcggtcagtt ctgcaatgag
120
aatccgatct ttaagcccg cactcagggc attggttacg ctgactctgc tacctgtatg
180
gccctgggag ttactgggtc tgctctgcgc gctaccggcc tgccgtggga cctgcgcaag
240
accagccctt attgcgatta cgacacgtat gacttcgacg tcgccacctg ggataacctg
300
gactgttacg ggcgtttccg catccgcctg gaagagatgg accagtcggt gcgcattctc
360
aagcaatgcc tcaaacgcct cgaggacacc cagggtgacc gtaatatggt cgagga
416

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```

<210> 1154
<211> 138
<212> PRT
<213> Homo sapiens

```

```

<400> 1154
Ala Trp Ile Arg Pro Gly Gly Val Ala Thr Asp Leu Pro Glu Thr Gly
1      5      10      15
Leu Asp Gln Leu Arg Asp Leu Ile Lys Arg Met Glu Lys Tyr Leu Pro
20     25     30
Glu Ile Gly Gln Phe Cys Asn Glu Asn Pro Ile Phe Lys Ala Arg Thr
35     40     45
Gln Gly Ile Gly Tyr Ala Asp Leu Ser Thr Cys Met Ala Leu Gly Val
50     55     60
Thr Gly Pro Ala Leu Arg Ala Thr Gly Leu Pro Trp Asp Leu Arg Lys
65     70     75     80
Thr Gln Pro Tyr Cys Asp Tyr Asp Thr Tyr Asp Phe Asp Val Ala Thr
85     90     95
Trp Asp Thr Cys Asp Cys Tyr Gly Arg Phe Arg Ile Arg Leu Glu Glu
100    105    110
Met Asp Gln Ser Val Arg Ile Leu Lys Gln Cys Leu Lys Arg Leu Glu
115    120    125
Asp Thr Gln Gly Asp Arg Asn Met Val Glu
130    135

```

<210> 1155
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 1155
 cttaaagttat ttggtctttt gcctctctcc tcaggttgtg aagattacag aaatctggga
 60
 tggtcttatgg gacgcttctc agccctaagt aggaaaacag cagtgaaaaa ggcaacaaaa
 120
 acatcacgca ggactggggg ttttggggaa acagctcact ttagagcagt gcagtgtaga
 180
 gctttccgtc ttctaccagg gtcacacctt aacactgttt atctgaaaaa ttccccctg
 240
 gcttactcgc ttgcagctgc ccactttgca gaaagatggc gctctgatct ctacgctccc
 300
 tgttccttca gggactccat agtatctttt ttcacgcgt
 339

<210> 1156
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1156
 Met Gly Arg Phe Ser Ala Leu Ser Arg Lys Thr Ala Val Lys Met Ala
 1 5 10 15
 Thr Lys Thr Ser Arg Arg Thr Gly Gly Phe Gly Glu Thr Ala His Phe
 20 25 30
 Arg Ala Val Gln Cys Arg Ala Phe Arg Leu Leu Pro Gly Ser Thr Phe
 35 40 45
 Asn Thr Val Tyr Leu Lys Ile Phe Pro Leu Ala Tyr Ser Leu Ala Ala
 50 55 60
 Ala His Phe Ala Glu Arg Trp Arg Ser Asp Leu Tyr Ala Pro Cys Ser
 65 70 75 80
 Phe Arg Asp Ser Ile Val Phe Phe Phe Thr Arg
 85 90

<210> 1157
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1157
 nnacagctc tctccgacc gcggcggtt gcacacgtcc ccgtctgagg agtattcgtg
 60
 ctggcaaaac tcgtgaccgc acacctgagg gcctatcggg tgcacgttgc cgtcatcatc
 120
 gttatgcagg ttgcgccca aatcgcggtc ctgaccttgc caaccatcaa cgcagacatc
 180
 atcaacaagg gcgtcgtgac agcgataacc ggatatgtca ccacccactc cctcttcatg
 240
 ctggcggtcg ctttagggca ggccatctgc cagggtcattg cggtttatct cgccgctcag
 300

gtggcgatgg gaatgggccc tgacgttcgc gacgccatct tcaccgcac ccttgacttc
 360
 tcggccccgg agatcaacaa attcggagca ccatcactca ttaccggac taccaacgac
 420
 gtccag
 426

<210> 1158
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1158
 Val Leu Ala Lys Leu Val Thr Arg His Leu Arg Ala Tyr Arg Leu His
 1 5 10 15
 Val Ala Val Ile Ile Val Met Gln Val Cys Ala Gln Ile Ala Ala Leu
 20 25 30
 Thr Leu Pro Thr Ile Asn Ala Asp Ile Ile Asn Lys Gly Val Val Thr
 35 40 45
 Ala Asp Thr Gly Tyr Val Thr Thr His Ser Leu Phe Met Leu Ala Val
 50 55 60
 Ala Leu Gly Gln Ala Ile Cys Gln Val Ile Ala Val Tyr Leu Ala Ala
 65 70 75 80
 Gln Val Ala Met Gly Met Gly Arg Asp Val Arg Asp Ala Ile Phe Thr
 85 90 95
 Arg Thr Leu Asp Phe Ser Ala Arg Glu Ile Asn Lys Phe Gly Ala Pro
 100 105 110
 Ser Leu Ile Thr Arg Thr Thr Asn Asp Val Gln
 115 120

<210> 1159
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 1159
 tctctccgac cgcgcctggg gcccggtggg gtccctgcggg gacgcggggc aggacggcgc
 60
 ggacgaggca ggagcaggcc gggctctcgc catgggtcac tgtcgctctt gccacgggaa
 120
 gttttctctg agaagcctgc gcagcatctc cgagaggcgc cctggagcga gcattggagag
 180
 gccatccgca gaggagcgcg gtctcgtacg ggacttccag cgcctgcttg gtgtggtgtg
 240
 ccgccaggac ccacacttgt ctccgtttgt ctgcaagagc tgccacgccc agttctacca
 300
 gtgccacagc cttctcaagt ctttctcgca gaggggtcaac gcctccccgg ctggtcgccc
 360
 gaagccttgt gcaaaggctg gtgccacgcc cccaacaggg gcagaggagg gaggctgtct
 420
 ggtggatctg atca
 434

<210> 1160

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1160

```

Met Gly His Cys Arg Leu Cys His Gly Lys Phe Ser Ser Arg Ser Leu
 1             5             10             15
Arg Ser Ile Ser Glu Arg Ala Pro Gly Ala Ser Met Glu Arg Pro Ser
 20             25             30
Ala Glu Glu Arg Val Leu Val Arg Asp Phe Gln Arg Leu Leu Gly Val
 35             40             45
Ala Val Arg Gln Asp Pro Thr Leu Ser Pro Phe Val Cys Lys Ser Cys
 50             55             60
His Ala Gln Phe Tyr Gln Cys His Ser Leu Leu Lys Ser Phe Leu Gln
 65             70             75             80
Arg Val Asn Ala Ser Pro Ala Gly Arg Arg Lys Pro Cys Ala Lys Val
 85             90             95
Gly Ala Gln Pro Pro Thr Gly Ala Glu Glu Gly Ala Cys Leu Val Asp
 100            105            110
Leu Ile

```

<210> 1161

<211> 355

<212> DNA

<213> Homo sapiens

<400> 1161

```

ctgcacacac accaggccac gccacgagg acggccagtc agcatgcagc caatacaccc
 60
acagaggggat ggggagcagc cctcagtgcc agctccaaca ggcccactgc aggtcctgtc
 120
actgcaccca aggagctgcc ttccatttca cctgacattt ccactaaggg cccagcgttt
 180
atcattccag aagagcagca ggcagaacct tcacctcca agagctgcaa gtgcgctgtg
 240
gcaggaaaaa aagatctggc gtctgaagtc agctcctgct ctccaggaaa agagggacga
 300
tgacatagga cttgagcaaa atgagagccc cgtgatggga gagaacacct gatca
 355

```

<210> 1162

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1162

```

Met Gln Pro Ile His Pro Gln Arg Asp Gly Glu Gln Pro Ser Val Pro
 1             5             10             15
Ala Pro Thr Gly Pro Leu Gln Val Leu Ser Leu His Pro Arg Ser Cys
 20             25             30
Leu Pro Phe His Leu Thr Phe Pro Leu Arg Ala Gln Arg Leu Ser Phe
 35             40             45
Gln Lys Ser Ser Arg Gln Asn Leu His Leu Pro Arg Ala Ala Ser Ala

```

```

      50              55              60
Leu Trp Gln Glu Lys Lys Ile Trp Arg Leu Lys Ser Ala Pro Ala Leu
65              70              75              80
Gln Glu Lys Arg Asp Asp Ile Gly Leu Glu Gln Asn Glu Ser Pro
      85              90              95
Val Met Gly Glu Asn Thr
      100

```

<210> 1163
 <211> 466
 <212> DNA
 <213> Homo sapiens

```

<400> 1163
ngcgcgccag gaagcgggag gtcagctgta caccacagggt aatagaacct ctaccctcag
60
aggaggtcaaa gagaaggcag aactatggca ggaaagctcc ggaagtccca catccctgga
120
gtgagcatctt ggcagctggt ggaggagatc cctgaaggct gcagcacgcc ggactttgag
180
cagaagccccg tcacctcggc tctgccagag gggaaaaatg ctgtcttttcg ggctgtggtc
240
tgtggggagc ccaggcccgga ggtgcgttgg cagaactcca aaggtgacct cagtgtattcc
300
agcaagtaca agatctcctc cagcctctggc agcaaggagc acgtgctgca gatcaacaag
360
ctgacaggcg aggacacgga tctgtaccac tgcacagcag taaatgcgta cggagaggcc
420
gcttgctcag tgagactcac cgtcatcgaa gttggctttc ggaaga
466

```

<210> 1164
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 1164
Met Ala Gly Lys Leu Arg Lys Ser His Ile Pro Gly Val Ser Ile Trp
1      5      10      15
Gln Leu Val Glu Glu Ile Pro Glu Gly Cys Ser Thr Pro Asp Phe Glu
20     25     30
Gln Lys Pro Val Thr Ser Ala Leu Pro Glu Gly Lys Asn Ala Val Phe
35     40     45
Arg Ala Val Val Cys Gly Glu Pro Arg Pro Glu Val Arg Trp Gln Asn
50     55     60
Ser Lys Gly Asp Leu Ser Asp Ser Ser Lys Tyr Lys Ile Ser Ser Ser
65     70     75     80
Pro Gly Ser Lys Glu His Val Leu Gln Ile Asn Lys Leu Thr Gly Glu
85     90     95
Asp Thr Asp Leu Tyr His Cys Thr Ala Val Asn Ala Tyr Gly Glu Ala
100    105    110
Ala Cys Ser Val Arg Leu Thr Val Ile Glu Val Gly Phe Arg Lys
115    120    125

```

<210> 1165
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 1165
 tgggtgggttc cggacacana aaatcacgtg ttgaaccgaa ttccaggcat ggtgaaaggc
 60
 tgcttttagta aagtccttgt tgagccgcgt ctgctcaagc tcaacttgac nattatgtgt
 120
 ctgcacattc tgctgatgtc caggttcgtg gccctgcccc gtcagttggc tgcagcagga
 180
 ttccccgcgc ctgaacactg gaaagtgtat ctggtgacga tgctcatctc cttcgtctcc
 240
 gttgtccctt tcattatcta tgcagaagtg aaacgccga tgaagcgcgt attcctgacg
 300
 tgtgttgccg tgctgttgat tgccgaaatc gtactatggg gtcctggccc acactctctg
 360
 gaactggtca tcggcgtaga gcttttcttc ctgccttta atctcatgga agcc
 414

<210> 1166
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 1166
 Trp Val Val Pro Asp Thr Xaa Asn His Val Leu Asn Arg Ile Ser Gly
 1 5 10 15
 Met Val Lys Gly Cys Phe Ser Lys Val Leu Val Glu Pro Arg Leu Leu
 20 25 30
 Lys Leu Asn Leu Thr Ile Met Cys Leu His Ile Leu Leu Met Ser Thr
 35 40 45
 Phe Val Ala Leu Pro Gly Gln Leu Ala Ala Ala Gly Phe Pro Ala Ala
 50 55 60
 Glu His Trp Lys Val Tyr Leu Val Thr Met Leu Ile Ser Phe Val Ser
 65 70 75 80
 Val Val Pro Phe Ile Ile Tyr Ala Glu Val Lys Arg Arg Met Lys Arg
 85 90 95
 Val Phe Leu Thr Cys Val Ala Leu Leu Leu Ile Ala Glu Ile Val Leu
 100 105 110
 Trp Gly Ser Gly Pro His Phe Trp Glu Leu Val Ile Gly Val Gln Leu
 115 120 125
 Phe Phe Leu Ala Phe Asn Leu Met Glu Ala
 130 135

<210> 1167
 <211> 464
 <212> DNA
 <213> Homo sapiens

<400> 1167
 gtcgaccccc tgggcaagag tcgcggcccc tgacgataac ttcaccccgc cggccttgag
 60

ctgttgggac cggctggcta aggcctgggc accggtagcg gcctgggtga taccctcatg
 120
 tagccgggtg acctgcctga ccatcttcgg caaacaccatg cgcagttgtg tggtaactc
 180
 attgacccct cgagacagtc gtgaggaacc gtcagcaagt tcgtcgatgc cgtcgtcgat
 240
 gctcttgcca gagttcggat ccttgatcgc catcgccctg acggccaccc ccgaccagc
 300
 ccgcacgccc agggcgatcc catcggtcat cgcgtcgcgg acgatgggta ccaggtcgtg
 360
 gcattcctgc gcggtgtggc ttgcacgca tcgacgcagg aagtcagcct cgccccggga
 420
 cagggccttc ttactaagtt ccgcgggtttt ctttcccgac gcgt
 464

<210> 1168

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1168

Met	Thr	Asp	Gly	Tyr	Ala	Leu	Gly	Val	Arg	Ala	Gly	Ser	Gly	Val	Ala
1			5					10					15		
Val	Lys	Ala	Met	Ala	Ile	Lys	Asp	Pro	Asn	Ser	Gly	Lys	Ser	Ile	Asp
			20					25					30		
Asp	Gly	Ile	Asp	Glu	Leu	Ala	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Arg	Gly
			35				40					45			
Val	Asn	Glu	Phe	Thr	Thr	Gln	Leu	Arg	Thr	Gly	Leu	Pro	Lys	Met	Val
			50			55					60				
Arg	Gln	Val	Thr	Arg	Leu	His	Glu	Gly	Ile	His	Gln	Ala	Ala	Thr	Gly
65					70					75				80	
Ala	Gln	Ala	Leu	Ala	Ser	Arg	Ser	Gln	Gln	Leu	Lys	Ala	Gly	Gly	Val
			85							90				95	
Lys	Leu	Ser	Ser	Gly	Ala	Ala	Thr	Leu	Ala	His	Gly	Val	Asp		
			100					105					110		

<210> 1169

<211> 486

<212> DNA

<213> Homo sapiens

<400> 1169

nacgcgtgaa gggagcagaa cggacaccag ttactagtgg ctctgggtcgg ggacagcctc
 60
 ctagagcctt tctggccaat gggaacagga atagcccggg gctttctagc tgctatggac
 120
 tctgctcgga tgggtccgaag ttggtctcta ggaacgagcc ctttggaagt gctggcagag
 180
 agggaaaagta ttacaggtt gctgcctcag accaccctg agaattgtgag taagaacttc
 240
 agccagtaca gtatcgaccc tgtcactcgg tatcccaata tcaacgtcaa cttcctccgg
 300
 ccaagccagg tgcgccattt atatgatact ggcgaaacaa aagatattca cctggaaaatg
 360

gagagcctgg tgaattcccc aaccaccccc aaattgactc gcaatgagtc tgtagctcgt
 420
 tcaagcaaac tgctgggttg gtgccagagg cagacagatg gctatgcagg ggtaaacgtg
 480
 acagat
 486

<210> 1170
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1170
 Arg Glu Gln Asn Gly His Gln Leu Leu Val Ala Leu Val Gly Asp Ser
 1 5 10 15
 Leu Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Ile Ala Arg Gly Phe
 20 25 30
 Leu Ala Ala Met Asp Ser Ala Trp Met Val Arg Ser Trp Ser Leu Gly
 35 40 45
 Thr Ser Pro Leu Glu Val Leu Ala Glu Arg Glu Ser Ile Tyr Arg Leu
 50 55 60
 Leu Pro Gln Thr Thr Pro Glu Asn Val Ser Lys Asn Phe Ser Gln Tyr
 65 70 75 80
 Ser Ile Asp Pro Val Thr Arg Tyr Pro Asn Ile Asn Val Asn Phe Leu
 85 90 95
 Arg Pro Ser Gln Val Arg His Leu Tyr Asp Thr Gly Glu Thr Lys Asp
 100 105 110
 Ile His Leu Glu Met Glu Ser Leu Val Asn Ser Arg Thr Pro Lys
 115 120 125
 Leu Thr Arg Asn Glu Ser Val Ala Arg Ser Ser Lys Leu Leu Gly Trp
 130 135 140
 Cys Gln Arg Gln Thr Asp Gly Tyr Ala Gly Val Asn Val Thr Asp
 145 150 155

<210> 1171
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 1171
 acgcgttcaa caaagcacag aaccggagat gcagtgggag ccgagagcag gaagcgcgga
 60
 ggacgcgcga ggtgctggcg ctgcccgagg ccccggtcca agtggggccc atagcagccg
 120
 actcgctaga cctcccaaaa acgcacacca cgcgcgacca ggaccgagag gcccgcacgg
 180
 ccctgctagg ccacaaacac tccactgtct ccagggtaaa agacaaacac agcctcgctt
 240
 gtcctcccaa gagtacaacc tctgtctgat gaaaaacaaa cgaccagag aggaggcagc
 300
 tgccgggaca ctgcaggctg ggcccgcgc gcccttgagg ggcaggtcaa aatccccgaa
 360
 caggcacagt gttcaggctg attgactgtc ccaggccagg gcgcctcaa ctgccagagc
 420

acctcctac
429

<210> 1172
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1172
Met Gln Trp Glu Pro Arg Ala Gly Ser Ala Glu Ala Ala Pro Gly Ala
1 5 10 15
Gly Ala Ala Arg Gly Pro Val Pro Ser Gly Ala His Ser Ser Arg Leu
20 25 30
Ala Arg Pro Ser Gln Asn Ala His His Ala Arg Pro Gly Pro Arg Gly
35 40 45
Pro His Gly Pro Ala Arg Pro Gln Thr Leu His Cys Leu Gln Gly Lys
50 55 60
Arg Gln Thr Gln Pro Arg Leu Ser Leu Gln Glu Tyr Asn Leu Cys Leu
65 70 75 80
Met Lys Asn Lys Arg Pro Arg Glu Glu Ala Ala Gly Thr Leu Gln
85 90 95
Ala Gly Pro Ala Ala Pro Leu Glu Gly Arg Ser Lys Ser Arg Asn Arg
100 105 110
His Ser Val Gln Ala Asp
115

<210> 1173
<211> 435
<212> DNA
<213> Homo sapiens

<400> 1173
cgcggtcaatg acgacggcga gcattctgcc gagcaggtga tgcgagccac ccgcggtgct
60
ggagctgggg cggaggccaa gcgtcgcatc atcttgggta cctatgcctt gtcgggtggg
120
tactatgacg cctactacgg ctccggctcag aaagtccgta ccctcatcca acgcgacttc
180
gagaaagcat ggcagatgtg cgatgtgctc gtgtcacccg ccacgccaac gactgccttc
240
cggtgggtg agegtactgc tgacccgatg gcgatgtacc gctccgatct atgcacggtc
300
ccggccaata tggccggaag tccgcgagga tctttcccca tcggtctatc agagaccgac
360
ggcatgcccc tcggcatgca ggtgatggcg ccaatcatgg cggacgatcg aatctaccga
420
gttggggcgc ctcta
435

<210> 1174
<211> 145
<212> PRT
<213> Homo sapiens

<400> 1174

```

Arg Val Asn Asp Asp Gly Glu His Ser Ala Glu Gln Val Met Arg Ala
1          5          10          15
Thr Arg Gly Ala Gly Leu Gly Ala Glu Ala Lys Arg Arg Ile Ile Leu
20          25          30
Gly Thr Tyr Ala Leu Ser Ala Gly Tyr Tyr Asp Ala Tyr Tyr Gly Ser
35          40          45
Ala Gln Lys Val Arg Thr Leu Ile Gln Arg Asp Phe Glu Lys Ala Trp
50          55          60
Gln Met Cys Asp Val Leu Val Ser Pro Ala Thr Thr Thr Ala Phe
65          70          75          80
Arg Leu Gly Glu Arg Thr Ala Asp Pro Met Ala Met Tyr Arg Ser Asp
85          90          95
Leu Cys Thr Val Pro Ala Asn Met Ala Gly Ser Pro Ala Gly Ser Phe
100          105          110
Pro Ile Gly Leu Ser Glu Thr Asp Gly Met Pro Val Gly Met Gln Val
115          120          125
Met Ala Pro Ile Met Ala Asp Asp Arg Ile Tyr Arg Val Gly Ala Ala
130          135          140
Leu
145

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<210> 1175

<211> 729

<212> DNA

<213> Homo sapiens

<400> 1175

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gacgcgactg caatccaccc acatctactt gatatgaaaa ttgggtcaagg caaatatgag
60
caggggttct ttccaaagt acagtccgat gtcttgcaa caggaccaac cagtaacaat
120
cgctgggttaa gtccgagtgc cactgcacag cgcaggaaag gacgccttcg ccagcattct
180
gagcatgttg ggctggacaa cgacttgagg gagaaatata tgcaagaggc acgaagttaa
240
ggaaaaaac tgaggcaacc caaactgtca gacctctctc ctgcagttat tgcaagagcc
300
aactgtaaat tcgtagaagg cttattaaaa gaatgtagaa ataagacaaa gcgcagtgtg
360
gtggagaaga tgggacatga agcgggtgaa cttggccatg gagaagcaaa catcaccggc
420
ctggaggaga acaccttgat ccgcagcctt tgtgacctgc tggagaggat atggagccat
480
ggcttcgagg tcaagcaggg gaagtcggtt ttgtggtcac atttaattcc ttttcaggac
540
agagaagaga accaagagcc ccttcagaaa tcaccagtgt ccttcggacc agaaagaaaa
600
aaatctgact caggagttaa gttgccaacg ctcagggtct ctcttattca ggacatgagg
660
catattcaaa acatgagtga gatcaagact gatgttgac gagctcgggc gtggataaga
720
ctgtctcta
729

```

<210> 1176
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 1176
 Asp Arg Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln
 1 5 10 15
 Gly Lys Tyr Glu Gln Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu
 20 25 30
 Ala Thr Gly Pro Thr Ser Asn Asn Arg Trp Val Ser Arg Ser Ala Thr
 35 40 45
 Ala Gln Arg Arg Lys Gly Arg Leu Arg Gln His Ser Glu His Val Gly
 50 55 60
 Leu Asp Asn Asp Leu Arg Glu Lys Tyr Met Gln Glu Ala Arg Ser Leu
 65 70 75 80
 Gly Lys Asn Leu Arg Gln Pro Lys Leu Ser Asp Leu Ser Pro Ala Val
 85 90 95
 Ile Ala Gln Thr Asn Cys Lys Phe Val Glu Gly Leu Leu Lys Glu Cys
 100 105 110
 Arg Asn Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly His Glu Ala
 115 120 125
 Val Glu Leu Gly His Gly Glu Ala Asn Ile Thr Gly Leu Glu Glu Asn
 130 135 140
 Thr Leu Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His
 145 150 155 160
 Gly Leu Gln Val Lys Gln Gly Lys Ser Val Leu Trp Ser His Leu Ile
 165 170 175
 Pro Phe Gln Asp Arg Glu Glu Asn Gln Glu Pro Leu Ala Glu Ser Pro
 180 185 190
 Val Ala Leu Gly Pro Glu Arg Lys Lys Ser Asp Ser Gly Val Met Leu
 195 200 205
 Pro Thr Leu Arg Val Ser Leu Ile Gln Asp Met Arg His Ile Gln Asn
 210 215 220
 Met Ser Glu Ile Lys Thr Asp Val Gly Arg Ala Arg Ala Trp Ile Arg
 225 230 235 240
 Leu Ser Leu

<210> 1177
 <211> 581
 <212> DNA
 <213> Homo sapiens

<400> 1177
 acgcgtgatg agttgcgcga gaccagcaac tgcagccgaa tacagttttc ttgtgtaccc
 60
 cgtcgacacag ctgcgagagg tgggcattgc cgagtggagg aacgatgtct aaggcggaaa
 120
 gctcatcctc ggcagacggg aagactttgt cgtcggggat gttgtcaatg agagcgggga
 180
 cgtcgatctc ggtactgccc atggcgtcat gaaggatcgc gcgatacggg gcgacgaccc
 240

cgatgagggc gtcgtcgaat ccagcgatga tcgatacttc tctcggtagc acgtccgtgg
 300
 ccaacaggtg gtcgacttgg gcgggggcta gccatgtaat tgttccgagc acatggaggg
 360
 tggctgccag gaggcggatg gccgggttctg gggcatcttt ggagatcttc agccggacat
 420
 cagtggggcag tccggccggg acttggcaga gggcctgggc gggatgggag cgctggggcga
 480
 cgacgaaacg ccccgacgcc gtaacgccgt gggcttgag atccagggtc cacttctctg
 540
 ggctttcacc ggcagagatc atgggtgtga ccaccattgt g
 581

<210> 1178

<211> 192

<212> PRT

<213> Homo sapiens

<400> 1178

Met	Val	Val	His	Thr	Met	Ile	Ser	Ala	Gly	Glu	Ser	Pro	Glu	Lys	Trp
1				5					10				15		
Thr	Cys	Asp	Leu	Gln	Ala	His	Gly	Val	Thr	Ala	Ser	Gly	Arg	Phe	Val
			20				25					30			
Val	Ala	Gln	Arg	Ser	His	Pro	Ala	Gln	Ala	Leu	Cys	Gln	Val	Pro	Ala
	35					40				45					
Gly	Leu	Pro	Thr	Asp	Val	Arg	Leu	Lys	Ile	Ser	Lys	Asp	Ala	Pro	Glu
	50				55					60					
Pro	Ala	Ile	Arg	Leu	Leu	Ala	Ala	Thr	Leu	His	Val	Leu	Gly	Thr	Ile
65				70				75						80	
Thr	Trp	Leu	Ala	Pro	Ala	Gln	Val	Asp	His	Leu	Leu	Ala	Thr	Asp	Val
			85					90					95		
Leu	Pro	Arg	Glu	Val	Ser	Ile	Ile	Ala	Gly	Phe	Asp	Asp	Ala	Leu	Ile
			100					105					110		
Gly	Val	Val	Ala	Pro	Tyr	Arg	Ala	Ile	Leu	His	Asp	Ala	Met	Gly	Ser
	115					120					125				
Thr	Glu	Ile	Asp	Val	Pro	Ala	Leu	Ile	Asp	Asn	Ile	Pro	Asp	Asp	Lys
	130				135					140					
Val	Phe	Pro	Ser	Ala	Glu	Asp	Glu	Leu	Ser	Ala	Leu	Asp	Ile	Val	Ala
145				150					155					160	
Ser	Leu	Gly	Asn	Ala	His	Leu	Ser	Gln	Leu	Cys	Asp	Gly	Val	His	Lys
			165						170				175		
Lys	Thr	Val	Phe	Gly	Cys	Ser	Cys	Trp	Ser	Arg	Ala	Thr	His	His	Ala
			180					185					190		

<210> 1179

<211> 597

<212> DNA

<213> Homo sapiens

<400> 1179

gtgcactttc tggcttctaa ctgtggcccc agccctgact ccttgagggtg ctctgtgct
 60
 gattggggct tctggacatg ctgccacaag atgtctggaa actccagggg gcacctgccg
 120

agaccctgcc ctgggaacgg ccggaagaat cccaaaacat gagattccgg tgcagctgag
 180
 ccccgccaat tcattgtctc ttctcagtc cttctgaaggc tgcatttggc aatgtgaccc
 240
 tcgggggtggg gaaggcatca gaggaatata ggctatggga cgccagaggc agcgtcctgg
 300
 ggacaaagcc cacttcttcc catgccaggc gcttctctcat ggacccagca tgggtggacgt
 360
 ggccctcaga cgtccatggg tgggtggggga ggcacgtgct gtttggccct gtctctgctc
 420
 agagtctcat aggaagatgc atgggtccaca caacagtggc tcggcagggg gtccaggctt
 480
 cccctcccaa ccagtgggtg tgagacgctt gggtttataac ccaagatccc ttgtccatt
 540
 ggtgacctct gaattcccca cctcccgagg cactgtcatg gcctctacct gacgcgt
 597

<210> 1180
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1180
 Met Gly Arg Gln Arg Gln Arg Pro Gly Asp Lys Ala His Phe Phe Pro
 1 5 10 15
 Cys Pro Gly Leu Pro His Gly Pro Ser Met Val Asp Val Ala Leu Arg
 20 25 30
 Arg Pro Trp Val Val Gly Glu Ala Arg Ala Val Trp Pro Cys Leu Cys
 35 40 45
 Ser Glu Ser His Arg Lys Met His Gly Pro His Asn Ser Glu Ser Ala
 50 55 60
 Gly Ser Pro Gly Phe Pro Ser Gln Pro Val Val Leu Arg Arg Leu Val
 65 70 75 80
 Tyr Asn Pro Arg Ser Leu Val Pro Leu Val Pro Pro Glu Ser Pro Thr
 85 90 95
 Ser Arg Gly Thr Cys Met Ala Ser Thr
 100 105

<210> 1181
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 1181
 gtgcactacc tcgatgtttc cccgcgtcag atgggtctccg tggtactctgc catgattccg
 60
 ttctctgagc acgacgacgc taacctgtgc ctgatgggtg cgaacatgca gcgtcaggct
 120
 gtgccgtgct tgcgttcgga ggctccgttc gtcgggtaccg gtatggagca gcgtgctgct
 180
 tacgacgcgg cgcatgtcat tgtcgcttcg gccacagggtg tgggtcgagac cgtgtcggga
 240
 ggcttcatca ccatcatgga cgatgagggc cagcgccaca cctacctgct gcgcaagttc
 300

gagcgaccca accagggcac ctgctacaac cagaagccac tgttgacgag gg
352

<210> 1182

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1182

```
Val Asp Tyr Leu Asp Val Ser Pro Arg Gln Met Val Ser Val Ala Thr
 1             5             10             15
Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met
          20             25             30
Gly Ala Asn Met Gln Arg Gln Ala Val Pro Leu Leu Arg Ser Glu Ala
          35             40             45
Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly
          50             55             60
Asp Val Ile Val Ala Ser Ala Thr Gly Val Val Glu Thr Val Ser Ala
65             70             75             80
Gly Phe Ile Thr Ile Met Asp Asp Glu Gln Arg His Thr Tyr Leu
          85             90             95
Leu Arg Lys Phe Glu Arg Thr Asn Gln Gly Thr Cys Tyr Asn Gln Lys
          100            105            110
Pro Leu Leu Thr Arg
          115
```

<210> 1183

<211> 432

<212> DNA

<213> Homo sapiens

<400> 1183

```
gacccctctcg ggcgctgggc caagcgctgt gtgaggccgt cctctcctgc agaaccgcg
60
cctctctgcc cctgccgct cactgttct gtcctgctca cctctccag gaagcctggc
120
tgccctctc catgctgatg ggcgtggccc ttgtccctgc agccatgcat tgacctccgt
180
ggctcctgga ggccaggcca cgtcctcatc ccctctgggt gagtgcaggg cacagcctgg
240
gtgcgtgggg ccgtggcggc tccgaggcgc caccgctgtg tcctctcatg agtgggtggc
300
gtccaggtct gtcctgggct ggctgcgagg aggaggttg cctgcgcggg ccatgtgcgt
360
gacagtggag acatcgccag cctctgctt gcacagctga cggcagcccc tctctctcca
420
gccatgtccc ca
432
```

<210> 1184

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1184

```

Met Ala Gly Glu Arg Gly Ala Ala Val Ser Cys Ala Ser Arg Arg Leu
 1           5           10           15
Ala Met Ser Pro Leu Ser Arg Thr Trp Pro Arg Glu Ala Asn Leu Leu
          20           25           30
Leu Ala Ala Ser Pro Gly Gln Thr Trp Thr Ala Pro Thr His Glu Arg
          35           40           45
Thr Gln Arg Trp Arg Leu Gly Ala Ala Thr Ala Pro Arg Thr Gln Ala
          50           55           60
Val Pro Leu Thr His Pro Glu Gly Met Arg Thr Trp Pro Gly Leu Gln
          65           70           75           80
Glu Pro Arg Arg Ser Met His Gly Cys Arg Asp Lys Gly His Ala His
          85           90           95
Gln His Gly Glu Gly Gln Ala Gly Phe Leu Glu Glu Val Ser Arg Thr
          100          105          110
Glu Gln Val Ser Gly Gln Gly Arg Arg Gly Ser Ala Gly Glu
          115          120          125
Asp Gly Leu Thr Thr Arg Leu Asp Gln Arg Pro Glu Gly
          130          135          140

```

<210> 1185

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1185

```

accggtgaat ttggccttaa cagcgatgga actcctggcc catcttatga acctggcatg
60
gaattacgcg gcaaatatgt attgttgggt gaagggtgtac ggggctctct atctaaacaa
120
gtcatcaata aataccaatt atccgagggt catgaaccac aaaagttcgg ccttggttta
180
aaagaaattt gggaaataga cccagaaaaa cacaagaaga gcagagtcag tcataccatg
240
ggctggccat taaatggcaa tgctggcggc ggttctttta ttatcatgc agaaaaaat
300
caagtcttta tcggctttgt ggtgcatctt aattacgcca acccttacct atccccttac
360
caagaatttc aacgctttaa acaccatccg attatcgagg agctattaac tggcggtaaa
420
cgc
423

```

<210> 1186

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1186

```

Thr Gly Glu Phe Gly Leu Asn Ser Asp Gly Thr Pro Gly Pro Ser Tyr
 1           5           10           15
Glu Pro Gly Met Glu Leu Arg Gly Lys Tyr Val Leu Leu Gly Glu Gly
          20           25           30
Val Arg Gly Ser Leu Ser Lys Gln Val Ile Asn Lys Tyr Gln Leu Ser

```

```

      35              40              45
Glu Gly His Glu Pro Gln Lys Phe Gly Leu Gly Leu Lys Glu Ile Trp
  50              55              60
Glu Ile Asp Pro Glu Lys His Lys Glu Gly Arg Val Ser His Thr Met
  65              70              75
Gly Trp Pro Leu Asn Gly Asn Ala Gly Gly Gly Ser Phe Ile Tyr His
      85              90              95
Ala Glu Asn Asn Gln Val Phe Ile Gly Phe Val Val His Leu Asn Tyr
      100              105              110
Ala Asn Pro Tyr Leu Ser Pro Tyr Gln Glu Phe Gln Arg Phe Lys His
      115              120              125
His Pro Ile Ile Ala Glu Leu Leu Thr Gly Gly Lys Arg
      130              135              140

```

<210> 1187

<211> 387

<212> DNA

<213> Homo sapiens

<400> 1187

```

acgcgtgctg gtgagtttaa attgaatgct gatggtaatt tggtagcagaa ttcaggggct
  60
aagggtccagg gctataatgc aatagatggc atagtcggtg ggaacttaga agatatggta
  120
gtaccacctg ctcgaatttc tctcaagca acatcaagtg ttgattttaa agtgaatcct
  180
aattccgaag gtgaggatgt gccgccttat attcgagcgg accttgatcc agccaatcca
  240
gatacttatg actatactca gacccaaacg gttgcggatg ggagtggttaa taatcattta
  300
attagttatt actatgctaa aagtgatgta gcaaatacct atcaggttta tgccacggta
  360
gatgggaagt cgactgatga taccggt
  387

```

<210> 1188

<211> 129

<212> PRT

<213> Homo sapiens

<400> 1188

```

Thr Arg Ala Gly Glu Phe Lys Leu Asn Ala Asp Gly Asn Leu Val Thr
  1              5              10              15
Asn Ser Gly Ala Lys Val Gln Gly Tyr Asn Ala Ile Asp Gly Ile Val
      20              25              30
Gly Gly Asn Leu Glu Asp Met Val Val Pro Thr Ala Arg Ile Ser Pro
      35              40              45
Gln Ala Thr Ser Ser Val Asp Leu Lys Val Asn Leu Asn Ser Glu Gly
      50              55              60
Glu Asp Val Pro Pro Tyr Ile Arg Ala Asp Phe Asp Pro Ala Asn Pro
      65              70              75              80
Asp Thr Tyr Asp Tyr Thr Gln Thr Gln Thr Val Ala Asp Gly Ser Gly
      85              90              95
Asn Asn His Leu Ile Ser Tyr Tyr Tyr Ala Lys Ser Asp Val Ala Asn

```

```

                100                105                110
Thr Tyr Gln Val Tyr Ala Thr Val Asp Gly Lys Ser Thr Asp Asp Thr
      115                120                125
Gly

```

<210> 1189
 <211> 330
 <212> DNA
 <213> Homo sapiens

```

<400> 1189
tcgatcgccg accgcccggg ccttgccccc ggcgatgatcg gtggcctgtt ggcagcacc
60
ctgggtgctg gtttcattgg cgccatcggt gcaggtttcc tggccggtta cagcgccaag
120
gccattgccc gctgggcacg gctgcccagc agcctggatg cgctcaaacc gattctgatc
180
attctcgtcg tggccagcct gtctactggg ttggtgatga tctactgggt cggccagccg
240
gtggcgggcca tgctcggagg cctgacacac ttctctgaca gcattgggtac caccaacgcc
300
attctcctgg gcntgttgct cggcggttag
330

```

<210> 1190
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 1190
Ser Ile Ala Asp Arg Pro Gly Leu Ala Pro Gly Met Ile Gly Gly Leu
  1             5             10             15
Leu Ala Ser Thr Leu Gly Ala Gly Phe Ile Gly Gly Ile Val Ala Gly
      20             25             30
Phe Leu Ala Gly Tyr Ser Ala Lys Ala Ile Ala Arg Trp Ala Arg Leu
      35             40             45
Pro Ser Ser Leu Asp Ala Leu Lys Pro Ile Leu Ile Ile Ser Leu Leu
      50             55             60
Ala Ser Leu Phe Thr Gly Leu Val Met Ile Tyr Val Val Gly Gln Pro
      65             70             75             80
Val Ala Ala Met Leu Gly Gly Leu Thr His Phe Leu Asp Ser Met Gly
      85             90             95
Thr Thr Asn Ala Ile Leu Leu Gly Xaa Leu Leu Gly Gly
      100             105

```

<210> 1191
 <211> 351
 <212> DNA
 <213> Homo sapiens

```

<400> 1191
cggccgacga tgtgcggtga gcaagagatt tggagagcca tgatgacgtc agcagacaaa
60

```

gcaggaggacta acggacagac catgcagaca ccgcccgttg tgctgccgca ggactgggag
 120
 gcagcccgtc agcaactgct cgtgaaggaa aaggccgata cccgtgcccc cgacgcactc
 180
 gccgcccgaac ggaggcgcat gccgtggatg gaagtgcaca aaacctacgc attcgaggcg
 240
 cccctggggca aggccagtct gctcgatctg ttccaggggcc ggaagcagct gatcctgtac
 300
 cgggccttctc tcgagccggg cgtgttcggc tggcccgacc atgcctgccg c
 351

<210> 1192

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1192

Met	Cys	Gly	Glu	Gln	Glu	Ile	Trp	Arg	Ala	Met	Met	Thr	Ser	Ala	Asp
1				5					10					15	
Lys	Ala	Gly	Thr	Asn	Gly	Gln	Thr	Met	Gln	Thr	Pro	Pro	Val	Val	Ser
			20					25					30		
Pro	Gln	Asp	Trp	Glu	Ala	Ala	Arg	Gln	Gln	Leu	Leu	Val	Lys	Glu	Lys
			35				40					45			
Ala	His	Thr	Arg	Ala	Arg	Asp	Ala	Leu	Ala	Ala	Glu	Arg	Arg	Arg	Met
	50				55					60					
Pro	Trp	Met	Glu	Val	Thr	Lys	Thr	Tyr	Ala	Phe	Glu	Ala	Pro	Ser	Gly
65					70				75					80	
Lys	Ala	Ser	Leu	Leu	Asp	Leu	Phe	Gln	Gly	Arg	Lys	Gln	Leu	Ile	Leu
			85					90					95		
Tyr	Arg	Ala	Phe	Phe	Glu	Pro	Gly	Val	Phe	Gly	Trp	Pro	Asp	His	Ala
			100				105						110		

Cys Arg

<210> 1193

<211> 722

<212> DNA

<213> Homo sapiens

<400> 1193

ggatcccagc ctccagatcc catcttgtag ctcttcttctc tctacactna ggttgctccc
 60
 cgacttagga cgcccagttt gtactcagtg tttgctcttt tatggcagag cctctgcact
 120
 cccagcctcc tggcccttc tgtacatgat ttcccttggt gccactccat gcatttttct
 180
 tggctcagga cttagtgggc ctccatggga cttgggtacct ctacttggtc cttctcggaa
 240
 tctgtaactt tgtgttcccc accattcttt cctttatgaa ccgatggtgc aacagcatga
 300
 ctacctgaaa ttcttagtca ctcccagctg ctttagtgga gggaaaaatgc ccacagcaca
 360
 ggaaatagtc ctgcccttcg agagaggcca ggggatggga gcgtgtccag agaaggcgga
 420

tgggttgatg aagggtggcc acagcgcccc ggaggaaggg gccagaacgc tctctgttct
 480
 gtcccatgag gaggattatg ttggtgtgtg tagtccctg gttcagagtt gtccagaaat
 540
 agctcagtgt aaggaacaat tttccaaaga tcaaaagagc tgtctcaaga tagcagtgcg
 600
 ttcccagccc ctacaggtgt atacagcaca aagggaggga ccccttagtg tggctgtcac
 660
 agagggaagt ggacgtcctg tggtttgacc ccaccagatg gctttagaga tctgggcccc
 720
 ag
 722

<210> 1194

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1194

Met	Val	Gln	Gln	His	Asp	Tyr	Leu	Lys	Phe	Leu	Val	Thr	Pro	Ser	Cys
1				5					10					15	
Phe	Ser	Gly	Gly	Lys	Met	Pro	Thr	Ala	Gln	Glu	Ile	Val	Leu	Pro	Phe
			20					25				30			
Glu	Arg	Gly	Gln	Gly	Met	Gly	Ala	Cys	Pro	Glu	Lys	Gly	Asp	Gly	Leu
		35					40				45				
Met	Lys	Gly	Gly	His	Ser	Ala	Arg	Glu	Glu	Gly	Ala	Arg	Thr	Leu	Ser
	50				55						60				
Val	Leu	Phe	His	Glu	Glu	Asp	Tyr	Val	Gly	Val	Cys	Ser	Pro	Leu	Val
65				70					75					80	
Gln	Ser	Cys	Pro	Glu	Ile	Ala	Gln	Cys	Lys	Glu	Gln	Phe	Ser	Lys	Asp
			85						90				95		
Gln	Lys	Ser	Cys	Leu	Lys	Ile	Ala	Val	Arg	Ser	Gln	Pro	Leu	Gln	Val
		100					105					110			
Tyr	Thr	Ala	Gln	Arg	Glu	Gly	Pro	Pro	Ser	Val	Ala	Val	Thr	Glu	Gly
	115					120					125				
Ser	Gly	Arg	Pro	Val	Val										
	130														

<210> 1195

<211> 391

<212> DNA

<213> Homo sapiens

<400> 1195

tctagagcat gatattccgc gggcgcgccc ggggtggactt tggttcgaga gtggaactaa
 60
 gtgagtaaat ggggcgggcg gggcagacgc gctcccagcc tcttgccgag agtgctgccc
 120
 ggtttcccgg gggcacggga gtgtgtctag gaggggaggg caggatccct cctcgagtcc
 180
 tgttctgaac aaaagaaaac gaggtgggtg gtgcttgaac ggcctgtgtt actctcgaga
 240
 tagccgaact ggtaggactc cggcgcgccc tatttatctt gattggctct gcctgaaggc
 300

aagcggttaat cccgtccaac ctgtatcact gcgaagagct cggtcgggag cgctttttgg
 360
 aaatgcagat tcttagcccc caccagatc t
 391

<210> 1196

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1196

Met Gly Ala Ala Arg Pro Asp Ala Leu Pro Ala Ser Trp Arg Glu Cys
 1 5 10 15
 Cys Pro Val Ser Arg Gly His Gly Ser Val Ser Arg Arg Gly Gly Gln
 20 25 30
 Asp Pro Ser Ser Ser Pro Val Leu Asn Lys Arg Lys Arg Gly Gly Trp
 35 40 45
 Cys Leu Asn Gly Pro Val Tyr Ser Ala Asp Ser Arg Thr Gly Arg Thr
 50 55 60
 Pro Ala Arg Pro Ile Tyr Leu Asp Trp Leu Cys Leu Lys Ala Ser Val
 65 70 75 80
 Asn Pro Val Gln Pro Val Ser Leu Arg Arg Ala Arg Ser Gly Ala Leu
 85 90 95
 Phe Gly Asn Ala Asp Ser
 100

<210> 1197

<211> 386

<212> DNA

<213> Homo sapiens

<400> 1197

acgcgtgatg atcatgaaaa tggtagacag cgtctagcag aagtcgcctc tgtgatgggc
 60
 tggcagcaag atgaaatcat cggttaacgta caaggggatg aaccttttct gcctgttgca
 120
 cttattcatg ccacgggttaa agcgttagcc gatgatgctg aatctgaaa ggccacgatt
 180
 gcctgtgcga ttgataacgt agcagagctg ttaaccctaa atgtagttaa agtcgtttgt
 240
 gatgaaaaac agcgcgcctt gtatttcagt cgtgcgccta tgccatggga ccgtaattgt
 300
 tttatggaaa aaacagacga tcaagcggtta ccagcggatt ttctctcggt gcgtcatatt
 360
 ggtccgtatg ttaccgcac gacatn
 386

<210> 1198

<211> 128

<212> PRT

<213> Homo sapiens

<400> 1198

Thr Arg Asp Asp His Glu Asn Gly Thr Glu Arg Leu Ala Glu Val Ala

```

      1           5           10           15
Ser Val Met Gly Trp Gln Gln Asp Glu Ile Ile Val Asn Val Gln Gly
      20           25           30
Asp Glu Pro Phe Leu Pro Val Ala Leu Ile His Ala Thr Val Lys Ala
      35           40           45
Leu Ala Asp Asp Ala Glu Ser Glu Met Ala Thr Ile Ala Cys Ala Ile
      50           55           60
Asp Asn Val Ala Glu Leu Phe Asn Pro Asn Val Val Lys Val Val Cys
      65           70           75           80
Asp Glu Lys Gln Arg Ala Leu Tyr Phe Ser Arg Ala Pro Met Pro Trp
      85           90           95
Asp Arg Asn Gly Phe Met Glu Lys Thr Asp Asp Gln Ala Leu Pro Ala
      100          105          110
Asp Phe Pro Ala Leu Arg His Ile Gly Pro Tyr Val Tyr Arg Thr Thr
      115          120          125

```

<210> 1199

<211> 318

<212> DNA

<213> Homo sapiens

<400> 1199

```

acgcgttcag cgctcatgtac agccccgggc cgggtcaattt gatgggcctc aatgccgggc
60
ttacgggcaa attcgctcgc tccagcggtt tctacatcgg cgtgggggtgc gcgatgctgc
120
tgatgggtcgg gctgggtggg ctcaccggcg aagcgatcat ctcccaggcg gcgctgccgt
180
atattttctt gattggcggg gtgtacacgc tgtacctcgc ctaccagggtg ttcaccgcac
240
gtaccgaagt ggatgacgcc ccaagcgcg ctcgccaagac cttgaccttc tggaatggcc
300
tggtgatcca gttgctcc
318

```

<210> 1200

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1200

```

Met Tyr Ser Pro Gly Pro Val Asn Leu Met Gly Leu Asn Ala Gly Leu
      1           5           10           15
Thr Gly Lys Leu Arg Arg Ser Ser Gly Phe Tyr Ile Gly Val Gly Cys
      20           25           30
Ala Met Leu Leu Met Val Gly Leu Val Gly Leu Thr Gly Glu Ala Ile
      35           40           45
Ile Ser Gln Ala Ala Leu Pro Tyr Ile Ser Leu Ile Gly Gly Val Tyr
      50           55           60
Thr Leu Tyr Leu Ala Tyr Gln Val Phe Thr Ala Arg Thr Glu Val Asp
      65           70           75           80
Asp Ala Pro Ser Ala Pro Ala Lys Thr Leu Thr Phe Trp Asn Gly Leu
      85           90           95
Val Ile Gln Leu Leu

```

100

<210> 1201
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 1201
 gtcgacgcac aactccagct ggtcgctccc aacagcccga acatccccct ttatcgcgat
 60
 atgacatccta ccgtgctgcg catggccaag gatgaccgca accgttggaa tgcaaaaatc
 120
 acgctgcagg cgatccgcga gctggataac gccttccgcg tgctggaaca gttcaagggc
 180
 cgccgcaagg tcacggtgtt tggtcggcg cgcacgccgg tcgaaagccc gctgtacgcc
 240
 ttggcaaggg aagtcggcac gctgctggcg caatccgacc tgatggtgat caccggcggt
 300
 ggccggcgga tcatggccgc tgcccacgag ggcgcaaggc ctggaacaca gcctgggggt
 360

<210> 1202
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1202
 Val Asp Ala Gln Leu Gln Leu Val Ala Pro Asn Ser Pro Asn Ile Pro
 1 5 10 15
 Leu Tyr Arg Asp Met Ile Leu Thr Val Leu Arg Met Ala Lys Asp Asp
 20 25 30
 Arg Asn Arg Trp Asn Ala Lys Ile Thr Leu Gln Ala Ile Arg Glu Leu
 35 40 45
 Asp Asn Ala Phe Arg Val Leu Glu Gln Phe Lys Gly Arg Arg Lys Val
 50 55 60
 Thr Val Phe Gly Ser Ala Arg Thr Pro Val Glu Ser Pro Leu Tyr Ala
 65 70 75 80
 Leu Ala Arg Glu Val Gly Thr Leu Leu Ala Gln Ser Asp Leu Met Val
 85 90 95
 Ile Thr Gly Gly Gly Gly Gly Ile Met Ala Ala Ala His Glu Gly Ala
 100 105 110
 Arg Ser Gly Thr Gln Pro Gly Gly
 115 120

<210> 1203
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 1203
 ccgcatatgg cagctcgact tcattcgacc agagttcttg gaacatttgg ctatcatgca
 60
 cctgagtatg caatgactgg acaacttagc tctaagagtg acgtttacag ttttggagtt
 120

ggtcttctgg agctcctgac tggagaaag cctgtggatc ttccattacc aagaggacag
 180
 caaagtcttg tgacatgggc aactccacgg ctttgtgaag ataaagttag gcaatgcgtt
 240
 gattcaagac ttggagtaga atatcctcct aaatccgttg caaagtttgc agctgttgct
 300
 gcactgtgtg tgcaatatga agctgacttt cgacccaaca tgagcatcgt ggtgaaggcg
 360
 cttcagcccc tgctgaatgc acgtgcatcc aacaaccctg gatgaatgaa tgaatgactg
 420
 ccgttgcttt tccctgacga gagtatctga atcagacaat catgtagcat tgaattc
 477

<210> 1204

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1204

Pro Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Thr Phe
 1 5 10 15
 Gly Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Ser Ser Lys
 20 25 30
 Ser Asp Val Tyr Ser Phe Gly Val Gly Leu Leu Glu Leu Leu Thr Gly
 35 40 45
 Arg Lys Pro Val Asp Leu Pro Leu Pro Arg Gly Gln Gln Ser Leu Val
 50 55 60
 Thr Trp Ala Thr Pro Arg Leu Cys Glu Asp Lys Val Arg Gln Cys Val
 65 70 75 80
 Asp Ser Arg Leu Gly Val Glu Tyr Pro Pro Lys Ser Val Ala Lys Phe
 85 90 95
 Ala Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ala Asp Phe Arg Pro
 100 105 110
 Asn Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Asn Ala Arg
 115 120 125
 Ala Ser Asn Asn Pro Gly
 130

<210> 1205

<211> 407

<212> DNA

<213> Homo sapiens

<400> 1205

acgcgttgcc attgaagact ggcaattaca cgatttacac atcattgatg ctgcagttga
 60
 tgtgcacagg gaaacactag ctaccgtgca gcaggaaatg atgggagaaa tcagccatgg
 120
 taacaagaac caagccatcc tggacacaga cggccggggg tgtgcgaacg gaacgttagt
 180
 ctatcaatgt gttgcggaac gattcaaggg atgctggccc ccccatcac ttgcccaatc
 240
 aagatgtgga ggggaatctgt ctgcgcagaa cctggatctc gtggtgtgac gacgttgtcc
 300

ccttctcgct cggacgccgc tcatgctccg ccacgtcgct gagcgagtga caaggtatcc
 360
 tgggaccatg cgtatggttt caactgaagc gctggcgaat cgtaaan
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<210> 1206

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1206

Met Met Gly Glu Ile Ser His Gly Asn Lys Asn Gln Ala Ile Leu Asp
 1 5 10 15
 Thr Asp Gly Arg Gly Cys Ala Asn Gly Thr Leu Val Tyr Gln Cys Val
 20 25 30
 Ala Glu Arg Phe Lys Gly Cys Trp Pro Pro Ser Leu Ala Gln Ser
 35 40 45
 Arg Cys Gly Gly Asn Leu Ser Ala Gln Asn Leu Asp Leu Val Val Val
 50 55 60
 Arg Arg Cys Pro Leu Leu Ala Arg Thr Pro Leu Met Leu Arg His Val
 65 70 75 80
 Ala Glu Arg Val Thr Arg Tyr Pro Gly Thr Met Arg Met Val Ser Thr
 85 90 95
 Glu Ala Leu Ala Asn Arg Lys
 100

<210> 1207

<211> 292

<212> DNA

<213> Homo sapiens

<400> 1207

gctagcatgt cacttttttc ttcagtagat ggcaactggag agacattgca ggatgaagag
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 120
 cagggggtgct caccacctag tgagtttcag ggacactcca catgtcccag caagtcttat
 180
 cagcatctta gctggcttct caacaagact cagtggcacc cctgtggatg tctcccatca
 240
 agtttcatta gtgccccagg gggagactcc cagaaaagttt cagcagcacc ac
 292

<210> 1208

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1208

Met Ser Leu Phe Ser Ser Val Asp Gly Thr Gly Glu Thr Leu Gln Asp
 1 5 10 15
 Glu Glu Ala Cys Leu His Ser Tyr Val Leu Ser Arg Pro Cys Phe Ser
 20 25 30
 Ser His Val Trp Asp Asn Gln Gly Cys Ser Pro Pro Ser Glu Phe Gln

130

135

140

<210> 1211
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 1211
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 agagccgaag ctgtgcttct ccatgagatg gatgaagatg atctggccaa tgccttgatc
 120
 tggcctgaga ttcaacagga gctgaaaatc attgaatctg aggaggagct ctcatcgctg
 180
 ccacctctg ctctgaagac cagcccaatt cagcctattc tegagtcgag tctggggccc
 240
 tttattccct cagagcctcc tgggagcttg cttgtggct ccttccctgc tccagtctcc
 300
 acccctctgg aggtgtggac tagggatcca gccaatcaga gcacacaggg ggcttccaca
 360
 gcagccagca gagagaagcc ggaacctgag cagggcctgc acccagacct cgccagcctg
 420
 gctcctctgg aaatagtctc ttttgagaag gcattctccag aggtctggagt gtgctcgcga
 480

<210> 1212
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 1212
 Glu Glu Gly Arg Glu Ala Gly Glu Met Glu Ser Ser Thr Leu Gln Glu
 1 5 10 15
 Ser Pro Arg Ala Arg Ala Glu Ala Val Leu Leu His Glu Met Asp Glu
 20 25 30
 Asp Asp Leu Ala Asn Ala Leu Ile Trp Pro Glu Ile Gln Gln Glu Leu
 35 40 45
 Lys Ile Ile Glu Ser Glu Glu Glu Leu Ser Ser Leu Pro Pro Pro Ala
 50 55 60
 Leu Lys Thr Ser Pro Ile Gln Pro Ile Leu Glu Ser Ser Leu Gly Pro
 65 70 75 80
 Phe Ile Pro Ser Glu Pro Pro Gly Ser Leu Pro Cys Gly Ser Phe Pro
 85 90 95
 Ala Pro Val Ser Thr Pro Leu Glu Val Trp Thr Arg Asp Pro Ala Asn
 100 105 110
 Gln Ser Thr Gln Gly Ala Ser Thr Ala Ala Ser Arg Glu Lys Pro Glu
 115 120 125
 Pro Glu Gln Gly Leu His Pro Asp Leu Ala Ser Leu Ala Pro Leu Glu
 130 135 140
 Ile Val Pro Phe Glu Lys Ala Ser Pro Glu Ala Gly Val Cys Ser Arg
 145 150 155 160

<210> 1213
 <211> 1141

<212> DNA

<213> Homo sapiens

<400> 1213

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cgtgatgctc aggggcgggt taccgggata gaggggcat cagggcggtt gagttacggc
120
tacaacgagg ctgggtcact catcagcgcg acggggcccc gcacacaaca taactggact
180
cacgacgcct atggccgggt caccagccac gccacatccg gaaccgacac caccttcgcc
240
tgggaccagg aaggccacct ggcgagacg tgtacgcgtg cacacgggca tggcactgcc
300
accagtatc gctatgacgc agcgggacgg cgcgtcagtg cgaccagctc agacggccag
360
gaggagcggt actcctggga tggacggggg tggctgtctg acatcaccac cgacgccacg
420
accgtatcga ctcacgtcga tgcattgggg cgcgccagtc gtatcaccac taagggccag
480
cagggtacgag tggactggga cctcgtgacc ggagccccca cctcgattga tggctgtcct
540
gtgcttcccc tgcccgaggg acgcatcctc ggccccaac ccacgcgcga taccaacctc
600
tggcgtgagg tcattgcccc cgaccctgac aaccttacc agcccgccac ggccactatt
660
gaggggtgtcc ccgagacgat caggatggcc gggaacacgc tagtggttga tggtcacctt
720
tgggtggggg gcgcctctac gacccaacta ccaccacctt ctgtctctct gaccggttaa
780
cccgccccgc cggcgcgcta tgggccaaca acccctacga ctacccaac aacaaccccc
840
tcaccctcac cgatcctctc gggacccacc ccgtcacga cgaccaactg gcaactcctc
900
ccaccccat cggcacactc gcacactacg tcgccaactc cgtcagcaca ctcgtgcac
960
acatcaccga tccgatcagc cactgggtggg ccaccacaaa agaccggatc ctctcccggg
1020
acttcctgat cggtgccggc ctctcatcgc gcgttatcgc gtagcgccca cgggcgtagg
1080
aggaccctc ctacgcgcgg ccatttcggg gggactcacc tcaggcggtt tttccgctag
1140
c
1141

```

<210> 1214

<211> 259

<212> PRT

<213> Homo sapiens

<400> 1214

```

Xaa His Asp Gly Gly Leu Val Cys Gly Tyr Val His Asp Gly Arg Val
1           5           10          15
Thr Arg Val Ala Arg Asp Ala Gln Gly Arg Val Thr Gly Ile Glu Gly

```



```

                20                25                30
Pro Ser Gly Arg Trp Ser Tyr Gly Tyr Asn Glu Ala Gly Ser Leu Ile
   35                40                45
Ser Ala Thr Gly Pro Arg Thr Gln His Asn Trp Thr His Asp Ala Tyr
   50                55                60
Gly Arg Leu Thr Ser His Ala Thr Ser Gly Thr Asp Thr Thr Phe Ala
   65                70                75                80
Trp Asp Gln Glu Gly His Leu Ala Gln Thr Cys Thr Arg Ala His Gly
   85                90                95
His Ala Thr Ala Thr Gln Tyr Arg Tyr Asp Ala Ala Gly Arg Arg Val
  100                105                110
Ser Ala Thr Ser Ser Asp Gly Gln Glu Glu Arg Tyr Ser Trp Asp Gly
  115                120                125
Arg Gly Trp Leu Ser Asp Ile Thr Thr Asp Ala Thr Thr Val Ser Thr
  130                135                140
His Val Asp Ala Leu Gly Arg Ala Ser Arg Ile Thr Thr Lys Gly Gln
  145                150                155                160
Gln Val Arg Val Asp Trp Asp Leu Val Thr Gly Ala Pro Thr Ser Ile
  165                170                175
Asp Gly Arg Pro Val Leu Pro Leu Pro Gly Gly Arg Ile Leu Gly Ala
  180                185                190
Thr Pro Ile Gly Asp Thr Asn Leu Trp Arg Glu Val Met Pro Thr Asp
  195                200                205
Pro Asp Asn Pro Tyr Gln Pro Ala Thr Ala Thr Ile Glu Gly Val Pro
  210                215                220
Glu Thr Ile Arg Met Ala Gly Asn Thr Leu Val Val Asp Gly His Pro
  225                230                235                240
Trp Trp Gly Arg Ala Ser Thr Thr Gln Leu Pro Pro Pro Ser Cys Leu
  245                250                255
Leu Thr Arg

```

<210> 1215

<211> 317

<212> DNA

<213> Homo sapiens

<400> 1215

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acgcgttcgc tgcagatcga gtcgccgggtg agctcgcgatc acctgtggat gtactacgtg
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ggcgtgcccga catccggcat cgggggggat cccaacctgc ttacctttta ttggaaccgc
120
ccccgggggtc aaccgggcca tcaccgggag aacgccgcctc ctcggaggggg gtgttctcgc
180
agtcgccggc gtgggtgcgt ggaagaagta ccgcggcaac accttcggcg ggctgctccc
240
gtcgtgtgcc ctcggcctcg tgctcgcgtt catcgtgctg aacaaggctg gctcggcgca
300
gtacatcgcc tggatcn
317

```

<210> 1216

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1216

```

Met Tyr Cys Gly Glu Pro Thr Leu Phe Ser Thr Met Asn Ala Ser Thr
 1             5             10             15
Arg Pro Arg Asp Ser Asp Gly Ser Ser Pro Pro Lys Val Val Pro Arg
 20             25             30
Tyr Phe Phe His Ala Pro Thr Pro Ala Thr Ala Arg Thr Pro Pro Pro
 35             40             45
Arg Ser Gly Val Leu Pro Val Met Ala Gly Leu Thr Pro Gly Ala Val
 50             55             60
Pro Ile Lys Gly Lys Gln Val Gly Ile Pro Pro Asp Ala Gly Cys Arg
 65             70             75             80
His Ala His Val Val His Pro Gln Val Asp Arg Ala His Arg Arg Leu
 85             90             95
Asp Leu Gln Arg Thr Arg
100

```

<210> 1217

<211> 548

<212> DNA

<213> Homo sapiens

<400> 1217

```

naccgctggg ttgacgcgct attaaacgat aagagcaaaa aaacatttcc tcatttatta
60
cgtttgcggg tgaatgatgt ttctggtgat agtcagtggg tagagatgcg aggcagtggt
120
acagggttggg acagccgtca tcgagctcag atggtgagag ggacattcga cggtattaac
180
catcttattg acgctgaaaa tgaattaatt gcggcccggtg aagatgctca cgcacgagag
240
cttattttat cggttttgct aaataatatt ccagaccctg tttggtctaa agatgaaagc
300
ggtcgttatt tggactgtaa ccatgcgttt tgtctgttta atggtttaga gcagagtgat
360
gttcaggggc aaaaagacag tgaattaaac ttagataata atggtcaata ttatcaagat
420
atgggcggtg aggtattagc gcgaggggag atttttcatg aacattgttg gggtagcctt
480
gcagatggaa gtgacaaccg cttgtttgaa gtatatcgag tccctatcaa agagcctacc
540
gtgaattc
548

```

<210> 1218

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1218

```

Xaa Ala Trp Val Asp Ala Leu Leu Asn Asp Lys Ser Lys Lys Thr Phe
 1             5             10             15
Pro His Leu Leu Arg Cys Arg Val Asn Asp Val Ser Gly Asp Ser Gln

```

```

      20      25      30
Trp Ile Glu Met Arg Gly Ser Val Thr Gly Trp Asp Ser Arg His Arg
      35      40      45
Ala Gln Met Val Arg Gly Thr Phe Glu Arg Ile Asn His Leu Ile Asp
      50      55      60
Ala Glu Asn Glu Leu Ile Ala Ala Arg Glu Asp Ala Gln Arg Arg Glu
      65      70      75      80
Leu Ile Leu Ser Ala Leu Leu Asn Asn Ile Pro Asp Pro Val Trp Ser
      85      90      95
Lys Asp Glu Ser Gly Arg Tyr Leu Asp Cys Asn His Ala Phe Cys Leu
      100      105      110
Phe Asn Gly Leu Glu Gln Ser Asp Val Gln Gly Gln Lys Asp Ser Glu
      115      120      125
Leu Asn Leu Asp Asn Asn Gly Gln Tyr Tyr Gln Asp Met Gly Gly Glu
      130      135      140
Val Leu Ala Arg Gly Glu Ile Phe His Glu His Cys Trp Gly Thr Pro
      145      150      155      160
Ala Asp Gly Ser Asp Asn Arg Leu Phe Glu Val Tyr Arg Val Pro Ile
      165      170      175
Lys Glu Pro Thr Val Asn
      180

```

<210> 1219

<211> 308

<212> DNA

<213> Homo sapiens

<400> 1219

```

acgcgtgaag ggaggaatac agatggagaa atgggtccac caaaaaatga tgaggggtacc
60
tccagagaaa attaccaaga ccattctgtt agtattttcc agctccacag gcctttggaa
120
gttcccagac caccctccct cttttcaaac taaaacaggg atgggtctta accaccaccc
180
aaaggcaagg ggggtcttaa aacccaaacc aagtggggca ggggccagcc tcttcaggag
240
ggcccaaccc tgcagcctct gcccatattgg gaaagaccgt gagttggaat tatgggtcgg
300
tgggggggc
308

```

<210> 1220

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1220

```

Met Glu Lys Trp Val His Gln Lys Met Met Arg Val Pro Pro Glu Lys
1      5      10      15
Ile Thr Lys Thr Ile Leu Leu Val Phe Ser Ser Ser Thr Gly Leu Trp
      20      25      30
Lys Phe Pro Asp His Pro Pro Ser Phe Gln Thr Lys Thr Gly Met Ala
      35      40      45
Leu Asn His His Pro Lys Ala Arg Gly Val Leu Lys Pro Lys Pro Ser

```


<212> DNA

<213> Homo sapiens

<400> 1223

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 ttgtgcgctc accgagaggg gccatacggg gtagacgagt ggtctcagcg catggttact
 120
 gtactttcag atgtgttgcc tgggtgttggc caaggccggt gggttctcgg cgaactcgca
 180
 atagtaacgc ataacctcgc acaattggga gtcaataacg gtgattgcgg ggtcatcggt
 240
 gaaacaaggc ccgtcccccac gatagctcta ccgggaccgc gtggagtccc cagacgggtg
 300
 ccctgttccc tcatcccatc gctgcaaccc ttacaggcga tgacgattca caaagcgcag
 360
 ggagccaat tcacggagct aacgggtggc ctgccaccac ccgaactgcc cctcctctct
 420
 cgtgagttgc tctataccgc catcacgcgt
 450

<210> 1224

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1224

Lys Leu Ala Gln Ala Ser Ala Asp Ala Ala Leu Lys Leu Val Asp
 1 5 10 15
 Ala His Arg Leu Leu Cys Ala His Arg Glu Gly Pro Tyr Gly Val Asp
 20 25 30
 Glu Trp Ser Gln Arg Met Val Thr Val Leu Ser Asp Val Leu Pro Gly
 35 40 45
 Val Gly Gln Gly Arg Trp Val Leu Gly Glu Thr Ala Ile Val Thr His
 50 55 60
 Asn Leu Ala Gln Leu Gly Val Asn Asn Gly Asp Cys Gly Val Ile Val
 65 70 75 80
 Glu Thr Arg Pro Val Pro Thr Ile Ala Leu Pro Gly Pro Gly Gly Val
 85 90 95
 Pro Arg Arg Leu Pro Cys Ser Leu Ile Pro Ser Leu Gln Pro Leu Gln
 100 105 110
 Ala Met Thr Ile His Lys Ala Gln Gly Ser Gln Phe Thr Asp Val Thr
 115 120 125
 Val Val Leu Pro Pro Pro Asp Ser Pro Leu Leu Ser Arg Glu Leu Leu
 130 135 140
 Tyr Thr Ala Ile Thr Arg
 145 150

<210> 1225

<211> 436

<212> DNA

<213> Homo sapiens

<400> 1225

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ncccatcccc caccgggat ggtgaacct gggatggcca cttgggagct caaagtgttg
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tcagtgggag gacaaggtcc tcaattctcg gcacattggc ccagagaagt catgaaaacc
120
caaaagcccc cgaaagtaag aagtagaaaa aaaccggacc cggaccagat gaagggacct
180
gggaagtttt tggaagagag actgctgaag tgtctccttg caggcatcac cgtgagctgg
240
ggctttgcac acagcatctt catggcttcc cacaatgatc ccagaactga tccagagaaa
300
cccagggatc aggggttgac ccgacctgt catcatccca ttctacaaat gaggacactg
360
aggcctgggtg aaaagggagg ggtggatgga accaggtggc ctggctctaa gaccagagg
420
ctggagtgtg ctcattg
436

```

<210> 1226

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1226

```

Met Val Asn Thr Gly Met Ala Thr Trp Glu Leu Lys Val Leu Ser Val
1 5 10 15
Gly Gly Gln Gly Pro Gln Phe Leu Ala His Trp Pro Arg Glu Val Met
20 25 30
Lys Thr Gln Ser Pro Pro Lys Val Arg Ser Arg Lys Lys Pro Asp Pro
35 40 45
Asp Gln Met Lys Gly Pro Gly Lys Phe Leu Glu Lys Arg Leu Leu Lys
50 55 60
Cys Leu Leu Ala Gly Ile Thr Val Ser Trp Gly Phe Ala His Ser Ile
65 70 75 80
Phe Met Ala Phe His Asn Asp Pro Arg Thr Asp Pro Glu Lys Pro Arg
85 90 95
Asp Gln Gly Leu Thr Arg Pro Cys His His Pro Ile Leu Gln Met Arg
100 105 110
Thr Leu Arg Pro Gly Glu Lys Gly Gly Val Asp Gly Thr Arg Trp Pro
115 120 125
Gly Ser Lys Thr Gln Arg Leu Glu Cys Ala His
130 135

```

<210> 1227

<211> 756

<212> DNA

<213> Homo sapiens

<400> 1227

```

gttgagtccc acgtgaaaca aaatgcactt tacaatagaa tgacgattcg tatcaagat
60
aatggtattg gaataccgat taacaaggta gataaaatct ttgatagatt ctaccgtgtc
120
gacaaagcac gtacacgtaa gatggggcgt acaggactag gtctagctat ttccaaagag
180

```

attgtcgaag cacataatgg ccgtatttgg gcaaatagtg tcgaaggaca aggtacatct
 240
 atcttcatta ccctaccatg tgaaattatt gaagatgggtg attgggatga atagtaaaga
 300
 atacatcaaa acgattatcc tgatactact tgtattaatg agtgcgtct taacctacat
 360
 ggtatggaac ttctcacctg atctatcaaa tgctgatagt acgtcatcag ataataagaa
 420
 agataattct aaacctattg gaaaaccaat gagtgcgaaa acggataaaa ccatacaccc
 480
 atttcaaatc gttcaatcta atggcgaaaa aacaaaaggt atgccagcaa caggctcatgc
 540
 agtatctcaa attttaagcc cattaagaaga taaaaatgtt gattcagtac aacatttaaa
 600
 acgaaatcat aacttaatta ttctgaatt aagtataaac tttatcggtc ttgatttcac
 660
 atatgattta ccgttatcaa tttacttaag ccaagtatta aacatagatg ctaagacacc
 720
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 756

<210> 1228

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1228

Val	Glu	Phe	His	Val	Lys	Gln	Asn	Ala	Leu	Tyr	Asn	Arg	Met	Thr	Ile
1				5					10					15	
Arg	Ile	Lys	Asp	Asn	Gly	Ile	Gly	Ile	Pro	Ile	Asn	Lys	Val	Asp	Lys
			20					25					30		
Ile	Phe	Asp	Arg	Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Thr	Arg	Lys	Met
		35					40					45			
Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Lys	Glu	Ile	Val	Glu	Ala
		50				55					60				
His	Asn	Gly	Arg	Ile	Trp	Ala	Asn	Ser	Val	Glu	Gly	Gln	Gly	Thr	Ser
65				70					75					80	
Ile	Phe	Ile	Thr	Leu	Pro	Cys	Glu	Ile	Ile	Glu	Asp	Gly	Asp	Trp	Asp
				85				90						95	

Glu

<210> 1229

<211> 377

<212> DNA

<213> Homo sapiens

<400> 1229

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 60
 cttgtgcgcc ccattggcaaa ccaggggggc gaggccactg gagcgatggg aaccgacacc
 120
 ccgctggccg tgctatctaa ctgtccgcgg atgctctggg actatttcag tcagcttttc
 180

gctcaggttaa ccaatccgcc cttggacgct atccgcgagg agcttgctac ctccctgacg
 240
 ggcaccatcg gcccgaggc gaacttgctt gagccttgccc cggaatcatg tcggcaagtg
 300
 gtcgtcaact acccgatcat cgattccgac cagcttgcca agatcattca catcgacgct
 360
 gacggggagc atccgga
 377

<210> 1230
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1230
 Thr Arg Arg Gln Gln Leu Phe Gly Tyr Thr Ser Glu Glu Pro Lys Met
 1 5 10 15
 Leu Val Ala Pro Met Ala Asn Gln Gly Val Glu Ala Thr Gly Ala Met
 20 25 30
 Gly Thr Asp Thr Pro Leu Ala Val Leu Ser Asn Cys Pro Arg Met Leu
 35 40 45
 Trp Asp Tyr Phe Ser Gln Leu Phe Ala Gln Val Thr Asn Pro Pro Leu
 50 55 60
 Asp Ala Ile Arg Glu Glu Leu Val Thr Ser Leu Thr Gly Thr Ile Gly
 65 70 75 80
 Pro Glu Ala Asn Leu Leu Glu Pro Gly Pro Glu Ser Cys Arg Gln Val
 85 90 95
 Val Val Asn Tyr Pro Ile Ile Asp Ser Asp Gln Leu Ala Lys Ile Ile
 100 105 110
 His Ile Asp Ala Asp Gly Glu His Pro
 115 120

<210> 1231
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1231
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 120
 cacactgttc tggctttggt agaacatggc gaagatgttg tagtggttaga taatttatca
 180
 aactcttcgc atgagtctct gcgtcgcgtt gagaaactcg cgggtagaag tgctcagttc
 240
 taccaaggcg atatcttgga tgctgagtg ctgcatcgca tcttcgaggc tcacgacatc
 300
 tcggtgtgta tccattttgc tgggctaaa ggtgtcggag agtcgacgcg t
 351

<210> 1232
 <211> 91
 <212> PRT

<213> Homo sapiens

<400> 1232

```

Met Ala Val Leu Ile Thr Gly Asp Ala Gly Tyr Ile Gly Ser His Thr
 1           5           10           15
Val Leu Ala Leu Leu Glu His Gly Glu Asp Val Val Val Leu Asp Asn
 20           25           30
Leu Ser Asn Ser Ser Asp Glu Ser Leu Arg Arg Val Glu Lys Leu Ala
 35           40           45
Gly Arg Ser Ala Gln Phe Tyr Gln Gly Asp Ile Leu Asp Ala Glu Cys
 50           55           60
Leu His Arg Ile Phe Glu Ala His Asp Ile Ser Ala Val Ile His Phe
 65           70           75           80
Ala Gly Leu Lys Gly Val Gly Glu Ser Thr Arg
 85           90

```

<210> 1233

<211> 4982

<212> DNA

<213> Homo sapiens

<400> 1233

```

nnggcttaag cagtggtaac aacgcagagt acgcgggggtg atggcctccc tgaaattaaa
60
catttctatt agtggcttcc cgtaaatactc atccttcttta gatcaaacct cggtatatctt
120
cctgcctatc tcttttgcac tccaaagtcc agttttatta aatcccaggg tctaagattt
180
tttctttgag aatttatctc cagtgtttct atggaaatta aaaaagaaaa ttaggataat
240
tcaatgtcga aatgttgcat gcatcttttg agaaatttat attttgtagg ttgaaggact
300
tgcttttttg gcagcgtatt tttggagggt gaatgtagtt attttaataa ccatgtccta
360
attatttata gcttcctgcc tgacacagct cacttcaaga agtgcaaat gtcagaacgt
420
ggaattaagt gggcttgtga atattgtacg tatgaaaaat ggccatctgc aatcaagtg
480
accatgtgtc gtgcccgaag acctagtggg acaattatta cagaagatcc atttaaaagt
540
ggttcaagtg atgttggtag agattgggat ccttcagca ccgaaggagg aagtagtcct
600
ttgatattgc cagactctag tgcaagacca agggtgaaat cttcgtatag catggaaaa
660
gcaataaagt ggtcatgcc catgtgtaca tatttgaact ggccaagagc aatcagatgt
720
accagtgct tatcccaacg taggaccagg agtccctacag aatctcctca gtcctcagg
780
ctcggctcaa gaccagttgc tttttctgtt gatccttgtg aggaatacaa tgatagaaat
840
aaactgaaca ctaggacaca gcaactggact tgctctgttt gcacatatga aaactgggcc
900
aaggctaaaa gatgtgtgtt ttgtgatcat ccagaccta ataacattga agcaatagaa
960

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ttggcagaga ctgaagaggc ttcttcaata ataatgagc aagacagagc tcgatggagg
1020
ggaagtgtga gtagtggtaa tagccaaagg agatcacctc ctgctacgaa gcgggactct
1080
gaagtgtaaa tggattttca gaggattgaa ttggctgggtg ctgtgggaag caaggaggaa
1140
cttgaagtga actttaaaaa actaaagcaa attaaaaaca ggatgaaaaa gactgattgg
1200
ctcttcctca atgcttggtg ggggggttgta gaagggtgatt tagctgccat agaagcatatc
1260
aagtcacag gagagagacat tgcacgtcag ctcaccgagc atgaagtacg cttgctgaat
1320
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 4860
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 4980
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 4982

<210> 1234

<211> 708

<212> PRT

<213> Homo sapiens

<400> 1234

Met Ser Glu Arg Gly Ile Lys Trp Ala Cys Glu Tyr Cys Thr Tyr Glu
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 Asn Trp Pro Ser Ala Ile Lys Cys Thr Met Cys Arg Ala Gln Arg Pro
 20 25 30
 Ser Gly Thr Ile Ile Thr Glu Asp Pro Phe Lys Ser Gly Ser Ser Asp
 35 40 45
 Val Gly Arg Asp Trp Asp Pro Ser Ser Thr Glu Gly Gly Ser Ser Pro
 50 55 60
 Leu Ile Cys Pro Asp Ser Ser Ala Arg Pro Arg Val Lys Ser Ser Tyr
 65 70 75 80
 Ser Met Glu Asn Ala Asn Lys Trp Ser Cys His Met Cys Thr Tyr Leu
 85 90 95
 Asn Trp Pro Arg Ala Ile Arg Cys Thr Gln Cys Leu Ser Gln Arg Arg
 100 105 110
 Thr Arg Ser Pro Thr Glu Ser Pro Gln Ser Ser Gly Ser Gly Ser Arg
 115 120 125
 Pro Val Ala Phe Ser Val Asp Pro Cys Glu Glu Tyr Asn Asp Arg Asn
 130 135 140
 Lys Leu Asn Thr Arg Thr Gln His Trp Thr Cys Ser Val Cys Thr Tyr

```

145          150          155          160
Glu Asn Trp Ala Lys Ala Lys Arg Cys Val Val Cys Asp His Pro Arg
      165          170          175
Pro Asn Asn Ile Glu Ala Ile Glu Leu Ala Glu Thr Glu Glu Ala Ser
      180          185          190
Ser Ile Ile Asn Glu Gln Asp Arg Ala Arg Trp Arg Gly Ser Cys Ser
      195          200          205
Ser Gly Asn Ser Gln Arg Arg Ser Pro Pro Ala Thr Lys Arg Asp Ser
      210          215          220
Glu Val Lys Met Asp Phe Gln Arg Ile Glu Leu Ala Gly Ala Val Gly
      225          230          235
Ser Lys Glu Glu Leu Glu Val Asp Phe Lys Lys Leu Lys Gln Ile Lys
      245          250          255
Asn Arg Met Lys Lys Thr Asp Trp Leu Phe Leu Asn Ala Cys Val Gly
      260          265          270
Val Val Glu Gly Asp Leu Ala Ala Ile Glu Ala Tyr Lys Ser Ser Gly
      275          280          285
Gly Asp Ile Ala Arg Gln Leu Thr Ala Asp Glu Val Arg Leu Leu Asn
      290          295          300
Arg Pro Ser Ala Phe Asp Val Gly Tyr Thr Leu Val His Leu Ala Ile
      305          310          315
Arg Phe Gln Arg Gln Asp Met Leu Ala Ile Leu Leu Thr Glu Val Ser
      325          330          335
Gln Gln Ala Ala Lys Cys Ile Pro Ala Met Val Cys Pro Glu Leu Thr
      340          345          350
Glu Gln Ile Arg Arg Glu Ile Ala Ala Ser Leu His Gln Arg Lys Gly
      355          360          365
Asp Phe Ala Cys Tyr Phe Leu Thr Asp Leu Val Thr Phe Thr Leu Pro
      370          375          380
Ala Asp Ile Glu Asp Leu Pro Pro Thr Val Gln Glu Lys Leu Phe Asp
      385          390          395
Glu Val Leu Asp Arg Asp Val Gln Lys Glu Leu Glu Glu Glu Ser Pro
      405          410          415
Ile Ile Asn Trp Ser Leu Glu Leu Ala Thr Arg Leu Asp Ser Arg Leu
      420          425          430
Tyr Ala Leu Trp Asn Arg Thr Ala Gly Asp Cys Leu Leu Asp Ser Val
      435          440          445
Leu Gln Ala Thr Trp Gly Ile Tyr Asp Lys Asp Ser Val Leu Arg Lys
      450          455          460
Ala Leu His Asp Ser Leu His Asp Cys Ser His Trp Phe Tyr Thr Arg
      465          470          475
Trp Lys Asp Trp Glu Ser Trp Tyr Ser Gln Ser Phe Gly Leu His Phe
      485          490          495
Ser Leu Arg Glu Glu Gln Trp Gln Glu Asp Trp Ala Phe Ile Leu Ser
      500          505          510
Leu Ala Ser Gln Pro Gly Ala Ser Leu Glu Gln Thr His Ile Phe Val
      515          520          525
Leu Ala His Ile Leu Arg Arg Pro Ile Ile Val Tyr Gly Val Lys Tyr
      530          535          540
Tyr Lys Ser Phe Arg Gly Glu Thr Leu Gly Tyr Thr Arg Phe Gln Gly
      545          550          555
Val Tyr Leu Pro Leu Leu Trp Glu Gln Ser Phe Cys Trp Lys Ser Pro
      565          570          575
Ile Ala Leu Gly Tyr Thr Arg Gly His Phe Ser Ala Leu Val Ala Met

```

```

      580              585              590
Glu Asn Asp Gly Tyr Gly Asn Arg Gly Ala Gly Ala Asn Leu Asn Thr
595              600              605
Asp Asp Asp Val Thr Ile Thr Phe Leu Pro Leu Val Asp Ser Glu Arg
610              615              620
Lys Leu Leu His Val His Phe Leu Ser Ala Gln Glu Leu Gly Asn Glu
625              630              635              640
Glu Gln Gln Glu Lys Leu Leu Arg Glu Trp Leu Asp Cys Cys Val Thr
645              650              655
Glu Gly Gly Val Leu Val Ala Met Gln Lys Ser Ser Arg Arg Arg Asn
660              665              670
His Pro Leu Val Thr Gln Met Val Glu Lys Trp Leu Asp Arg Tyr Arg
675              680              685
Gln Ile Arg Pro Cys Thr Ser Leu Ser Asp Gly Glu Glu Asp Glu Asp
690              695              700
Asp Glu Asp Glu
705

```

```

<210> 1235
<211> 383
<212> DNA
<213> Homo sapiens

```

```

<400> 1235
gcgtctcagg ccgtgacctca gatacctgtc gatatgacga ccttggggcg tgatttggtg
60
gccttcaccg gtcacaagat gtgcgggtccg acgggtatcg gcattctctg gggacgctat
120
gacctctctg ctgagctacc gcccttcctc ggaggcgccg agatgatcga ggtcgtgcgc
180
atggagggat cgacctacgc cgagcctcca catcgttttg aggcaggcac cccgccgatc
240
gcacagctgg ctgccctcgg ggtggccgcc gactacctag atggcatcgg gatgcaggcc
300
atcgccgagc acgaacatga gctggctgct cggatgctcg aagactacca gaccgtcaag
360
ggagtgcagc cggagagagg ctg
383

```

```

<210> 1236
<211> 127
<212> PRT
<213> Homo sapiens

```

```

<400> 1236
Ala Ser Gln Ala Val Xaa Gln Ile Pro Val Asp Met Thr Thr Leu Gly
1          5          10          15
Ala Asp Leu Val Ala Phe Thr Gly His Lys Met Cys Gly Pro Thr Gly
20          25          30
Ile Gly Ile Leu Trp Gly Arg Tyr Asp Leu Leu Ala Glu Leu Pro Pro
35          40          45
Phe Leu Gly Gly Gly Glu Met Ile Glu Val Val Arg Met Glu Gly Ser
50          55          60
Thr Tyr Ala Glu Pro Pro His Arg Phe Glu Ala Gly Thr Pro Pro Ile

```

65		70		75		80
Ala	Gln	Leu	Ala	Ala	Leu	Gly
		85		90		95
Gly	Met	Gln	Ala	Ile	Ala	Glu
		100		105		110
Leu	Glu	Asp	Tyr	Gln	Thr	Val
		115		120		125

<210> 1237

<211> 1608

<212> DNA

<213> Homo sapiens

<400> 1237

```

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acaccagcac attctgactc aacatggcta tacgggtgtc atcgctgaag aaaggctcaa
120
tgctggccta gggccggggc tactagaaca aggtgatctg ggctcttggt atctgtcat
180
ttgacctgtc tctaagaaag cagaaggaac accctgtata tccaaggaag tcatgtgcca
240
gttaggttta catcaaaagg caaacagatt accagaaata cagcagccac ttgtgcagaa
300
ggaaggatta tgtcaaatag ttagaagatt ccagaaactg caacttccag tgagtccctc
360
tgtgtgtctg gatcaggga tgcaattaaa gccgagtact tcgagtcacc ttttaaaaaa
420
agtgaagcca cgtgtgtgga aaccagggga ctggagtcgt gaacagctga atgaaacgac
480
agtccctgtc ccacatgaaa caatctttcg agccaaagat ctatctgtga ttcttaaaagc
540
gtatgtgttg gtgacgtcct taaccccttt gcgtgcattc attcattcga ctggcacagt
600
ttggaatcca ccaagaaaa aacgcttcac tgtcaagctg caaacatttt ttgagacatt
660
cctgagagcc agttcacctc aacaggcttt tgacattatg aaggaagcaa ttggcaaaat
720
actgctagcc gctgaagtat tcagtgaaac atctactctg ggaccaaaga ccttccatag
780
atgcagattc tgctttcaac ttctaacttt tgatattggt tatggcagtt tcattgaccc
840
tgtagtgctc cagggtacac agcatattaaa ttttcaagat tatgataata tggattttga
900
ggacccaaaat acagaagaat tcctttttaa tgacactttc aattttctct tcctaatga
960
atcatcactt tccatatttt ctgagatatt tcagagactt tatagatcag atgttttcaa
1020
gggtgaaaaa tatcaaaagg aactaaatca gtgtctgtcc ttagaagaaa ttaactcaat
1080
tatgactttc ataaaggaac ttggaagtct gggacaattc caactgctct tcccatctac
1140
tactcctggg attcagtcac tgatgcatga attttatgat gtggcaaatc ctgtgggaaa
1200

```

tcctgggtca gtcctgaccc aatactgggc tctttttaa gatttgaac aatttcagtt
 1260
 catgaataaa aagacacagc cacatccact ggaatggaat tctttcacag aagataagaa
 1320
 cattgaaaaa ccacaagtgc catttgatgc aatagaaaaa aaaaaagctg cagttccaca
 1380
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 1440
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 1608

<210> 1238

<211> 458

<212> PRT

<213> Homo sapiens

<400> 1238

Met Cys Gln Leu Gly Leu His Gln Lys Ala Asn Arg Leu Pro Glu Ile
 1 5 10 15
 Gln Gln Pro Leu Cys Arg Lys Glu Gly Leu Cys Gln Ile Val Arg Arg
 20 25 30
 Phe Pro Glu Leu Gln Leu Pro Val Ser Pro Ser Val Cys Leu Asp Gln
 35 40 45
 Gly Met Gln Leu Lys Pro Ser Thr Ser Ser His Leu Leu Lys Thr Val
 50 55 60
 Lys Pro Arg Val Trp Lys Pro Gly Asp Trp Ser Arg Glu Gln Leu Asn
 65 70 75 80
 Glu Thr Thr Val Leu Ala Pro His Glu Thr Ile Phe Arg Ala Lys Asp
 85 90 95
 Leu Ser Val Ile Leu Lys Ala Tyr Val Leu Val Thr Ser Leu Thr Pro
 100 105 110
 Leu Arg Ala Phe Ile His Ser Thr Gly Thr Val Trp Asn Pro Pro Lys
 115 120 125
 Lys Lys Arg Phe Thr Val Lys Leu Gln Thr Phe Phe Glu Thr Phe Leu
 130 135 140
 Arg Ala Ser Ser Pro Gln Gln Ala Phe Asp Ile Met Lys Glu Ala Ile
 145 150 155 160
 Gly Lys Leu Leu Leu Ala Ala Glu Val Phe Ser Glu Thr Ser Thr Leu
 165 170 175
 Gly Pro Lys Thr Phe His Arg Cys Arg Phe Cys Phe Gln Leu Leu Thr
 180 185 190
 Phe Asp Ile Gly Tyr Gly Ser Phe Met Tyr Pro Val Val Leu Gln Val
 195 200 205
 His Glu His Leu Asn Phe Gln Asp Tyr Asp Asn Met Asp Phe Glu Asp
 210 215 220
 Gln Asn Thr Glu Glu Phe Leu Leu Asn Asp Thr Phe Asn Phe Leu Phe
 225 230 235 240
 Pro Asn Glu Ser Ser Leu Ser Ile Phe Ser Glu Ile Phe Gln Arg Leu
 245 250 255
 Tyr Arg Ser Asp Val Phe Lys Gly Glu Asn Tyr Gln Lys Glu Leu Asn


```

                260                265                270
Gln Cys Leu Ser Leu Glu Glu Ile Asn Ser Ile Met Thr Phe Ile Lys
      275                280                285
Glu Leu Gly Ser Leu Gly Gln Phe Gln Leu Leu Phe Pro Ser Thr Thr
      290                295                300
Pro Gly Ile Gln Ser Leu Met His Glu Phe Tyr Asp Val Ala Asn Pro
      305                310                315                320
Val Gly Asn Pro Gly Ser Val Leu Thr Gln Tyr Trp Ser Leu Leu Asn
      325                330                335
Val Phe Glu Gln Phe Gln Phe Met Asn Lys Lys Thr Gln Pro His Pro
      340                345                350
Leu Glu Trp Asn Ser Phe Thr Glu Asp Lys Asn Ile Glu Lys Pro Gln
      355                360                365
Val Pro Phe Asp Ala Ile Glu Asn Lys Lys Ala Ala Val Pro Gln Ile
      370                375                380
Lys Asn Glu Asn Lys Glu Ile His Cys Ser Asp Asp Glu Asn Thr Pro
      385                390                395                400
Cys His Ile Lys Gln Ile Phe Thr His Pro His Leu Glu Leu Asn Pro
      405                410                415
Asp Phe His Pro Lys Ile Lys Asp Tyr Tyr Cys Glu Val Pro Phe Asp
      420                425                430
Val Val Thr Val Thr Ile Gly Val Glu Thr Pro Lys Cys Leu Cys Lys
      435                440                445
Val His Leu Tyr Glu Gln Ala Gly Pro Ser
      450                455

```

<210> 1239

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1239

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atacctactg aacgtgaacg aacagaaagg ctaattaaaa ccaaattaag ggagatcatg
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atgcagaagg attggagaa tattacatcc aaagagataa gaacagagtt ggaaatgcaa
120
atggtgtgca acttgcggga attcaaggaa tttatagaca atgaaatgat agtgcactctt
180
gggtcaaatgg atagccctac acagatatatt gagcatgtgt tcctggggctc agaatggaat
240
gcctccaact tagaggactt acagaaccga ggggtacggg atatcttgaa tgtcactcga
300
gagatagata actttttccc aggagtcctt gagtatcata acattcgggt atatgatgaa
360
gaggcaacgg atctcctggc gtactggaat gacacttaca aattcatctc taaagcaaag
420
aaacatggat ctaaatgcct tgtgcac
447

```

<210> 1240

<211> 149

<212> PRT

<213> Homo sapiens

<400> 1240

```

Ile Pro Thr Glu Arg Glu Arg Thr Glu Arg Leu Ile Lys Thr Lys Leu
 1           5           10           15
Arg Glu Ile Met Met Gln Lys Asp Leu Glu Asn Ile Thr Ser Lys Glu
          20           25           30
Ile Arg Thr Glu Leu Glu Met Gln Met Val Cys Asn Leu Arg Glu Phe
          35           40           45
Lys Glu Phe Ile Asp Asn Glu Met Ile Val Ile Leu Gly Gln Met Asp
          50           55           60
Ser Pro Thr Gln Ile Phe Glu His Val Phe Leu Gly Ser Glu Trp Asn
          65           70           75           80
Ala Ser Asn Leu Glu Asp Leu Gln Asn Arg Gly Val Arg Tyr Ile Leu
          85           90           95
Asn Val Thr Arg Glu Ile Asp Asn Phe Phe Pro Gly Val Phe Glu Tyr
          100          105          110
His Asn Ile Arg Val Tyr Asp Glu Glu Ala Thr Asp Leu Leu Ala Tyr
          115          120          125
Trp Asn Asp Thr Tyr Lys Phe Ile Ser Lys Ala Lys Lys His Gly Ser
          130          135          140
Lys Cys Leu Val His
145

```

<210> 1241

<211> 489

<212> DNA

<213> Homo sapiens

<400> 1241

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acgcgtgtgc agcgtatcca gcaccgtcct cagaataata gctgtgaaaa ggaggaaggg
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120
taggaagatc aatgagggcg gagtgtgtgt gtgtacgtgt gcgcgtgtgt gtgtgagaga
180
gagagaaaga aagaagaaag gtccccgattg caacgtgtca gatcttgcaa ctttcccccc
240
accaaacaca acaacctca gacacaaaaa caccattgct gactgatacc ccaggctcttc
300
aggggttaaag gaaccgtgtg ttggcagcgc aattgtgcag acgctgtaag gccaaaacga
360
ggattttgtg tgtgaggtcg gtggtgcgtt cttttcttct tcttctcgcc tgttttcccg
420
gagtgcctgg gttgcgagaa aggcgcacgc caggctgtgc agccgaatcg cttcgcaatt
480
attcatgct
489

```

<210> 1242

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1242

```

Met Asn Asn Cys Glu Ala Ile Arg Leu His Ser Leu Arg Cys Ala Phe

```

```

      1           5           10           15
Leu Ala Thr Gln Ala Leu Arg Glu Asn Arg Arg Glu Glu Lys Glu Lys
      20           25           30
Asn Ala Pro Pro Thr Ser Gln His Lys Ser Ser Phe Trp Pro Tyr Ser
      35           40           45
Val Cys Thr Ile Ala Leu Pro Thr His Gly Ser Phe Asn Pro Glu Asp
      50           55           60
Leu Gly Tyr Gln Ser Ala Met Val Phe Leu Cys Leu Arg Val Val Val
      65           70           75           80
Leu Gly Gly Gly Lys Val Ala Arg Ser Asp Thr Leu Gln Ser Gly Pro
      85           90           95
Phe Phe Phe Leu Ser Leu Ser Leu Thr His Thr Arg Ala His Val His
      100          105          110
Thr His Thr Arg Ala Ser Leu Ile Phe Leu Leu Val Arg Thr His
      115          120          125

```

<210> 1243

<211> 390

<212> DNA

<213> Homo sapiens

<400> 1243

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gagatgatat acctaccggg aatgttcact gtctacttgc atggccagtt ctgggtcggg
120
gtcctagaga ggcgcgacga ggggttgggt cgtgccgtaa aagtcacgtt tggcgccgaa
180
ccgtctgaca cggaattgta cgggtggggt agccgtcatg gcaacgcact tatagagcga
240
ttggagtcta ccgctgctgt ccctaccacc cgcagtcgcc gagccaagcg actgaacccc
300
aagagggcgt tacgagatgc agcgcgagct gcccaagcac accgtgccag cagcnccgca
360
caggccgcga ttaaggccga tcaggaagct
390

```

<210> 1244

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1244

```

Xaa Asp Ser Val Asp Pro Leu Met Glu Asn Pro Val Cys Gln Val Pro
      1           5           10           15
Ser Ala Tyr Trp Glu Met Ile Tyr Leu Pro Gly Met Phe Thr Val Tyr
      20           25           30
Phe Asp Gly Gln Phe Trp Val Gly Val Leu Glu Arg Arg Asp Glu Gly
      35           40           45
Leu Val Arg Ala Val Lys Val Thr Phe Gly Ala Glu Pro Ser Asp Thr
      50           55           60
Glu Leu Tyr Gly Trp Val Ser Arg His Gly Asn Ala Leu Ile Glu Arg
      65           70           75           80
Leu Glu Ser Thr Ala Ala Val Pro Thr Thr Arg Ser Pro Arg Ala Lys

```

```

      85              90              95
Arg Leu Asn Pro Lys Arg Ala Leu Arg Asp Ala Ala Arg Ala Ala Gln
      100              105              110
Ala His Arg Ala Ser Thr Xaa Ala Gln Ala Ala Ile Lys Ala Asp Gln
      115              120              125
Glu Ala
      130

```

```

<210> 1245
<211> 339
<212> DNA
<213> Homo sapiens

```

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<400> 1245
gccaaagcagc aaaaaccaca gatcattgct atgggaaatg tgtcattttc ttgttcacaa
60
ccacaatcta tgcccgtgac ttttctgagc tccaggagtt ttttagcact gccagacttc
120
tctggagagg aggaggtttc tgccactttt caatttcgaa cttggaataa ggcagggttt
180
ctgctgttca gtgaacttca gctgatttca gggggtatcc tcctctttct gagtgatgga
240
aaacttaagt cgaatctcta ccagccaaga aaattaccca gtgacatcac agcagggtgc
300
gaattaaatg atgggcagtg gcattctgtc tctttatct
339

```

```

<210> 1246
<211> 113
<212> PRT
<213> Homo sapiens

```

```

<400> 1246
Ala Lys Gln Gln Lys Pro Gln Ile Ile Ala Met Gly Asn Val Ser Phe
1      5      10      15
Ser Cys Ser Gln Pro Gln Ser Met Pro Val Thr Phe Leu Ser Ser Arg
      20      25      30
Ser Phe Leu Ala Leu Pro Asp Phe Ser Gly Glu Glu Glu Val Ser Ala
      35      40      45
Thr Phe Gln Phe Arg Thr Trp Asn Lys Ala Gly Leu Leu Leu Phe Ser
      50      55      60
Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu Leu Phe Leu Ser Asp Gly
65      70      75      80
Lys Leu Lys Ser Asn Leu Tyr Gln Pro Arg Lys Leu Pro Ser Asp Ile
      85      90      95
Thr Ala Gly Val Glu Leu Asn Asp Gly Gln Trp His Ser Val Ser Leu
      100      105      110
Ser

```

```

<210> 1247
<211> 366
<212> DNA
<213> Homo sapiens

```

<400> 1247

ttgacctcca acccgggcac gcgcatacctg cccagatcc cgatggatgg gcatacctc
 60
 aaccgggtgt ggccggacgt cggcctgacg gtgcacccgc cgatgctcta catgggctac
 120
 gtcggtttct cctgggcctt tgcgtttgcc atcgccgcct tgctcggcgg gcgcctcgat
 180
 gcggcctggg cgcgctggtc gcggccatgg accattgtgg cctgggcgtt cctcggtatc
 240
 ggtatcaccc tcggttcctg gtgggcctac tacgaactcg gctggngcgg ctggtgggtc
 300
 tgggaccccg gggaaaaccc cttcttcctg ccctggctgg ggggcacccc gctgattcac
 360
 tcgctg
 366

<210> 1248

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1248

Leu	Thr	Ser	Asn	Pro	Gly	Thr	Arg	Ile	Leu	Pro	Gln	Ile	Pro	Met	Asp
1			5						10					15	
Gly	His	Asp	Leu	Asn	Pro	Val	Trp	Arg	Asp	Val	Gly	Leu	Ile	Val	His
		20						25					30		
Pro	Pro	Met	Leu	Tyr	Met	Gly	Tyr	Val	Gly	Phe	Ser	Val	Ala	Phe	Ala
		35					40					45			
Phe	Ala	Ile	Ala	Ala	Leu	Leu	Gly	Gly	Arg	Leu	Asp	Ala	Ala	Trp	Ala
	50					55					60				
Arg	Trp	Ser	Arg	Pro	Trp	Thr	Ile	Val	Ala	Trp	Ala	Phe	Leu	Gly	Ile
	65				70				75					80	
Gly	Ile	Thr	Leu	Gly	Ser	Trp	Trp	Ala	Tyr	Tyr	Glu	Leu	Gly	Trp	Xaa
			85						90					95	
Gly	Trp	Trp	Phe	Trp	Asp	Pro	Gly	Glu	Asn	Pro	Phe	Phe	Met	Pro	Trp
			100					105					110		
Leu	Gly	Gly	Thr	Pro	Leu	Ile	His	Ser	Leu						
		115					120								

<210> 1249

<211> 374

<212> DNA

<213> Homo sapiens

<400> 1249

acgctgtgcc tcaacaccct ggcgcccacg ctgattgccg tggaaccggt gccggcaatg
 60
 ggcgcgacgt tgagcaagct gctgccggat gtgcacctgg tcaatggcac tgccgagggc
 120
 attccactgg aaagcgccgt ggcggtatgct gtggtgtgctg cacaagcctt ccattggttt
 180
 tccagcgagg cggccctggc ggaaatccat cgggtactca aaccggatgg gcgcctgggg
 240

ctgggtgtgga atgtgcgcga cgagtcggtg gattgggtcg ccgccattac tcaaatcatc
 300
 acgccttatg aaggcgacac gccgcgcttt cataccggcc gttggcgaga agccttcaact
 360
 ggcgagtatt ttg
 374

<210> 1250

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1250

Thr	Arg	Val	Leu	Asn	Thr	Leu	Ala	Pro	Thr	Leu	Ile	Ala	Val	Glu	Pro
1				5					10					15	
Val	Pro	Ala	Met	Gly	Ala	Gln	Leu	Ser	Lys	Leu	Leu	Pro	Asp	Val	His
			20					25					30		
Leu	Val	Asn	Gly	Thr	Ala	Glu	Ala	Ile	Pro	Leu	Glu	Ser	Ala	Val	Ala
			35				40					45			
Asp	Ala	Val	Val	Cys	Ala	Gln	Ala	Phe	His	Trp	Phe	Ser	Ser	Glu	Ala
	50					55					60				
Ala	Leu	Ala	Glu	Ile	His	Arg	Val	Leu	Lys	Pro	Asp	Gly	Arg	Leu	Gly
	65				70					75				80	
Leu	Val	Trp	Asn	Val	Arg	Asp	Glu	Ser	Val	Asp	Trp	Val	Ala	Ala	Ile
			85						90				95		
Thr	Gln	Ile	Ile	Thr	Pro	Tyr	Glu	Gly	Asp	Thr	Pro	Arg	Phe	His	Thr
			100					105					110		
Gly	Arg	Trp	Arg	Glu	Ala	Phe	Thr	Gly	Glu	Tyr	Phe				
			115					120							

<210> 1251

<211> 742

<212> DNA

<213> Homo sapiens

<400> 1251

accggtctct tcctcgga aa ggagggcg aggggcttgc ggggcagcca tggaggcgac
 60
 gcggaggcgg cagcacgtgg gagcgacggg cggcccaggc gcgcagttgg gcgcctcctt
 120
 ccctgcaggc caggcatggc tctgtgagcg ctgatgaggc tgcccgcacg gtcctcttcc
 180
 acctcgacct ctggttttac ttcactgc agaactgggt tctggacttt gggcgctcca
 240
 ttgccatgct ggtattccct ctcgagtggg ttccactcaa caagcccagt gttggggact
 300
 acttcacat ggcctacaac gtcatacgc cctttctctt gctcaagctc atcgagcggg
 360
 cccccccgac cctgctacgc tccatcacgt acgtgagcat catcatcttc atcatgggtg
 420
 ccagcatcca cctgggtggg gactctgtca accaccgcct gctcttcagt ggctaccagg
 480
 accacctgtc tgctcgtgag aaccccatca tcaagaatct caagccggag acgctgatcg
 540

actcctttga gctgctctac tattatgatg agtacctggg tcaactgcatg tggatcatcc
 600
 ccttcttctc catcctcttc atgtacttca gcggctgctn ttactgcctc taaagctgag
 660
 agcttgatcc cagggcctgc cctgctcctg gtggcaccca gtggcctgta ctactggtag
 720
 ctgggtcacgc agggccagat ct
 742

<210> 1252

<211> 80

<212> PRT

<213> Homo sapiens

<400> 1252

Met	Arg	Leu	Pro	Ala	Arg	Leu	Pro	Ser	Thr	Ser	Thr	Ser	Gly	Ser	Thr
1				5					10					15	
Ser	His	Cys	Arg	Thr	Gly	Phe	Trp	Thr	Leu	Gly	Val	Pro	Leu	Pro	Cys
			20				25						30		
Trp	Tyr	Ser	Leu	Ser	Ser	Gly	Phe	His	Ser	Thr	Ser	Pro	Val	Leu	Gly
		35				40						45			
Thr	Thr	Ser	Thr	Trp	Pro	Thr	Thr	Ser	Ser	Arg	Pro	Phe	Ser	Cys	Ser
	50					55					60				
Ser	Ser	Ser	Ser	Gly	Pro	Pro	Ala	Pro	Cys	Tyr	Ala	Pro	Ser	Arg	Thr
65					70					75					80

<210> 1253

<211> 675

<212> DNA

<213> Homo sapiens

<400> 1253

gggccccctc ccaggcgctt tctgggagct tttagaactg cgctctgaag tttccagaga
 60
 gcgaggagct tttgcccag gcagagacaa tggaagaaaa tgaaagccag aaatgtgagc
 120
 cgtgccttcc ttactcagca gacagaagac agatgcagga acaaggcaaa ggcaatctgc
 180
 atgtaacatc accagaagat gcagaatgcc gcagaaccaa ggaacgcctt tctaattggaa
 240
 acagtctgtg ttcaagttcc aagtcttccc gcaatatccc aaggagacac accttagggg
 300
 ggccccgaag ttccaaggaa atactgggaa tgcaaacatc tgagatggat cggaagagag
 360
 gaaaaagcgt tcctagaaca tctgaagcag aagtaccccc accacgcctc tgcaatcatg
 420
 ggtcaccaag agaggctgag agaccagaca aggateccca aactgtctca cagtctctca
 480
 ccaccagctg tgggtgaccc ggtcgagcat ttatcagaga cgtccgctga ttctttggaa
 540
 gccatgtctg agggggatgc tccaaccctt tttccagag gcagccggac tcgtgagcag
 600
 ctctctgtg tgaggtcaac caaccagacg aaagaaagat ctctgggggt tctctatctc
 660

cagtatggag atgaa

675

<210> 1254

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1254

```
Met Gly His Gln Glu Arg Leu Arg Asp Gln Thr Arg Ile Pro Lys Leu
 1             5             10             15
Ser His Ser Pro Gln Pro Pro Ser Val Gly Asp Pro Val Glu His Leu
                20             25             30
Ser Glu Thr Ser Ala Asp Ser Leu Glu Ala Met Ser Glu Gly Asp Ala
 35             40             45
Pro Thr Pro Phe Ser Arg Gly Ser Arg Thr Arg Ala Ser Leu Pro Val
 50             55             60
Val Arg Ser Thr Asn Gln Thr Lys Glu Arg Ser Leu Gly Val Leu Tyr
 65             70             75             80
Leu Gln Tyr Gly Asp Glu
                        85
```

<210> 1255

<211> 401

<212> DNA

<213> Homo sapiens

<400> 1255

```
ncgccgatta ccaaggctat ggatgtgtgg gccttggggc taacgctata ctgtctgctg
 60
ttcggtcgag tgccatttga tgcagagacg gagtacttgc tgctggaaag tatectgcat
120
gacgattatg ccgtcccgcac gcacatgggt agcgaccgcg tgttggtagg cccgcgacca
180
gcacgttggc cctcgtcgca agagacgccc aacgtgccgc tgtccggcga ggcgcatgca
240
gtacgcccatc tgctcgatgc ccttctcgac aaggatccag cgacgcgcct cactctcgat
300
cgtgttataa cacacccatg gctcgtggca gagtcattgt aatagtagca attgtatata
360
ccctcatcac caagatggcc aaagcggtag aagggccgcg g
401
```

<210> 1256

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1256

```
Xaa Pro Ile Thr Lys Ala Met Asp Val Trp Ala Leu Gly Val Thr Leu
 1             5             10             15
Tyr Cys Leu Leu Phe Gly Arg Val Pro Phe Asp Ala Glu Thr Glu Tyr
 20             25             30
Leu Leu Leu Glu Ser Ile Leu His Asp Asp Tyr Ala Val Pro Thr His
```



```

          35              40              45
Met Gly Ser Asp Arg Val Leu Val Gly Pro Arg Pro Ala Arg Trp Pro
   50              55              60
Ser Ser Gln Glu Thr Pro Asn Val Pro Leu Ser Gly Glu Ala His Ala
65              70              75              80
Val Arg His Leu Leu Asp Ala Leu Leu Asp Lys Asp Pro Ala Thr Arg
          85              90              95
Leu Thr Leu Asp Arg Val Ile Thr His Pro Trp Leu Val Ala Glu Ser
          100              105              110
Trp

```

<210> 1257

<211> 294

<212> DNA

<213> Homo sapiens

<400> 1257

```

cgcgtagacgc tgattgaagg tgatgtcgcc aacgccgacc tgggtggcgca agccgccatc
60
ggcgccacgg cggtggtgca tttggcagcg gtggcttcgg tgcaagcctc ggtggatgac
120
ccggtcagca cgcgccagag caatcttctc ggcacctga atgtctcgca agccatgcgc
180
aaggccgggtg tgaagcgtgt ggtatttctc tccagcgttg cggtgtatgg caacaatggc
240
gagggcgctt cgattgacga agagaccatc aaggcccccgc tgacgcctta cgcg
294

```

<210> 1258

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1258

```

Arg Val Gln Leu Ile Glu Gly Asp Val Ala Asn Ala Asp Leu Val Ala
1              5              10              15
Gln Ala Ala Ile Gly Ala Thr Ala Val Val His Leu Ala Ala Val Ala
20              25              30
Ser Val Gln Ala Ser Val Asp Asp Pro Val Ser Thr Arg Gln Ser Asn
35              40              45
Phe Val Gly Thr Leu Asn Val Cys Glu Ala Met Arg Lys Ala Gly Val
50              55              60
Lys Arg Val Val Phe Ala Ser Ser Val Ala Val Tyr Gly Asn Asn Gly
65              70              75              80
Glu Gly Ala Ser Ile Asp Glu Glu Thr Ile Lys Ala Pro Leu Thr Pro
          85              90              95
Tyr Ala

```

<210> 1259

<211> 417

<212> DNA

<213> Homo sapiens

<400> 1259
 nnacactcta gcctctgact caaggaagct gccagggtc ttgcccttcg gtttggggg
 60
 atcccgcttc ccttcgctcg gagcagacat agtgagaacg tgagaagctg caggcggtggc
 120
 ctcaccgtgg tgtgttccaa gatgtccagg gccaaaggatg ccgtgtcctc cgggggtggc
 180
 agcggtggtg acgtggctaa gggagtggtc caggggaggcc tggacaccac tcgggtctgca
 240
 cttacgggca ccaaggaggc ggtgtccagc ggggtcacag gggccatgga catggctaag
 300
 ggggcccgtc aagggggtct ggacacctcg aaggctgtcc tcaccggcac caaggacacg
 360
 gtgtccactg gggtcacagg ggcagtgaat gtggccaaag ggcccgtaca ggccggc
 417

<210> 1260

<211> 133

<212> PRT

<213> Homo sapiens

<400> 1260

Leu	Lys	Glu	Ala	Ala	Gln	Gly	Leu	Ala	Leu	Arg	Phe	Gly	Gly	Ile	Pro
1				5					10					15	
Ser	Pro	Phe	Val	Trp	Ser	Arg	His	Ser	Glu	Asn	Val	Arg	Ser	Cys	Arg
			20					25					30		
Arg	Gly	Leu	Thr	Val	Val	Cys	Ser	Lys	Met	Ser	Arg	Ala	Lys	Asp	Ala
			35				40				45				
Val	Ser	Ser	Gly	Val	Ala	Ser	Val	Val	Asp	Val	Ala	Lys	Gly	Val	Val
		50				55				60					
Gln	Gly	Gly	Leu	Asp	Thr	Thr	Arg	Ser	Ala	Leu	Thr	Gly	Thr	Lys	Glu
				70					75					80	
Ala	Val	Ser	Ser	Gly	Val	Thr	Gly	Ala	Met	Asp	Met	Ala	Lys	Gly	Ala
			85					90					95		
Val	Gln	Gly	Gly	Leu	Asp	Thr	Ser	Lys	Ala	Val	Leu	Thr	Gly	Thr	Lys
			100				105					110			
Asp	Thr	Val	Leu	Ser	Thr	Gly	Leu	Thr	Gly	Ala	Val	Asn	Val	Ala	Lys
			115				120					125			
Pro	Val	Gln	Ala	Gly											
			130												

<210> 1261

<211> 330

<212> DNA

<213> Homo sapiens

<400> 1261

ngtgcactg cegttcggca tcaggagatg aacatggatt tgaacgctga agtcgatcag
 60
 ctggtccgcc aatcccagac ctggatcccc ttgatcatgg agtaacggcag ccgcctgctg
 120tgaccctggc ggtcggtcgg tggatcgaca acaaggctcag cgcccgcctg 180
 ggcaaacctgg taggcctcgc caacgccgac ctggcactgc aaggctttat cagcaccttg
 240

tcgaacatcg ggctgaaagt gctgctgttc gtcagtgtgg cgctcatgat cggcattgag
 300
 accacctcgt tcgtcgcgga catcggtgct
 330

<210> 1262
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1262
 Xaa Ala Arg Ala Val Arg His Gln Glu Met Asn Met Asp Leu Asn Ala
 1 5 10 15
 Glu Val Asp Gln Leu Val Arg Gln Ser Gln Thr Trp Ile Pro Leu Ile
 20 25 30
 Met Glu Tyr Gly Ser Arg Leu Leu Leu Ala Leu Leu Thr Leu Ala Val
 35 40 45
 Gly Trp Trp Ile Asp Asn Lys Val Ser Ala Arg Leu Gly Lys Leu Val
 50 55 60
 Gly Leu Arg Asn Ala Asp Leu Ala Leu Gln Gly Phe Ile Ser Thr Leu
 65 70 75 80
 Ser Asn Ile Gly Leu Lys Val Leu Leu Phe Val Ser Val Ala Ser Met
 85 90 95
 Ile Gly Ile Glu Thr Thr Ser Phe Val Ala Asp Ile Gly Ala
 100 105 110

<210> 1263
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1263
 acgctggac gatggacttc gtcggtctgc ggtacgacga agggctcaac attgccggtg
 60
 gcatcgatga tgagtttgct cgcctgggca acacctagca gcaatggcat cgaatagtc
 120
 tgcccagcct gctccatttc gaagcagatg gtcgccgggt tcagtttctt ctcgctccac
 180
 gtcaacagac cgtcaccgtg gttgacgac tcgccgggtgg aggcgtcctt gacgacgatc
 240
 tggccacgcg ccagggaata catctcccca tccacccaaa agaagcggcc caagctgggg
 300
 atcttgccca gcccgatgat cgagagggtt tcaacaagcg actcggggatc c
 351

<210> 1264
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1264
 Met Pro Ser Leu Gly Ala Phe Phe Trp Val Asp Gly Glu Met Tyr Ser
 1 5 10 15
 Leu Ala Arg Gly Gln Ile Val Val Lys Asp Ala Ser Thr Gly Glu Ile

```

                20                25                30
Val Asn His Gly Asp Gly Leu Leu Thr Trp Ser Glu Lys Lys Leu Asn
      35                40                45
Pro Ala Thr Ile Val Val Glu Met Glu Gln Ala Gly Gln Gly Leu Ser
      50                55                60
Met Pro Leu Leu Leu Gly Val Ala Gln Ala Ser Lys Leu Ile Ile Asp
      65                70                75                80
Ala Thr Gly Asn Val Glu Pro Phe Val Val Pro Gln Thr Asp Glu Val
      85                90                95
His Arg Pro Arg
      100

```

<210> 1265

<211> 318

<212> DNA

<213> Homo sapiens

<400> 1265

```

accggtgtat gcaactgaaa tgctgtccga tatgcttgcg ctccagctcg tgaatcgaaa
60
gttgataaac gctcgcttgg tggaatcgtc gctacggaag cttatcaagg atacggatgc
120
tgctgcaccg ccaaaattat ggacgcccc cgacccact cgctctgacg ataccattgc
180
acagccgaaa gtgcaaccag cccaagcagt gggagatgac tcgatcatgt cggtcgatga
240
gcctgatgca accgtccatg acatgccact caccacgaca ctcgacaacg tgggtcgctc
300
agatccatcg cgacgcgt
318

```

<210> 1266

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1266

```

Met Leu Ser Asp Met Pro Ala Leu Gln Leu Val Asn Arg Lys Leu Asp
  1                5                10                15
Asn Ala Arg Leu Val Glu Ser Ser Leu Arg Lys Leu Ile Lys Asp Thr
      20                25                30
Asp Ala Ala Ala Pro Pro Lys Leu Trp Thr Pro Pro Asp Pro Thr Arg
      35                40                45
Ser Asp Asp Thr Ile Ala Gln Pro Lys Val Gln Pro Ala Gln Ala Val
      50                55                60
Gly Asp Asp Ser Ile Met Ser Val Asp Glu Pro Asp Ala Thr Val His
      65                70                75                80
Asp Met Pro Leu Thr Thr Thr Leu Asp Asn Val Gly Arg Ser Asp Pro
      85                90                95
Ser Arg Arg

```

<210> 1267

<211> 343

<212> DNA

<213> Homo sapiens

<400> 1267

nggacacttg tgggaaatgc cccacagcct gtgtttttat tccccttggtg aacacttgtg
 60
 ggaactgtcc caccgcccgt gtttctgtgc gcctgcagac actcgtggga aatgccccac
 120
 aacctgtgtt tttgttcccc ttgtgaacac tcgtgggaaa tgcaccacaa cctgtgtttt
 180
 tattccccct gtgaacactc gtgggaaatg tcccatggcc cgtgtttccg tgcacctgog
 240
 gatactcatc aaacaccagg ctgtcattgg ggacagggtg agctctggct gttggtgcag
 300
 catggtagga agagcaccaa gtccctggact ctgttgattt ata
 343

<210> 1268

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1268

Met	Pro	His	Ser	Leu	Cys	Phe	Tyr	Ser	Pro	Cys	Glu	His	Leu	Trp	Glu
1				5					10				15		
Leu	Ser	His	Gly	Pro	Cys	Phe	Cys	Ala	Pro	Ala	Asp	Thr	Arg	Gly	Lys
			20					25					30		
Cys	Pro	Thr	Thr	Cys	Val	Phe	Val	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
			35					40					45		
Cys	Pro	Thr	Thr	Cys	Val	Phe	Ile	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
			50				55				60				
Cys	Pro	Met	Ala	Arg	Val	Ser	Val	His	Leu	Arg	Ile	Leu	Ile	Lys	His
65					70				75					80	
Gln	Ala	Val	Ile	Gly	Asp	Arg	Val	Ser	Ser	Gly	Cys	Trp	Cys	Ser	Met
					85				90					95	
Val	Gly	Arg	Ala	Pro	Ser	Pro	Gly	Leu	Cys						
			100					105							

<210> 1269

<211> 391

<212> DNA

<213> Homo sapiens

<400> 1269

tcgcatccg gagegatcgg tgctgcagat ggctggcgac gccctgcggg gcgcattgog
 60
 ggacgcgcgac ctggagccgg ccgccctaga cgggctgac gtccagggtg ggtccccccg
 120
 cgccgcggac tacgacacg gtccgaaac ctttggctt tcgccacaat tctgcagcca
 180
 gacctggggc gcacggccgg ttaccgcaa cggtgatcct ggcagcgccc atggcggtgt
 240
 ccagcggcct cgccggcggg gtggcttgcc tcatgggcat gaagaattcg gacctcgggc
 300

ggttgggtga ggcggacaat ccctttcatc atgagcaatt ccgggagaat ggcgggccc
 360
 acggggaaga ggggttgatc ggcattggcct c
 391

<210> 1270
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1270
 Met Met Lys Gly Ile Val Arg Leu Thr Gln Pro Pro Glu Val Arg Ile
 1 5 10 15
 Leu His Ala His Glu Ala Ser His Pro Arg Glu Ala Ala Gly His
 20 25 30
 Arg His Gly Arg Cys Gln Asp His Arg Cys Gly Glu Pro Ala Val Arg
 35 40 45
 Pro Arg Ser Gly Cys Arg Ile Val Ala Lys Asp Gln Arg Phe Arg Thr
 50 55 60
 Arg Cys Arg Ser Pro Arg Arg Gly Gly Thr Pro Pro Gly Arg Ser Ala
 65 70 75 80
 Arg Leu Gly Arg Pro Ala Pro Gly Arg Arg Pro Ala Met Arg Pro Ala
 85 90 95
 Gly Arg Arg Gln Pro Ser Ala Ala Pro Ile Ala Pro Asp Arg
 100 105 110

<210> 1271
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 1271
 acgcgtcggtt actggccacc tgcgagcgca ccagggtagg cagcactcgg tctccgtcga
 60
 accagaaagc gtcattcggg tgggtgaacga gaacgggcca tggtgtggtg ggacggataa
 120
 cccccgggtt cgtcaccata tggcccacta aagagttcac cagggttgat ttaccagccc
 180
 cggtcgacc tcctaccacc gccagaagcg gcgcatcaat agtctctaag cgcggcaaaa
 240
 tatagtcggtt aagctgggta gcgatgcgtc gtgccagccc ggcttgagta atagcctccg
 300
 gcaaatccaa ggggaactgg gcctgacgca ggttgtgccc gagatcggc aacgacagca
 360
 gtatctgctc agtgttcatt gtgattcttc ctggtcactc gtcaggcctg tggcgggcgc
 420
 cactgcaact cgttgttgac cggctgggtg cgacgtcgct tgaggaatgc gggcagttct
 480
 ggcttcgaca atttggcacc tcggggcagc gtgatagccg ccgggagcag cacgttcata
 540
 cgggttgatga gtcgatctg aagcggacca ggatcatcgt ccaaccacg cacaatggcg
 600
 tcacgaagat aagcaagatc tgtcccaacg cgcaggaact ctaacgtgtg ccaccacggg
 660

t

661

<210> 1272

<211> 126

<212> PRT

<213> Homo sapiens

<400> 1272

```

Met Asn Thr Glu Gln Ile Leu Leu Ser Leu Thr Asp Leu Arg His Asn
 1           5           10           15
Leu Arg Gln Ala Gln Phe Pro Leu Asp Leu Pro Glu Ala Ile Thr Gln
      20           25           30
Ala Gly Leu Ala Arg Arg Ile Ala Asn Gln Leu Asn Asp Tyr Ile Leu
 35           40           45
Pro Arg Leu Glu Thr Ile Asp Ala Pro Leu Leu Ala Val Val Gly Gly
 50           55           60
Ser Thr Gly Ala Gly Lys Ser Thr Leu Val Asn Ser Leu Val Gly His
 65           70           75           80
Met Val Thr Gln Pro Gly Val Ile Arg Pro Thr Thr Thr Ser Pro Val
      85           90           95
Leu Val His His Pro Asp Asp Ala Phe Trp Phe Asp Gly Asp Arg Val
 100           105           110
Leu Pro Thr Leu Val Arg Ser Gln Val Ala Ser Asn Asp Ala
 115           120           125

```

<210> 1273

<211> 489

<212> DNA

<213> Homo sapiens

<400> 1273

```

gccggcgaga ccgggtgccg aaagaccatg gtggtcaccg gtattggttt gctgctcggc
 60
gacaaggctg acattggatt ggtccggcat ggctcgcgac gtgccgtcgt cgaagccggt
 120
ctcgacacgc ctgatgccgg tcgcgtcagc gagcttggcg gaacagtcga ggaatggtgag
 180
gttatctgcg ctcgacacat cacgagtcgt cgctctcgag cgctgcttgg aggagctcaa
 240
gttacccgcta gtcagctggc ccacatcggt ggggatcagg tgaccatcca tggccaatct
 300
gaacaagtga ggttggtcga cgcagcgccg cagctcgacg tcgttgaccg gggtgccgga
 360
gatgagctgg caggctacct aagtcgacat gcacagctgt ggtcggagtt tcgtgctgca
 420
tcccagcgtc ttcagcgccct caacgaggat cgcgctgggg ccgagatgga acgcgaggtg
 480
cttacgcgt
 489

```

<210> 1274

<211> 163

<212> PRT

<213> Homo sapiens

<400> 1274

Ala Gly Glu Thr Gly Ala Gly Lys Thr Met Val Val Thr Gly Ile Gly
 1 5 10 15
 Leu Leu Leu Gly Asp Lys Ala Asp Thr Gly Leu Val Arg His Gly Cys
 20 25 30
 Asp Arg Ala Val Val Glu Ala Val Leu Asp Thr Pro Asp Ala Gly Arg
 35 40 45
 Val Ser Glu Leu Gly Gly Thr Val Glu Asp Gly Glu Val Ile Cys Ala
 50 55 60
 Arg His Ile Thr Ser Arg Arg Ser Arg Ala Leu Gly Gly Ala Gln
 65 70 75 80
 Val Thr Ala Ser Gln Leu Ala His Ile Val Gly Asp Gln Val Thr Ile
 85 90 95
 His Gly Gln Ser Glu Gln Val Arg Leu Val Asp Ala Ala Arg Gln Leu
 100 105 110
 Asp Val Val Asp Arg Ala Ala Gly Asp Glu Leu Ala Gly Tyr Leu Ser
 115 120 125
 Arg His Ala Gln Leu Trp Ser Glu Phe Arg Ala Ala Ser Gln Arg Leu
 130 135 140
 Gln Arg Leu Asn Glu Asp Arg Ala Gly Ala Glu Met Glu Arg Glu Val
 145 150 155 160
 Leu Thr Arg

<210> 1275

<211> 384

<212> DNA

<213> Homo sapiens

<400> 1275

nngctagcaa gtgcaagtac gagcaaaagt tatcagcaac agcgggagggc tgaacttctc
 60
 gtcgcacggc tagaggggga aatgcacgca cacagcgacc cgaccccgtc gccacaacca
 120
 cccgaggatg cagggttgat tgatgttgcc ctgaaagagg cgaagaaagc ctttgatgaa
 180
 ggcaaggtcg atctaattgga taaactcaat caggagatac ttcgcctggc aaacgaattc
 240
 ggtgcgctcg ggcttgaatc tattgagctt ggctccgacg cgaagatggc agtacgcaaa
 300
 ggcaaatcaga aatcagcggt cagcaggctg actcccggtg aacgtctcag gctgcgcatt
 360
 gctacagcca tcgctgtggt acgc
 384

<210> 1276

<211> 128

<212> PRT

<213> Homo sapiens

<400> 1276

Xaa Leu Ala Ser Ala Ser Thr Ser Lys Ser Tyr Gln Gln Gln Arg Glu


```

      1             5             10             15
Ala Glu Leu Leu Val Ala Arg Leu Glu Gly Glu Met His Ala His Ser
      20             25             30
Asp Pro Thr Pro Ser Pro Gln Pro Pro Glu Asp Ala Gly Leu Ile Asp
      35             40             45
Val Ala Leu Lys Glu Ala Lys Lys Ala Phe Asp Glu Gly Lys Val Asp
      50             55             60
Leu Met Asp Lys Leu Asn Gln Glu Ile Leu Arg Leu Ala Asn Glu Phe
      65             70             75             80
Gly Ala Leu Gly Leu Glu Ser Ile Glu Leu Gly Ser Asp Ala Lys Met
      85             90             95
Ala Val Arg Lys Gly Asn Gln Lys Ser Ala Phe Ser Arg Leu Thr Pro
      100             105             110
Gly Glu Arg Leu Arg Leu Arg Ile Ala Thr Ala Ile Ala Leu Leu Arg
      115             120             125

```

<210> 1277

<211> 392

<212> DNA

<213> Homo sapiens

<400> 1277

```

cagtttcagc cccgctgtgt gtccccaatt cctgtctctc ctaccagcgg gattcagaac
60
ccagtggcct tcctcagctc tgttctgcct tctctccctg ccattcccacc cacaaatgcc
120
atgggggtgc ctagaagtgc accatccatg ccattcccagg gattagcgaa gaaaaataca
180
aagtctcttc aaccagttaa tgatgataac attcgtgaaa ctaagaacgc agtgattcga
240
gacttgggga aaaaaataac ttctcagtgt gtcagaccaa accagcagga gtacaaaaat
300
tcaagctttg agcagaggct gatgaatgaa atagagtttc gcttggaaac tactcctgtt
360
gatgaatcac atgatgaaat tcaacatgat gg
392

```

<210> 1278

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1278

```

Gln Phe Gln Pro Arg Cys Val Ser Pro Ile Pro Val Ser Pro Thr Ser
      1             5             10             15
Arg Ile Gln Asn Pro Val Ala Phe Leu Ser Ser Val Leu Pro Ser Leu
      20             25             30
Pro Ala Ile Pro Pro Thr Asn Ala Met Gly Leu Pro Arg Ser Ala Pro
      35             40             45
Ser Met Pro Ser Gln Gly Leu Ala Lys Lys Asn Thr Lys Ser Pro Gln
      50             55             60
Pro Val Asn Asp Asp Asn Ile Arg Glu Thr Lys Asn Ala Val Ile Arg
      65             70             75             80
Asp Leu Gly Lys Lys Ile Thr Phe Ser Asp Val Arg Pro Asn Gln Gln

```

```

      85              90              95
Glu Tyr Lys Ile Ser Ser Phe Glu Gln Arg Leu Met Asn Glu Ile Glu
      100              105              110
Phe Arg Leu Glu Arg Thr Pro Val Asp Glu Ser His Asp Glu Ile Gln
      115              120              125
His Asp
      130

```

<210> 1279

<211> 297

<212> DNA

<213> Homo sapiens

<400> 1279

```

atggagtcgc agactctccg ccacatgatc gaggacgact gcgccgacaa cggcatccca
60
ctccccaacg tcaactccag gatcctctct aaggtcatcg agtactgcaa cagtcacgct
120
cacgcccgcc ccaaacccgc tgactccgct gcctccgagg gcggcgagga cctcaagagc
180
tgggacgcga agttcgtaaa ggtggaccag gctacgctct tcgacctcat cctggctgcc
240
aactatctga acatcaaggg attgctggac ctgacctgcc agacgggtgc tgacatg
297

```

<210> 1280

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1280

```

Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp Cys Ala Asp
1              5              10              15
Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val
      20              25              30
Ile Glu Tyr Cys Asn Ser His Val His Ala Ala Ala Lys Pro Ala Asp
      35              40              45
Ser Ala Ala Ser Glu Gly Gly Glu Asp Leu Lys Ser Trp Asp Ala Lys
      50              55              60
Phe Val Lys Val Asp Gln Ala Thr Leu Phe Asp Leu Ile Leu Ala Ala
      65              70              75              80
Asn Tyr Leu Asn Ile Lys Gly Leu Leu Asp Leu Thr Cys Gln Thr Gly
      85              90              95
Ala Asp Met

```

<210> 1281

<211> 515

<212> DNA

<213> Homo sapiens

<400> 1281

```

acgcgtgaag ggggctttgg aggggatggc ttctggactg cacgatgggt gaacacagtt
60

```

ttttaaactc ttttccacat ctgtataggt ttgaaaatta tcaacaactc atggggaggg
 120
 tggcgtgccca ggctcatggct gcttgaggac cttctgagga gggccggctc aaccgaggac
 180
 gccctcccca ctaccaagta ggcactgcgg gcaggagtcg cccccccac cccaaggaag
 240
 ttcagaacag gcaacaggag gagcctgact ccaacagagt tgggtgtcatc cggcgcatcg
 300
 ctaaggagct cacaacacat caactctggg agcccaaggg ggtgtgtggt ccaactcaagg
 360
 ggaagatgat ccagaagctc tgcctccctcc ctttgccttt gaagaacaca ggagtgcac
 420
 gtggggaatc taccggctta atttctctt agtaacaggc atagtaggat caaaaaattt
 480
 ttgcttctaa tttttaaaaa cattcaatgt gtaca
 515

<210> 1282

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1282

Met Gly Glu His Ser Phe Leu Asn Ser Phe Pro His Leu Tyr Arg Phe
 1 5 10 15
 Glu Asn Tyr Gln Gln Leu Met Gly Arg Val Ala Cys Gln Val Met Ala
 20 25 30
 Ala Trp Ser Pro Ser Glu Glu Gly Arg Leu Asn Arg Gly Arg Pro Pro
 35 40 45
 His Tyr Gln Val Gly Thr Ala Gly Arg Ser Arg His Pro His Pro Lys
 50 55 60
 Glu Val Gln Asn Arg Gln Gln Glu Glu Pro Asp Ser Asn Arg Val Gly
 65 70 75 80
 Val Ile Arg Arg Ile Ala Lys Asp Val Thr Thr His Gln Leu Trp Glu
 85 90 95
 Pro Lys Gly Val Cys Gly Pro Leu Lys Gly Lys Met Ile Gln Lys Leu
 100 105 110
 Cys Ser Leu Pro Leu Leu Leu Lys Asn Thr Gly Val Thr Arg Gly Glu
 115 120 125
 Ser Thr Gly Leu Ile Ser Ser
 130 135

<210> 1283

<211> 296

<212> DNA

<213> Homo sapiens

<400> 1283

gaattctca caatgaactg cagtgtctgg aggaccagtt gggtagcctt actccgggtc
 60
 tcactcgac aacttatata tatatgcttt gtgcacacaa agaaaaacag cagcccaaaa
 120
 gaatcccgcc tggggctctt aggaggagg aaagtccca caggtaactc actggttaat
 180

tttaaagagc tcaggaaagg aaggaaggat ggctttttct cttgtgagtc aagacaaggt
 240
 cctgatgata accctcccag atcagaacgt aactttcaac ccacgagtgc tgctcn
 296

<210> 1284

<211> 94

<212> PRT

<213> Homo sapiens

<400> 1284

Met	Asn	Cys	Ser	Val	Trp	Arg	Thr	Ser	Trp	Val	Ala	Leu	Leu	Arg	Val
1				5					10					15	
Ser	Thr	Ala	Glu	Leu	Ile	His	Ile	Cys	Phe	Val	His	Thr	Lys	Lys	Asn
			20					25					30		
Ser	Ser	Pro	Lys	Glu	Ser	Arg	Leu	Gly	Leu	Leu	Gly	Gly	Arg	Lys	Val
		35					40				45				
Pro	Thr	Gly	Asn	Ser	Leu	Val	Asn	Phe	Lys	Glu	Leu	Arg	Lys	Gly	Arg
	50					55					60				
Lys	Asp	Gly	Phe	Phe	Ser	Cys	Glu	Ser	Arg	Gln	Gly	Pro	Asp	Asp	Asn
65					70				75					80	
Pro	Pro	Arg	Ser	Glu	Arg	Asn	Phe	Gln	Pro	Thr	Ser	Ala	Ala		
				85					90						

<210> 1285

<211> 526

<212> DNA

<213> Homo sapiens

<400> 1285

gggccccttc ttacctgccc cttcccctgt ccaccaaccc gtagacaggg agggcaagca
 60
 gtgaaaggtc catctagagg aggtaaaaga cagggtctgag ggaaaacgcc ttgtacagtc
 120
 aggatggcag atgtactctg tcagggaaga cagccccaca gaaaaggctc ggcttgccca
 180
 agaagcaaca aaagggattc tacacctcag accaggggagg gggaatgtgt acaaaagattg
 240
 gatttactaa attcagagcc acagacttct aggtactctg gtgaagatca gtgctctttc
 300
 aaaccacac ttcagaggca ggctttaaaa cgcctgactt ctgtcagggc cacaggctgg
 360
 gctgccccaa gctcctacgg ggctggggga tccgagagag gacttcccac tagtccaaga
 420
 tgtggtgact agtttcaagc cacagattga ggagcagacc tgatgccctt tcggggccct
 480
 gctaagaacc tgattcgagg aaaaggaagt gaagacagta acgcgt
 526

<210> 1286

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1286

```

Met Ala Asp Val Leu Cys Gln Gly Arg Gln Pro His Arg Lys Gly Ser
 1           5           10          15
Ala Trp Pro Arg Ser Asn Lys Arg Asp Ser Thr Pro Gln Thr Arg Glu
          20           25           30
Gly Glu Cys Val Gln Arg Leu Asp Leu Leu Asn Ser Glu Pro Gln Thr
 35           40           45
Phe Arg Tyr Phe Gly Glu Asp Gln Cys Ser Phe Lys Pro Thr Leu Gln
 50           55           60
Arg Gln Ala Leu Lys Arg Leu Thr Ser Val Arg Ala Thr Gly Trp Ala
 65           70           75           80
Ala Gln Ser Ser Tyr Gly Ala Gly Gly Ser Glu Arg Gly Leu Pro Thr
          85           90           95
Ser Pro Arg Cys Gly Asp
          100

```

<210> 1287

<211> 333

<212> DNA

<213> Homo sapiens

<400> 1287

```

acgcgtgaag gggagaggca gctccagggtg gagggaagtg catgaggaag cagagaggca
 60
ggcgacaggc agcgtggctg gggctgggca ggccttcagg ttgtattgca gccagagggt
120
caggtagaag gaaggtacaa caagcaagga agggccagg aagccactgg ggggtgtttga
180
gccattgaat attctggatt ttaggacatt tctgtggctg actccactgc catcagagtt
240
catccacccc aactccagcc tgagagtgtc ggggcactgg gcaactccgga attcttcaaa
300
gtctgtatgc aacatgtccc cagggtgtct gac
333

```

<210> 1288

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1288

```

Met Leu His Gln Ser Phe Glu Glu Phe Arg Ser Ala Gln Cys Pro Ser
 1           5           10          15
Thr Leu Arg Leu Glu Leu Gly Trp Met Asn Ser Asp Gly Ser Gly Val
          20           25           30
Ser His Arg Asn Val Leu Lys Ser Arg Ile Phe Asn Gly Ser Asn Thr
 35           40           45
Pro Ser Gly Phe Leu Gly Pro Ser Leu Leu Val Val Pro Ser Ser His
 50           55           60
Leu Thr Ser Gly Leu Gln Ser Asn Trp Lys Ala Cys Pro Ala Pro Ala
 65           70           75           80
Thr Leu Pro Val Ala Cys Leu Ser Ala Ser Ser Cys Thr Ser Leu His
          85           90           95
Leu Glu Leu Pro Leu Pro Phe Thr Arg

```

100

105

<210> 1289
 <211> 336
 <212> DNA
 <213> Homo sapiens

<400> 1289
 accggtgtct gtgtacaggt ggaaggggat gggatatgaga tgggtgcagcg tgtgcatggg
 60
 caccggcgtat ggtgtgtgag tgcactcgtg tgccggagag ctgtaagctg ctggcgtgagt
 120
 cctgcacggt ggaggaggca aggtggcccc tgcctgtggg cacagagccc accttccggg
 180
 ccagcccagag gcccttttcc cagagcccc tccaaggagg ccataaccacc tgcattccca
 240
 agatggcgtg gggcgctccct ggtgcaggag caggggacag tcagggaggc gtgtggcgga
 300
 cagtagcagc cccccagccc ccctccccc accggt
 336

<210> 1290
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 1290
 Met Val Cys Glu Cys Thr Arg Val Pro Glu Ser Cys Lys Leu Leu Ala
 1 5 10 15
 Glu Ser Cys Thr Val Glu Glu Ala Arg Trp Pro Leu Pro Val Gly Thr
 20 25 30
 Glu Pro Thr Phe Arg Ser Ser Pro Arg Pro Leu Ser Gln Ser Pro Leu
 35 40 45
 Pro Arg Gly His Thr Thr Cys Ile Pro Lys Met Ala Trp Gly Val Pro
 50 55 60
 Gly Ala Gly Ala Gly Asp Ser Gln Gly Gly Val Trp Arg Thr Val Ala
 65 70 75 80
 Ala Pro Gln Pro Pro Ser Pro His Arg
 85

<210> 1291
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 1291
 tggccatcca cctctgtcag ctgttccggc aacccattca gatcattgtg gtagtaacga
 60
 atcttctgca acggcccggc accgtccacg cgagccagag gttgatagcc ttcattctca
 120
 taaactgaca ggcttgtctg gctgtgttta tgctcctgca ataaccgcaa accatcccg
 180
 gtaaaccggg tttcccccaa cggataccca tcaactgccat gctcggtttt tctatccga
 240

cgccccagcg ggtcatcac catcctgacc acgctacat cgtcattacg cacttcaacc
 300
 agccggcttt cagcgctcata cgcaaaccgc tgcacgccac gcttggcact gcgcttctcg
 360
 accatccgcc caaacgcgt
 379

<210> 1292
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1292
 Met Val Glu Lys Arg Ser Ala Lys Arg Gly Val Gln Arg Phe Ala Tyr
 1 5 10 15
 Asp Ala Glu Ser Arg Leu Val Glu Val Arg Asn Asp Asp Gly Ser Val
 20 25 30
 Val Arg Met Val Tyr Asp Pro Leu Gly Arg Arg Ile Glu Lys Thr Glu
 35 40 45
 His Gly Ser Asp Gly Tyr Pro Leu Gly Glu Thr Arg Phe Thr Trp Asp
 50 55 60
 Gly Leu Arg Leu Leu Gln Glu His Lys His Ser Gln Thr Ser Leu Tyr
 65 70 75 80
 Val Tyr Glu Asp Glu Gly Tyr Gln Pro Leu Ala Arg Val Asp Gly Ala
 85 90 95
 Gly Pro Leu Gln Lys Ile Arg Tyr Tyr His Asn Asp Leu Asn Gly Leu
 100 105 110
 Pro Glu Gln Leu Thr Glu Val Asp Gly
 115 120

<210> 1293
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 1293
 nngccggcgc ccgagagct gttcgaggcg tgccgcaacg gggacgtgga acgagtcgaag
 60
 aggcctggtga cgcttgagaa ggtgaacagc cgcgacacgg cgggcaggaa atccaccccg
 120
 ctgcacttgc ccgaggttt tgggcggaaa gacgtagttg aatatttctc tcagaatggt
 180
 gcaaatgtcc aagcacgtga tgatgggggc cttattcttc ttcataatgc atgctctttt
 240
 ggtcatgctg aagtagtcaa tctctctttg cgacatggtg cagaccccaa tgcttgagat
 300
 aattggaatt atactcctag aggggtggagt gtgctcgcga
 340

<210> 1294
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 1294

```

Xaa Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys Arg Asn Gly Asp Val
 1             5             10             15
Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys Val Asn Ser Arg Asp
             20             25             30
Thr Ala Gly Arg Lys Ser Thr Pro Leu His Phe Ala Ala Gly Phe Gly
             35             40             45
Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala Asn Val Gln
             50             55             60
Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala Cys Ser Phe
             65             70             75             80
Gly His Ala Glu Val Val Asn Leu Leu Arg Arg His Gly Ala Asp Pro
             85             90             95
Asn Ala

```

<210> 1295

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1295

```

ggatcccga gacctcgctcg gcgaacgtca cctcgccag gccgcaggcg cggaacaccg
60
acgtgtcgat gccctcgccc tcgatgcagt cggtcagcgg tacgcaggcg ccgcggggagg
120
cgaaggtgcc gatctggctg cgctcggcgt agaccagcga cggcggttcg cccgacgcga
180
cggaggagag gaactgctgg atgtcgaggt cacctcgat cagcttgacc ttggcgctcg
240
cgagctcctc cttcgcccg tcgagccgca ccgtcgcgat ctcgtcgccg gcaccgaagc
300
ccatcacctc gacctcgccg gagagcttcg ccccgctgtc gaaagacgcg t
351

```

<210> 1296

<211> 75

<212> PRT

<213> Homo sapiens

<400> 1296

```

Gly Ser Arg Arg Pro Arg Arg Arg Thr Ser Pro Arg Pro Gly Pro Arg
 1             5             10             15
Arg Gly Thr Pro Thr Cys Arg Cys Pro Arg Pro Arg Cys Ser Arg Ser
             20             25             30
Ala Val Arg Arg Arg Arg Gly Arg Arg Arg Cys Arg Ser Gly Cys Ala
             35             40             45
Arg Arg Arg Pro Ala Thr Ala Val Arg Pro Thr Pro Arg Arg Arg Gly
             50             55             60
Thr Ala Gly Cys Arg Gly His Pro Arg Ser Ala
             65             70             75

```

<210> 1297

<211> 356

<212> DNA

<213> Homo sapiens

<400> 1297

gtgcaccgg attccattg ccaccgactt cgagtaaact ccagtcccga ggacacgaga
 60
 gacacccagg cctcaggccc catgggcacg ctccacgcc aaggctcctac cagagggaga
 120
 gatacatctt acaaatctcg gggcccacca caccaagaag acacggagga gccaaacaaa
 180
 gaaggaccat acgaaatgca cccccaaagc aaccaaccaa tccaagaaaa aatacgtctc
 240
 aggggttctgt gggccctctt gcatgggctg cctgcccccc ctgtttctgc ctggctcaag
 300
 caccttacc cagcctgctc gaaagagccc tggctaccag agcagagcac tggcct
 356

<210> 1298

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1298

Met	Gly	Thr	Leu	His	Ala	Thr	Ala	Pro	Thr	Arg	Gly	Thr	Asp	Thr	Leu
1				5					10				15		
Tyr	Lys	Ser	Arg	Gly	Pro	Pro	His	Gln	Glu	Asp	Thr	Glu	Glu	Pro	Thr
			20					25					30		
Lys	Glu	Gly	Pro	Tyr	Glu	Met	His	Pro	Gln	Ser	Asn	Gln	Pro	Ile	Gln
		35					40					45			
Glu	Lys	Ile	Arg	Leu	Arg	Val	Leu	Trp	Ala	Leu	Leu	His	Gly	Leu	Pro
		50				55				60					
Cys	Pro	Pro	Val	Leu	Ala	Trp	Leu	Lys	His	Leu	Thr	Pro	Ala	Cys	Ser
65					70				75					80	
Lys	Glu	Pro	Trp	Leu	Pro	Glu	Gln	Ser	Thr	Gly					
			85						90						

<210> 1299

<211> 307

<212> DNA

<213> Homo sapiens

<400> 1299

ggatccactt ctaagatgtc tcaactcacgt ggtgatggca gcaggcctca gactctgggtg
 60
 gttgttgcca ggtgtgtctc gttccttgcc atgtgggtct ctacacaggg cagcttctctg
 120
 tgtctttgccc atatggcaac tgagaatgat cttggctacc ttctccagcc cgaggatcgg
 180
 gaggttttctg ggggtgggtc acgggtcttg cccggagttc gccctggcaa aggcctgtgc
 240
 cagtgatctt ggagcggagc gaagtgttcc cgtgactctg cagccgcagt tcttaggggt
 300
 tccttag
 307

<210> 1300
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 1300
 Met Ala Ala Gly Leu Arg Leu Trp Trp Leu Leu Ala Gly Cys Leu Ser
 1 5 10 15
 Ser Leu Pro Cys Gly Ser Leu His Arg Ala Ala Ser Cys Val Phe Ala
 20 25 30
 Ile Trp Gln Leu Arg Met Ile Leu Ala Thr Phe Ser Ser Pro Gly Val
 35 40 45
 Gly Ser Phe Leu Gly Trp Gly His Gly Ser Cys Pro Glu Phe Ala Leu
 50 55 60
 Ala Lys Ala Cys Ala Ser Asp Pro Gly Ala Glu Arg Ser Val Ser Val
 65 70 75 80
 Thr Leu Gln Pro Gln Phe Leu Gly Leu Pro
 85 90

<210> 1301
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 1301
 ctgagcaagt taaaagaagt tcttgaattt tataacttta ttttgacaaa ctattataaa
 60
 gttgagccta tttcctttga tgcagtatac gctgaagggt tggaaatggc tgagtctcttg
 120
 cgccctatgg tgtcagatac gattacactt ttgcatgacc ttagaagggtc tggcgcaaac
 180
 atcatgtttg aaggcgcgca aggggtctttg ttggatgttg atcatggtac ttaccgcgtat
 240
 gtgacttcat ctaatacgac tgcgggcgga gcgcagcgg gaacagggtt ttgtcctttg
 300
 tacttagatt atgtattagg taccactaag gcttatacga ctgcggttgg ttctggacct
 360
 ttccctactg agttgtttga cgaagatggt gagcgtcttg gtacgcgt
 408

<210> 1302
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 1302
 Leu Ser Lys Leu Lys Glu Val Leu Glu Phe Tyr Asn Phe Ile Leu Thr
 1 5 10 15
 Asn Tyr Tyr Lys Val Glu Pro Ile Ser Phe Asp Ala Val Tyr Ala Glu
 20 25 30
 Gly Leu Glu Met Ala Glu Phe Leu Arg Pro Met Val Ser Asp Thr Ile
 35 40 45
 Thr Leu Leu His Asp Leu Arg Arg Ser Gly Ala Asn Ile Met Phe Glu

50	55	60
Gly Ala Gln Gly Ser Leu Leu Asp Val Asp His Gly Thr Tyr Pro Tyr		
65	70	75
Val Thr Ser Ser Asn Thr Thr Ala Gly Gly Ala Pro Ala Gly Thr Gly		80
	85	90
Phe Gly Pro Leu Tyr Leu Asp Tyr Val Leu Gly Ile Thr Lys Ala Tyr		95
	100	105
Thr Thr Arg Val Gly Ser Gly Pro Phe Pro Thr Glu Leu Phe Asp Glu		110
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<210> 1303

<211> 1037

<212> DNA

<213> Homo sapiens

<400> 1303

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<210> 1304

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1304

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          20          25          30
Arg Arg Pro Pro Arg Ala Ser Thr Lys Thr Gly Ser Gln Pro Ala
 35          40          45
Met Pro Ser Pro Leu Arg Pro Gln Gly Ser Ala Gly Val Leu Pro Glu
 50          55          60
Pro Arg Val Pro Val Gln Lys Pro Gly Ile Asn Ala Ala Ser Pro Ile
 65          70          75          80
Gly Thr Val Arg Val Glu Arg Gly Arg Pro Thr Val Ser Pro Ala Gly
          85          90          95
Arg Gly Ser Pro Arg Gly Gly His Val Gly Gly Leu Thr Ala Pro Ser
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Thr Pro Gly His Ser Asp His Gly Leu His Thr Gln Lys Gln Ser Gly
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Ser His Ala Trp
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<210> 1305

<211> 775

<212> DNA

<213> Homo sapiens

<400> 1305

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660

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gataatccac ataccaagcc tctgaatttc tgggcctggc tcatggaaca gggtcatcgt
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<210> 1306

<211> 258

<212> PRT

<213> Homo sapiens

<400> 1306

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 35 40 45
 Asp Ala Asp Gly His Trp Val Ser Gly Thr Phe Asp Thr Ser Trp Glu
 50 55 60
 Arg Leu Asp Ala Ala Ala Met Gly Phe Asp Val Val Tyr Leu Pro
 65 70 75 80
 Ala Ile His Pro Met Gly Gln Ala Phe Arg Lys Gly Lys Asp Asn Thr
 85 90 95
 Leu Thr Pro Gly Pro Asp Asp Pro Gly Ser Pro Trp Ala Ile Gly Ser
 100 105 110
 Ser Asp Gly Gly His Asp Thr Ile His Pro Asp Leu Gly Thr Phe Asp
 115 120 125
 Asp Leu Asp Arg Phe Val Ala His Ala His Asp Leu Gly Met Glu Val
 130 135 140
 Ala Leu Asp Phe Ala Leu Gln Ala Ser Pro Asp His Pro Trp Val His
 145 150 155 160
 Gln His Pro Glu Trp Phe Thr Thr Arg Val Asp Gly Thr Ile Ala Tyr
 165 170 175
 Ala Glu Asn Ser Pro Lys Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe
 180 185 190
 Asp Asn Asp Pro Asp Gly Ile Tyr Gln Glu Cys Leu Arg Leu Leu Glu
 195 200 205
 Leu Trp Ile Ser His Gly Val Thr Ile Phe Arg Val Asp Asn Pro His
 210 215 220
 Thr Lys Pro Leu Asn Phe Trp Ala Trp Leu Met Glu Gln Val His Arg
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 Arg His Pro Glu Val Ile Phe Leu Ala Glu Ala Phe Thr Arg Pro Glu
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<210> 1307

<211> 624

<212> DNA

<213> Homo sapiens

<400> 1307

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<210> 1308

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1308

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His	Ala	Ala	Thr	Ala	Trp	Gly	Cys	Arg	Ala	Leu	Leu	Gly	Ala	Val	Cys
			20				25					30			
Leu	Cys	Ser	Gly	Ser	Leu	Gly	Trp	Gln	Gly	Leu	Ala	Pro	Ser	Gly	Thr
		35				40					45				
Arg	Gly	Ala	Leu	Ala	Ser	Gly	Cys	Gly	Thr	Glu	His	Val	Glu	Trp	Leu
	50				55				60						
Trp	Ser	Ser	Thr	Ala	Gln	Ala	Gln	Gly	Pro	Asp	Arg	Met	Cys	Pro	Ala
65				70				75					80		
Ser	Leu	Thr	Ser	Pro	Glu	Val	Gly	Cys	Arg	Glu	Pro	Gly	Ala	Trp	His
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Ser	Pro	Pro	Ala												
			100												

<210> 1309

<211> 563

<212> DNA

<213> Homo sapiens

<400> 1309

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<210> 1310

<211> 183

<212> PRT

<213> Homo sapiens

<400> 1310

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 35 40 45
 Ile Asp Arg Gly Asn Ala His Lys Ala Arg Arg Ser Met Leu Thr Thr
 50 55 60
 Thr His Thr Leu Gln His Lys Asp Thr Ser Ile Trp Val Phe Ala Glu
 65 70 75 80
 Gly Thr Arg Asn Phe Gly Glu Thr Leu Leu Pro Phe Lys Lys Gly Ala
 85 90 95
 Phe Gln Met Ala Ile Ala Ala Gly Val Pro Ile Val Gln Val Cys Val
 100 105 110
 Ser Thr Tyr Val Lys His Met Lys Leu Asn Arg Trp Asp Ser Gly Asp
 115 120 125
 Ile Leu Ile Arg Ser Leu Pro Pro Ile Pro Thr Thr Gly Leu Thr Leu
 130 135 140
 Asp Asp Met Pro Arg Leu Met Glu Thr Cys Arg Gln Gln Met Arg Glu
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 Cys Ile Glu Ala Met Asp Arg Glu Leu Glu Ile Val Pro Cys Arg Asn
 165 170 175
 Glu Leu Ala Arg Glu Gly Arg
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<210> 1311

<211> 674

<212> DNA

<213> Homo sapiens

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<210> 1312

<211> 196

<212> PRT

<213> Homo sapiens

<400> 1312

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		20						25					30		
Gln	Asp	Pro	Ala	Cys	Glu	Pro	His	Arg	Asp	Asn	Arg	Gly	Asp	His	Pro
		35					40				45				
Ala	Tyr	Gln	Gly	Gly	Gln	His	Cys	Gly	Ser	His	Leu	His	Lys	Asp	Asp
	50				55						60				
Leu	Val	His	Pro	Thr	Pro	Ala	Gln	Ser	Asp	Ala	Phe	Glu	Ala	Gly	His
	65			70					75					80	
Gln	Ile	Thr	Val	Gly	Gly	Ser	Leu	Leu	Leu	Arg	Gln	Gln	Ala	Arg	His
		85						90					95		
Asp	Gly	Arg	Gln	His	Asp	Glu	Gly	Asp	Gly	Arg	Asp	Asp	Gly	Asp	Arg
	100						105					110			
Trp	Gln	Arg	Asp	Ile	Thr	Glu	Asp	Ser	Gly	Gly	His	Asp	Ile	Lys	Phe
	115					120					125				
Pro	Gln	Pro	Val	Arg	Leu	Arg	Pro	Leu	Val	Gly	Gln	Ser	Ile	Leu	Ile
	130				135						140				
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	145				150				155					160	
Ser	Gly	Phe	Arg	Arg	Pro	Gly	Asp	Ala	Leu	Asp	Pro	Ala	Gln	Ile	Ile
		165					170						175		
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 35 40 45
 Ser Ser Ser Arg Ala Pro Leu Leu Ala Lys Thr Pro Leu Ser Thr Ser
 50 55 60
 Tyr Thr His Gln Lys Pro Arg Ser His Thr Arg Leu Cys Pro Leu Pro
 65 70 75 80
 Ser Leu Pro Pro Pro Ser Ile Leu Ser Pro Lys Ser Arg Asp Cys Pro
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4620
ggtctaaagg tagaatgtga atattgccac agagtttcatt gctctcagta taagatttta
4680
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4740
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4800
taaagtctga ggattttcgt caaccttact gaaacacact ggtgctttca tcatcagagg
4860
tcaaatatt atgataacta ttccattaag tttgccaaac atttgtcgtg gttaccagtg
4920

cagcctgtca aattctgcta ttgacacag ctttggaag atttagttct tggtttttcc
 4980
 gttttgtatt agaagactg ttacagtttt atttggtgtg ttaagccaa attcagctat
 5040
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 5100
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 5245

<210> 1316

<211> 856

<212> PRT

<213> Homo sapiens

<400> 1316

Met	Asp	Glu	Asp	Ser	Ser	Leu	Arg	Asp	Tyr	Thr	Val	Ser	Leu	Asp	Ser
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Asp	Met	Asp	Asp	Ala	Ser	Lys	Leu	Leu	Gln	Asp	Tyr	Asp	Ile	Arg	Thr
			20				25						30		
Gly	Asn	Thr	Arg	Glu	Ala	Leu	Ser	Pro	Cys	Pro	Ser	Thr	Val	Ser	Thr
			35				40					45			
Lys	Ser	Gln	Pro	Gly	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Gly	Val	Lys	Met
			50				55					60			
Thr	Ser	Phe	Ala	Glu	Gln	Lys	Phe	Arg	Lys	Leu	Asn	His	Thr	Asp	Gly
							70					75			80
Lys	Ser	Ser	Gly	Ser	Ser	Ser	Gln	Lys	Thr	Thr	Pro	Glu	Gly	Ser	Glu
							85					90			95
Leu	Asn	Ile	Pro	His	Val	Val	Ala	Trp	Ala	Gln	Ile	Pro	Glu	Glu	Thr
							100					105			110
Gly	Leu	Pro	Gln	Gly	Arg	Asp	Thr	Thr	Gln	Leu	Leu	Ala	Ser	Glu	Met
							115					120			125
Val	His	Leu	Arg	Met	Lys	Leu	Glu	Glu	Lys	Arg	Arg	Ala	Ile	Glu	Ala
							130					135			140
Gln	Lys	Lys	Lys	Met	Glu	Ala	Ala	Phe	Thr	Lys	Gln	Arg	Gln	Lys	Met
							145					150			155
Gly	Arg	Thr	Ala	Phe	Leu	Thr	Val	Val	Lys	Lys	Lys	Gly	Asp	Gly	Ile
							160					165			170
Ser	Pro	Leu	Arg	Glu	Glu	Ala	Ala	Gly	Ala	Glu	Asp	Glu	Lys	Val	Tyr
							175					180			185
Thr	Asp	Arg	Ala	Lys	Glu	Lys	Glu	Ser	Gln	Lys	Thr	Asp	Gly	Gln	Arg
							190					195			200
Ser	Lys	Ser	Leu	Ala	Asp	Ile	Lys	Glu	Ser	Met	Glu	Asn	Pro	Gln	Ala
							205					210			215
Lys	Trp	Leu	Lys	Ser	Pro	Thr	Thr	Pro	Ile	Asp	Pro	Glu	Lys	Gln	Trp
							220					225			230
Asn	Leu	Ala	Ser	Pro	Ser	Glu	Glu	Thr	Leu	Asn	Glu	Gly	Glu	Ile	Leu
							235					240			245
Glu	Tyr	Thr	Lys	Ser	Ile	Glu	Lys	Leu	Asn	Ser	Ser	Leu	His	Phe	Leu
							250					255			260
Gln	Gln	Glu	Met	Gln	Arg	Leu	Ser	Leu	Gln	Gln	Glu	Met	Leu	Met	Gln
							265					270			

275					280					285					
Met	Arg	Glu	Gln	Gln	Ser	Trp	Val	Ile	Ser	Pro	Pro	Gln	Pro	Ser	Pro
290					295					300					
Gln	Lys	Gln	Ile	Arg	Asp	Phe	Lys	Pro	Ser	Lys	Gln	Ala	Gly	Leu	Ser
305	310					315					320				
Ser	Ala	Ile	Ala	Pro	Phe	Ser	Ser	Asp	Ser	Pro	Arg	Pro	Thr	His	Pro
325					330					335					
Ser	Pro	Gln	Ser	Ser	Asn	Arg	Lys	Ser	Ala	Ser	Phe	Ser	Val	Lys	Ser
340					345					350					
Gln	Arg	Thr	Pro	Arg	Pro	Asn	Glu	Leu	Lys	Ile	Thr	Pro	Leu	Asn	Arg
355					360					365					
Thr	Leu	Thr	Pro	Pro	Arg	Ser	Val	Asp	Ser	Leu	Pro	Arg	Leu	Arg	Arg
370	375					380					385				
Phe	Ser	Pro	Ser	Gln	Val	Pro	Ile	Gln	Thr	Arg	Ser	Phe	Val	Cys	Phe
385	390					395					400				
Gly	Asp	Asp	Gly	Glu	Pro	Gln	Leu	Lys	Glu	Ser	Lys	Pro	Lys	Glu	Glu
405					410					415					
Val	Lys	Lys	Glu	Glu	Leu	Glu	Ser	Lys	Gly	Thr	Leu	Glu	Gln	Arg	Gly
420					425					430					
His	Asn	Pro	Glu	Glu	Lys	Glu	Ile	Lys	Pro	Phe	Glu	Ser	Thr	Val	Ser
435					440					445					
Glu	Val	Leu	Ser	Leu	Pro	Val	Thr	Glu	Thr	Val	Cys	Leu	Thr	Pro	Asn
450	455					460					465				
Glu	Asp	Gln	Leu	Asn	Gln	Pro	Thr	Glu	Pro	Pro	Pro	Lys	Pro	Val	Phe
465	470					475					480				
Pro	Pro	Thr	Ala	Pro	Lys	Asn	Val	Asn	Leu	Ile	Glu	Val	Ser	Leu	Ser
485					490					495					
Asp	Leu	Lys	Pro	Pro	Glu	Lys	Ala	Asp	Val	Pro	Val	Glu	Lys	Tyr	Asp
500					505					510					
Gly	Glu	Ser	Asp	Lys	Glu	Gln	Phe	Asp	Asp	Asp	Gln	Lys	Val	Cys	Cys
515					520					525					
Gly	Phe	Phe	Phe	Lys	Asp	Asp	Gln	Lys	Ala	Glu	Asn	Asp	Met	Ala	Met
530					535					540					
Lys	Arg	Ala	Ala	Leu	Leu	Glu	Lys	Arg	Leu	Arg	Arg	Glu	Lys	Glu	Thr
545	550					555					560				
Gln	Leu	Arg	Lys	Gln	Gln	Leu	Glu	Ala	Glu	Met	Glu	His	Lys	Lys	Glu
565					570					575					
Glu	Thr	Arg	Arg	Lys	Thr	Glu	Glu	Glu	Arg	Gln	Lys	Lys	Glu	Asp	Glu
580					585					590					
Arg	Ala	Arg	Arg	Glu	Phe	Ile	Arg	Gln	Glu	Tyr	Met	Arg	Arg	Lys	Gln
595					600					605					
Leu	Lys	Leu	Met	Glu	Asp	Met	Asp	Thr	Val	Ile	Lys	Pro	Arg	Pro	Gln
610					615					620					
Val	Val	Lys	Gln	Lys	Lys	Gln	Arg	Pro	Lys	Ser	Ile	His	Arg	Asp	His
625	630					635					640				
Ile	Glu	Ser	Pro	Lys	Thr	Pro	Ile	Lys	Gly	Pro	Pro	Val	Ser	Ser	Leu
645					650					655					
Ser	Leu	Ala	Ser	Leu	Asn	Thr	Gly	Asp	Asn	Glu	Ser	Val	His	Ser	Gly
660					665					670					
Lys	Arg	Thr	Pro	Arg	Ser	Glu	Ser	Val	Glu	Gly	Phe	Leu	Ser	Pro	Ser
675					680					685					
Arg	Cys	Gly	Ser	Arg	Asn	Gly	Glu	Lys	Asp	Trp	Glu	Asn	Ala	Ser	Thr
690	695					700					705				
Thr	Ser	Ser	Val	Ala	Ser	Gly	Thr	Glu	Tyr	Thr	Gly	Pro	Lys	Leu	Tyr

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705              710              715              720
Lys Glu Pro Ser Ala Lys Ser Asn Lys His Ile Ile Gln Asn Ala Leu
              725              730              735
Ala His Cys Cys Leu Ala Gly Lys Val Asn Glu Gly Gln Lys Lys Lys
              740              745              750
Ile Leu Glu Glu Met Glu Lys Ser Asp Ala Asn Asn Phe Leu Ile Leu
              755              760              765
Phe Arg Asp Ser Gly Cys Gln Phe Arg Ser Leu Tyr Thr Tyr Cys Pro
              770              775              780
Glu Thr Glu Glu Ile Asn Lys Leu Thr Gly Ile Gly Pro Lys Ser Ile
785              790              795              800
Thr Lys Lys Met Ile Glu Gly Leu Tyr Lys Tyr Asn Ser Asp Arg Lys
              805              810              815
Gln Phe Ser His Ile Pro Ala Lys Thr Leu Ser Ala Ser Val Asp Ala
              820              825              830
Ile Thr Ile His Ser His Leu Trp Gln Thr Lys Arg Pro Val Thr Pro
              835              840              845
Lys Lys Leu Leu Pro Thr Lys Ala
              850              855

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<210> 1317

<211> 1123

<212> DNA

<213> Homo sapiens

<400> 1317

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120
gagggttagcc agcctagcac catggacgcc accgcagtag caggcatcga gaccaagaaa
180
gagaaggagg acctgtgctt gctaaagaag gaggagaagg aggagccagt agccccggag
240
ctggcaacaa cgggtgcctga gagcgagag cctgaggcag agggcgagcg ggaggagctg
300
gacggcagcg acatgtcagc catcatctat gaaatcccca aggagcctga gaagaggcgg
360
cggagcaagc ggtcgcggtt gatggatgct gacggcctgc tcgagatgtt ccactgccca
420
tacgagggtc gcagccaagt ctacgtggcc ctacagcagt tccagaacca cgtcaatett
480
gtgcatcgga aaggaaagac caaagtgtgc cctcatcctg gctgtggcaa gaagtcttat
540
ttatccaacc acctcgcgcg gcacatgac atccattcag gtgtccgtga attcacctgc
600
gagacctgag gcaagtcctt caagaggaag aaccacctgg aggtacatcg gcgcacccac
660
accggcgaga cccccctgca gtgcgtgac tgtggctacc agtgcgggca gcgcgcgtcg
720
ctcaactggc acatgaagaa gcacactgag gaggtgcagt acaacttcac gtgcgatgcc
780
tcggggaagc gcttcgagaa gctggacagc gtcaagttcc acacgctcaa aagccacccg
840

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gatacacaagc ccacctgacc cacctgacca ctgaccgccc ctattttatc gtcgctcgg
 900
 acaccacagc cggggttg cggggcctgg acagctgcga gggccggcgg gaccgcggggc
 960
 cggaaggagc gccccgccc cgccccagag ctggcgcccc tgggcaggtt cccaccccg
 1020
 cccacacgca tccttctcgg agctggtgcc tggggtgca ttgctggaac tgtgtcaaga
 1080
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 1123

<210> 1318

<211> 285

<212> PRT

<213> Homo sapiens

<400> 1318

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Gly	Ser	Gly	Leu	Gly	Glu	Glu	Val	Pro	Cys	Ala	Met	Met	Glu	Gly	Val
			20					25					30		
Ala	Ala	Tyr	Thr	Gln	Thr	Glu	Pro	Glu	Gly	Ser	Gln	Pro	Ser	Thr	Met
		35					40				45				
Asp	Ala	Thr	Ala	Val	Ala	Gly	Ile	Glu	Thr	Lys	Lys	Glu	Lys	Glu	Asp
	50					55					60				
Leu	Cys	Leu	Leu	Lys	Lys	Glu	Glu	Lys	Glu	Glu	Pro	Val	Ala	Pro	Glu
65					70					75				80	
Leu	Ala	Thr	Thr	Val	Pro	Glu	Ser	Ala	Glu	Pro	Glu	Ala	Glu	Ala	Asp
				85					90					95	
Gly	Glu	Glu	Leu	Asp	Gly	Ser	Asp	Met	Ser	Ala	Ile	Ile	Tyr	Glu	Ile
			100					105					110		
Pro	Lys	Glu	Pro	Glu	Lys	Arg	Arg	Arg	Ser	Lys	Arg	Ser	Arg	Val	Met
			115					120					125		
Asp	Ala	Asp	Gly	Leu	Leu	Glu	Met	Phe	His	Cys	Pro	Tyr	Glu	Gly	Cys
	130					135					140				
Ser	Gln	Val	Tyr	Val	Ala	Leu	Ser	Ser	Phe	Gln	Asn	His	Val	Asn	Leu
145					150					155					160
Val	His	Arg	Lys	Gly	Lys	Thr	Lys	Val	Cys	Pro	His	Pro	Gly	Cys	Gly
				165					170					175	
Lys	Lys	Phe	Tyr	Leu	Ser	Asn	His	Leu	Arg	Arg	His	Met	Ile	Ile	His
			180					185					190		
Ser	Gly	Val	Arg	Glu	Phe	Thr	Cys	Glu	Thr	Cys	Gly	Lys	Ser	Phe	Lys
			195				200					205			
Arg	Lys	Asn	His	Leu	Glu	Val	His	Arg	Arg	Thr	His	Thr	Gly	Glu	Thr
	210					215					220				
Pro	Leu	Gln	Cys	Val	Ile	Cys	Gly	Tyr	Gln	Cys	Arg	Gln	Arg	Ala	Ser
225					230					235					240
Leu	Asn	Trp	His	Met	Lys	Lys	His	Thr	Ala	Glu	Val	Gln	Tyr	Asn	Phe
				245					250					255	
Thr	Cys	Asp	Ala	Cys	Gly	Lys	Arg	Phe	Glu	Lys	Leu	Asp	Ser	Val	Lys
			260					265					270		
Phe	His	Thr	Leu	Lys	Ser	His	Pro	Asp	His	Lys	Pro	Thr			
			275				280						285		

<210> 1319

<211> 538

<212> DNA

<213> Homo sapiens

<400> 1319

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 120
 ctgaatgtgt gaatgggtcc ctgggtgctt tccttcctct gggagctccg tgggagagtg
 180
 gagtcgatgc caagtcagag agcagttggg gaggaaccca gaagccctgg gatggtgtct
 240
 gcatggggaat gtgtagggag gcagccacaa tgggcctggg ccttccttcc tctccttcc
 300
 gtccccctcc cccatcccc tctctcctcc ctctcttctg gaaacccagt actgggggaa
 360
 acacacacag gtgggatgca ggtatccggg aagctcatag aagctgccac gctgctggag
 420
 tttgcctcat acaggagcgt gggcatgccc cgcgtggagt tgtgctgtgt gtgtgcatat
 480
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 538

<210> 1320

<211> 169

<212> PRT

<213> Homo sapiens

<400> 1320

Met	Arg	Ala	Trp	Lys	Gln	Met	Ala	Ser	Gln	Ser	Ser	Ile	Trp	Glu	Asp
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Ser	Gln	Asn	Ser	Ala	Gly	Ser	Arg	Gly	Trp	Gly	Met	Ala	Pro	Ala	Glu
		20					25					30			
Cys	Val	Asn	Gly	Ser	Leu	Gly	Ala	Phe	Leu	Pro	Leu	Gly	Ala	Pro	Trp
		35				40						45			
Glu	Ser	Gly	Val	Asp	Ala	Lys	Ser	Glu	Ser	Ser	Trp	Gly	Gly	Thr	Gln
	50					55					60				
Lys	Pro	Trp	Asp	Gly	Val	Cys	Met	Gly	Met	Cys	Arg	Glu	Ala	Ala	Thr
	65				70				75					80	
Met	Gly	Leu	Gly	Leu	Pro	Phe	Ser	Pro	Ser	Cys	Pro	Pro	Pro	Pro	Ser
			85						90					95	
Pro	Ser	Leu	Leu	Pro	Ser	Phe	Trp	Lys	Pro	Ser	Thr	Gly	Gly	Asn	Thr
		100						105					110		
His	Arg	Trp	Asp	Ala	Gly	Ile	Arg	Glu	Ala	His	Arg	Ser	Cys	His	Ala
		115					120					125			
Ala	Gly	Val	Cys	Leu	Ile	Gln	Glu	Arg	Gly	His	Ala	Pro	Arg	Gly	Val
		130				135					140				
Val	Leu	Cys	Val	Cys	Ile	Cys	Met	Val	Val	Cys	Ala	Trp	Gly	Trp	Gly
	145				150					155				160	
Ile	Leu	Thr	Trp	Gly	His	Ser	Gln	Ser							
					165										

<210> 1321

<211> 1292

<212> DNA

<213> Homo sapiens

<400> 1321

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120
cgccccgacg gctcacggtg cgcaacgacg aagcagggat cgtcagacc cgggcacgtc
180
atcgtcaaga agatttataa caacaatgtc cttctcggcg tcaacggttc ggggaccgaa
240
atggctcgtca atgctcgcgg tatcgccctac ggacgacacc gcggggagat cgtcagtgcc
300
tcgctcgccc agcgatatgt cgcagagggg gcctatcgca cgaccgccat cgcacactg
360
ctaacgaacg ccaactcacg cgaggtgcga gtggcacagg caatcgtcga attggcgcgc
420
gaagagctgg gcaactccca tgcccgacgg atgatgctgc ccatcctcga tcacctcgtc
480
gcagctgtgc accgagctaa gcaggggggc gtcacgatt tccccctgga atgggaagtc
540
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600
gctctcgaaa tccatttgca acccgaggaa tgggtggcat tctccctgca cttcatcaat
660
cagcgggtgg acagtagaga cgttttcgcg accatgtcga tgactcagac gatctcgac
720
gttttcaccg agctggagga cctgtggcac gttgagatcg accgttcgtc catgagcgca
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840
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900
gcagctagcc aagtggccga gcacatatcg aaagcaatcg gcaacgacct gacggaagcc
960
gaaatcaact acatcgccct acacaccacc cggctctaca acgaggtgat ggggatggat
1020
gactgacgat cgcgcacctg ttaaggctca tcggtagtgg gcaatacaca aaatggcgat
1080
gaccttcctg ccgaaaagcc agcaccaaa gtcaccagat caaaattcag atgcgtgcct
1140
aattcccacc ccgacatcca agaggtcagg ggggggttgt tgggggttgt ggggtggggg
1200
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1292

<210> 1322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 1322

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Arg Pro Asp Arg Ser Arg Tyr Ala Thr Thr Lys Gln Gly Ser Leu Arg
      20           25           30
Pro Gly His Val Ile Val Lys Lys Ile Tyr Asn Asn Asn Val Leu Leu
 35           40           45
Gly Val Asn Gly Ser Gly Thr Glu Met Val Val Asn Ala Arg Gly Ile
 50           55           60
Ala Tyr Gly Arg His Arg Gly Glu Ile Val Asp Ala Ser Ser Ala Gln
65           70           75           80
Arg Tyr Val Ala Glu Gly Ala Tyr Arg Thr Thr Ala Ile Ala Ser Leu
      85           90           95
Leu Thr Asn Ala Thr His Thr Glu Val Arg Val Ala Gln Ala Ile Val
      100          105          110
Glu Leu Ala Arg Glu Glu Leu Gly Thr Pro His Ala Arg Arg Met Met
      115          120          125
Leu Pro Ile Leu Asp His Leu Val Ala Ala Val His Arg Ala Lys Gln
      130          135          140
Gly Ala Val Ile Asp Phe Pro Leu Glu Trp Glu Val Arg Gln Leu Tyr
      145          150          155          160
Pro Asp Glu Ala Glu Leu Gly Arg Arg Ala Val Glu Ile Val Asp Gly
      165          170          175          180
Ala Leu Glu Ile His Leu Gln Pro Glu Glu Trp Val Ala Phe Ser Leu
      180          185          190
His Phe Ile Asn Gln Arg Trp Asp Ser Arg Asp Val Ser Arg Thr Met
      195          200          205
Ser Met Thr Gln Thr Ile Cys Asp Val Phe Thr Glu Leu Glu Asp Leu
      210          215          220
Trp His Val Glu Ile Asp Arg Ser Ser Met Ser Ala Ser Arg Phe Val
      225          230          235          240
Thr His Leu Arg Tyr Leu Phe Ala Arg Ala Ser Asp Asn Lys Gln Leu
      245          250          255
Ser His Val Asp Leu Asp Ile Val Gly Leu Met Ser Asp Arg Tyr Pro
      260          265          270
Glu Ala Thr Leu Ala Ala Ser Gln Val Ala Glu His Ile Ser Lys Ala
      275          280          285
Ile Gly Asn Asp Leu Thr Glu Ala Glu Ile Asn Tyr Ile Ala Leu His
      290          295          300
Thr Thr Arg Leu Tyr Asn Glu Val Met Gly Met Asp Asp
      305          310          315

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<210> 1323

<211> 306

<212> DNA

<213> Homo sapiens

<400> 1323

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60
ggcaaaattg ctgagatgcg tacaggtgaa ggtaaaaccc tgatgggtac tttagcgtgt
120

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tacctcaatg cattgagtg tgagggtgtg catgtcatca cegtcaatga ctatcttgca
 180
 caacgtgatg ctgaactcaa cegcccatga tttgagtttt tgggtttaag catcggtgtg
 240
 atttattcga tgcaaatgcc tgctgagaaa gcacaagctt atttagcaga cactacttac
 300
 ggtacc
 306

<210> 1324
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1324
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 Thr Leu His Glu Gly Lys Ile Ala Glu Met Arg Thr Gly Glu Gly Lys
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 Thr Leu Met Gly Thr Leu Ala Cys Tyr Leu Asn Ala Leu Ser Gly Gln
 35 40 45
 Gly Val His Val Ile Thr Val Asn Asp Tyr Leu Ala Gln Arg Asp Ala
 50 55 60
 Glu Leu Asn Arg Pro Leu Phe Glu Phe Leu Gly Leu Ser Ile Gly Val
 65 70 75 80
 Ile Tyr Ser Met Gln Met Pro Ala Glu Lys Ala Gln Ala Tyr Leu Ala
 85 90 95
 Asp Ile Thr Tyr Gly Thr
 100

<210> 1325
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 1325
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 attgtcgccg catgttccgt ctccgctcat gccggaagct ggccagagaa accgatcacg
 120
 atggctcgtgc cgtttcccgc cggaggcggc accgatctcg tggcgcgctc gatccagccg
 180
 cttttgcagc gcgaactcgg acaaccgggtg gtgatcgaca accgcagcgg cgcaggcgggc
 240
 acgctcggct ccagcttcgt ggcgcgggcc gttgccgacg gctacacggc tggcgtggtc
 300
 accacgagca cccacgcggt aagcgtcgcg ctctatcccc ggctggccta caaccgaca
 360
 gcggactttg catacgccgg cttcatcggc n
 391

<210> 1326
 <211> 130
 <212> PRT

<213> Homo sapiens

<400> 1326

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Val His Met Gly Pro Leu Ala Asn Pro Thr Arg Gly Leu Arg Arg Ala
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Ile Leu Ala Ala Ile Val Ala Ala Cys Ser Val Ser Ala His Ala Gly
      20           25           30
Ser Trp Pro Glu Lys Pro Ile Thr Met Val Val Pro Phe Pro Ala Gly
      35           40           45
Gly Gly Thr Asp Leu Val Ala Arg Ser Ile Gln Pro Leu Leu Gln Arg
      50           55           60
Glu Leu Gly Gln Pro Val Val Ile Asp Asn Arg Ser Gly Ala Gly Gly
65           70           75           80
Thr Leu Gly Ser Ser Phe Val Ala Arg Ala Val Ala Asp Gly Tyr Thr
      85           90           95
Ala Gly Val Val Thr Thr Ser Thr His Ala Val Ser Val Ala Leu Tyr
      100          105          110
Pro Arg Leu Ala Tyr Asn Pro Thr Ala Asp Phe Ala Tyr Ala Gly Phe
      115          120          125
Ile Gly
      130

```

<210> 1327

<211> 324

<212> DNA

<213> Homo sapiens

<400> 1327

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nnacgcgtga ttctcggaact gcagcagttc gagcagtcgc atggacacag cgacgggagc
60
tacttgctat ggttcgagct gctgtggcga gactatttcc gctttctgca tcttcggcat
120
ggcgctcgcc tgtaccgcgc acgcggcctc gcaaatgagg tacggcacgc ggagcgccca
180
gatgtgcagg gcttcgagcg ctggcgctcgt gcacgcaccg gcgagccgct cgtcgatgcc
240
gcgatgcgcg agctggagac caccggctac ctcagcaaca ggctcagaca ggtgtgcgcg
300
agctacctcg tgcacgagct ggga
324

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<210> 1328

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1328

```

Xaa Arg Val Ile Ser Glu Leu Gln Gln Phe Glu Gln Ser His Gly Gln
 1           5           10           15
Ser Asp Gly Ser Tyr Trp Leu Trp Phe Glu Leu Leu Trp Arg Asp Tyr
      20           25           30
Phe Arg Phe Leu His Leu Arg His Gly Ala Arg Leu Tyr Arg Ala Arg
      35           40           45
Gly Leu Ala Asn Glu Val Arg His Ala Glu Arg Pro Asp Val Gln Gly

```

```

      50              55              60
Phe Glu Arg Trp Arg Arg Ala Ser Thr Gly Glu Pro Leu Val Asp Ala
65              70              75              80
Ala Met Arg Glu Leu Glu Thr Thr Gly Tyr Leu Ser Asn Arg Leu Arg
      85              90              95
Gln Val Val Ala Ser Tyr Leu Val His Glu Leu Gly
      100              105

```

<210> 1329

<211> 438

<212> DNA

<213> Homo sapiens

<400> 1329

```

ngtgcacgct tagcattaga tttagcttcc agtggcaaaa ctacgtcggt gatttcaagc
60
ggcgatatacg gcatttacgc gatggcgacc ctgggtgttg aactgctgga tagacaactc
120
cagggccttg aagaccatcc tgaatgggta gatgttgaaa tcgatgtggt acctggcatc
180
tctgcaatgc aagctggtgc aagtcgtatt ggtgcatgt taggtcatga cttttgtacg
240
gtgagtttgt ctgatttatt aaccctttgg gaaactatta ataaactgat tcatagtcca
300
ggtgaggggg attttgttat ctctttttat aaccctgttt ctaagaaacg tgattggcag
360
cttaaccacg cgcgtgatgt attattgaaa taccgtccag catcaacgcc agttttatta
420
ggtcgtcagt tgacgcgt
438

```

<210> 1330

<211> 146

<212> PRT

<213> Homo sapiens

<400> 1330

```

Xaa Ala Arg Leu Ala Leu Asp Leu Ala Ser Ser Gly Lys Thr Thr Ser
1      5      10      15
Leu Ile Ser Ser Gly Asp Ile Gly Ile Tyr Ala Met Ala Thr Leu Val
      20      25      30
Phe Glu Leu Leu Asp Arg Gln Leu Gln Gly Leu Glu Asp His Pro Glu
      35      40      45
Trp Leu Asp Val Glu Ile Asp Val Val Pro Gly Ile Ser Ala Met Gln
      50      55      60
Ala Gly Ala Ser Arg Ile Gly Ala Met Leu Gly His Asp Phe Cys Thr
65      70      75      80
Val Ser Leu Ser Asp Leu Leu Thr Pro Trp Glu Thr Ile Asn Lys Arg
      85      90      95
Ile His Ser Ala Gly Glu Gly Asp Phe Val Ile Ser Phe Tyr Asn Pro
      100      105      110
Val Ser Lys Lys Arg Asp Trp Gln Leu Asn His Ala Arg Asp Val Leu
      115      120      125
Leu Lys Tyr Arg Pro Ala Ser Thr Pro Val Leu Leu Gly Arg Gln Leu

```

130
 Thr Arg
 145
 <210> 1331
 <211> 453
 <212> DNA
 <213> Homo sapiens
 <400> 1331
 gcgtaccgct ccgcggaact ggtgatgatg accgaggcac cgggatgcgg aatcccttgg
 60
 catcttcttg ccggcatcgg acgcatcgaa tccggtcacg ccaacggcgg caagacgacc
 120
 tcggtgggta cgaacgtcac cccgatcctc ggccccatcc tcgacggacg gctggcaggc
 180
 aacgaagtca ttcgggacac cgacaagggc aatcgacggc gaccactca cgaccgcgcc
 240
 gtcggggccga tgcagttcat tccggccacc tgggccggat atgccagcga cggcaacggg
 300
 gacggaatca aggaccccaa caacgtcttc gatgcggcac tctcggcagc gaagtacctc
 360
 tgcagcggcg gactcaacct gcgcgatgtc gcccaggaga ccaaagctgt tctgcgatac
 420
 aacaactcgg ccgcttacgc agcaaacgtg atc
 453
 <210> 1332
 <211> 151
 <212> PRT
 <213> Homo sapiens
 <400> 1332
 Ala Tyr Arg Ser Ala Glu Leu Val Met Met Thr Glu Ala Pro Gly Cys
 1 5 10 15
 Gly Ile Pro Trp His Leu Leu Ala Gly Ile Gly Arg Ile Glu Ser Gly
 20 25 30
 His Ala Asn Gly Gly Lys Thr Thr Ser Val Gly Thr Asn Val Thr Pro
 35 40 45
 Ile Leu Gly Pro Ile Leu Asp Gly Arg Leu Ala Gly Asn Glu Val Ile
 50 55 60
 Arg Asp Thr Asp Lys Gly Asn Arg Arg Arg Pro Thr His Asp Arg Ala
 65 70 75 80
 Val Gly Pro Met Gln Phe Ile Pro Ala Thr Trp Ala Gly Tyr Ala Ser
 85 90 95
 Asp Gly Asn Gly Asp Gly Ile Lys Asp Pro Asn Asn Val Phe Asp Ala
 100 105 110
 Ala Leu Ser Ala Ala Lys Tyr Leu Cys Ser Gly Gly Leu Asn Leu Arg
 115 120 125
 Asp Val Ala Gln Glu Thr Lys Ala Val Leu Arg Tyr Asn Asn Ser Ala
 130 135 140
 Ala Tyr Ala Ala Asn Val Ile
 145 150

<210> 1333

<211> 540

<212> DNA

<213> Homo sapiens

<400> 1333

acgcgtcgcc cacactgttg ccgccgaggg ggctcgagcc ggggtgtgagg aaggatccgc
 60
 ggacacagctc gtcggtcaag atgggtctag tgctgtctgt atggcgccgg aggcattccgc
 120
 gcgaagggtt aaagcggatg gactaagcca gcttgtctat gatgtcaatg gagacgcccgt
 180
 cagcgtcgcg acggaaatca cccggcctac tcgtctatta gcccttattg gactaaccga
 240
 agtacacggt cgggcgagcg aaatgtgtat ttgtgtggtt cgctgagggc gttgcagcga
 300
 tacaatgatg aggtgtctaa gtattttccg gtccaccggc agaaccgcga gcagcgttct
 360
 ctcaatcaga tcgtcgacat cctgcacat ggcggtctta tcgctaccac gacagacacg
 420
 gggttatgct tcggtgccc gntaggggat aaggatgccg tggaccggat tcgcaaaactt
 480
 cgccagttat ttgacaagca tcacttcacc ctggtcatga gccagtttgc gcagggttggc
 540

<210> 1334

<211> 70

<212> PRT

<213> Homo sapiens

<400> 1334

Val His Pro Glu Asn Pro Gln Gln Arg Ser Leu Asn Gln Ile Val Asp
 1 5 10 15
 Ile Leu His His Gly Gly Leu Ile Ala Tyr Pro Thr Asp Thr Gly Tyr
 20 25 30
 Ala Phe Gly Ala Arg Xaa Gly Asn Lys Asp Ala Val Asp Arg Ile Arg
 35 40 45
 Lys Leu Arg Gln Leu Phe Asp Lys His His Phe Thr Leu Val Met Ser
 50 55 60
 Gln Phe Ala Gln Val Gly
 65 70

<210> 1335

<211> 748

<212> DNA

<213> Homo sapiens

<400> 1335

ncctctatcac tttttttccc tattctctatc cccctctctt ccgaccgcgt gaagcgttct
 60
 gtgaatgccca agaagaagcg tcgtgaggtc ctcgatcagg cctccgggta ccgtgggtcag
 120
 cgctcgcgcc tgtaccgcaa ggccaaggag cagaccctcc attcgccac ttattcgttc
 180

cgtgaccgctc gtgctaagaa gggtgacttc cgctcgctgt ggatccagcg catcaatgct
 240
 gcttcccgtg cccagggcat gacctacaac cgtttcatca acggtctgaa gaacgctggc
 300
 gtcgaggtcg accgcaagat gctcgtgtag cttgccgtct cgcacattaa cgccttcaac
 360
 agcctggtcg aggtcgctaa ggctagccag ccgcagaacg ctgctgcctg agatggccat
 420
 gactggcggg ccgaacgacg actatttggg atgggagtcg atctcgaagg ggtcattgcg
 480
 ttcggcccggt cgtctttcat ctccggcggg acgcgatgag tccgggctgt tcttggtaga
 540
 aggtgcgtag gcagttcgtg aagccctagc atggccgggt aaagtcaatt tgttggcaac
 600
 ctccggaccca gctcgcgatg ctgagcatgt cgaggtgggt acatgctggt gcgttcgggt
 660
 cgtggtgctc actgacgagg atgtcaatgc gctttctgat accgtcacca gtcagggggt
 720
 cttcgcggta tgctggcagg ttacgcgt
 748

<210> 1336

<211> 136

<212> PRT

<213> Homo sapiens

<400> 1336

Xaa	Leu	Ile	Leu	Phe	Phe	Pro	Ile	Pro	Ile	Pro	Pro	Leu	Ser	Asp	Arg
1				5					10					15	
Val	Lys	Arg	Ser	Val	Asn	Ala	Lys	Lys	Lys	Arg	Arg	Glu	Val	Leu	Asp
			20					25					30		
Gln	Ala	Ser	Gly	Tyr	Arg	Gly	Gln	Arg	Ser	Arg	Leu	Tyr	Arg	Lys	Ala
		35					40				45				
Lys	Glu	Gln	Thr	Leu	His	Ser	Ala	Thr	Tyr	Ser	Phe	Arg	Asp	Arg	Arg
	50				55					60					
Ala	Lys	Lys	Gly	Asp	Phe	Arg	Ser	Leu	Trp	Ile	Gln	Arg	Ile	Asn	Ala
65				70					75					80	
Ala	Ser	Arg	Ala	Gln	Gly	Met	Thr	Tyr	Asn	Arg	Phe	Ile	Asn	Gly	Leu
			85						90				95		
Lys	Asn	Ala	Gly	Val	Glu	Val	Asp	Arg	Lys	Met	Leu	Ala	Glu	Leu	Ala
		100					105					110			
Val	Ser	Asp	Ile	Asn	Ala	Phe	Asn	Ser	Leu	Val	Glu	Val	Ala	Lys	Ala
		115					120					125			
Ser	Gln	Pro	Gln	Asn	Ala	Ala									
	130					135									

<210> 1337

<211> 364

<212> DNA

<213> Homo sapiens

<400> 1337

acgcgtgagg ccaggccact gggcaccgcc gttagccagg gcagctcct tcagtggtca
 60

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aggcagactc agctcatggg cgagcatgtc agtgaagggc acagcaaggc tcacgagtgg
120
gcctcttgcc tcatgggtcag tgtgggtcag tgctttcgct gtatgagact acaggggttc
180
tctgcctcac catgggggac gattgggtct gggtcacttc ctgctgtggg acctgtcctg
240
ggcaactcgc gatgtggggc agggctccta cgtgccagct accagatgcc agcagcaccc
300
ccagaagtga caaccacaac catctccagg tgttgccagt gtccctctgg ggtagagtg
360
gccc
364

```

<210> 1338

<211> 96

<212> PRT

<213> Homo sapiens

<400> 1338

```

Met Gly Glu His Val Ser Glu Gly His Ser Lys Ala His Glu Trp Ala
 1             5             10             15
Ser Cys Leu Met Val Ser Val Gly Gln Cys Phe Arg Cys Met Arg Leu
                20             25             30
Gln Gly Phe Ser Ala Ser Pro Trp Gly Thr Ile Gly Ser Gly Ser Leu
                35             40             45
Pro Ala Val Gly Pro Val Leu Gly Thr Ala Gly Cys Gly Ala Gly Leu
 50             55             60
Leu Arg Ala Ser Tyr Gln Met Pro Ala Ala Pro Glu Val Thr Thr
65             70             75             80
Thr Thr Ile Ser Arg Cys Cys Gln Cys Pro Leu Gly Val Arg Val Ala
                85             90             95

```

<210> 1339

<211> 653

<212> DNA

<213> Homo sapiens

<400> 1339

```

cgcggtgtct tcaacatcga cgaaaagcag tgcattgacc tggcgccacc tggtagtgag
60
tggtgctgca ggtacgccga caagtacctc ggcgacgttg agttcggtca cgagtactct
120
ccggagatgt ttagccagac ccgacccggc ttcgctatcg acgtctgtca etccgtgatg
180
gacgtgtggc agccgggggc agggcgtgag attatcctta atctgccggc tacccgtcag
240
atgagtactc cgaacaccta ccgccaccaa atcgagtact tctgccgcaa tatccgtgat
300
cgtgagcacg tgtgcgtctc ttgcaaccg cacaatgata gtggcacggc gatcgcgggc
360
gccagattcg cgcagatggc gggcgccgat cgcgtcgagg gctgtttctt tggccccggc
420
gagcgcccg gacccgtcga cctgggtcac ctgggcatag acctcgtag ccagggagtt
480

```

gacgcggtta tcgactttctc cgacatgccc aagatccgcc gcaccgtcga gtactgcacc
 540
 tgtctgccac tacgggcccc ccagccctac tccggcgatc tggctcttcac cgccttctcc
 600
 ggttcccacc aggacgcat caagaagggt ctggaagacc tggcccgccg cgc
 653

<210> 1340
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 1340
 Arg Val Val Phe Asn Ile Asp Glu Lys Gln Cys Ile Asp Leu Ala His
 1 5 10 15
 Arg Gly Thr Glu Trp Val Val Arg Tyr Ala Asp Lys Tyr Leu Gly Asp
 20 25 30
 Val Glu Phe Gly Tyr Glu Tyr Ser Pro Glu Met Phe Ser Gln Thr Arg
 35 40 45
 Thr Asp Phe Ala Ile Asp Val Cys His Ser Val Met Asp Val Trp Gln
 50 55 60
 Pro Gly Pro Gly Arg Glu Ile Ile Leu Asn Leu Pro Ala Thr Val Glu
 65 70 75 80
 Met Ser Thr Pro Asn Thr Tyr Ala Asp Gln Ile Glu Tyr Phe Cys Arg
 85 90 95
 Asn Ile Arg Asp Arg Glu His Val Cys Val Ser Leu His Pro His Asn
 100 105 110
 Asp Arg Gly Thr Ala Ile Ala Ala Glu Phe Ala Gln Met Ala Gly
 115 120 125
 Ala Asp Arg Val Glu Gly Cys Phe Phe Gly Pro Glu Glu Arg Pro Gly
 130 135 140
 Thr Val Asp Leu Val Thr Leu Gly Met Asn Leu Val Ser Gln Gly Val
 145 150 155 160
 Asp Ala Gly Ile Asp Phe Ser Asp Met Pro Lys Ile Arg Arg Thr Val
 165 170 175
 Glu Tyr Cys Thr Cys Leu Pro Val Pro Ala Arg Gln Pro Tyr Ser Gly
 180 185 190
 Asp Leu Val Phe Thr Ala Phe Ser Gly Ser His Gln Asp Ala Ile Lys
 195 200 205
 Lys Gly Leu Glu Asp Leu Ala Arg Arg
 210 215

<210> 1341
 <211> 666
 <212> DNA
 <213> Homo sapiens

<400> 1341
 accggttgct gatttctctt ttggagtctt caccactatg agcagtgact ccattgtttt
 60
 gcaaaagtctt ttgccttgct ttgatcatat ttccacaact ggattcccaa cagaagtgtg
 120
 gcaatctgta atagaaaagt tggcaaaaga aggattatgg cattcatttc tgcttctgtc
 180

agcaaaaaaa gaccgattac caagaaatat tcatgtccca gagttatcac tgaaaagtct
 240
 ctttgagaaa tacgttttca ttggacttta tgagaagatg gaacaagtgc ccaagttagt
 300
 ccagtggtc atctccattg gtgcaagtgt tgagactata ggaccgtatc cccttcatgc
 360
 cctcatgcga ctctgtatcc aagccagaga aaaccatctt ttccggtggt taatggatca
 420
 caagcccag tggaaggcc gcattaacca gaaggatggg gatgggtgca ctgtctcgca
 480
 cgtcgtcgt gccactccc caggatacct cgtaagcga caaacagagg atgtgcagat
 540
 gctcctgcgc ttggggcag atcccacttt gctggatcga cagtctcggt ctgttggtga
 600
 tgtcctgaag aggaataaga acttcaaagc catcgagaaa atcaacagtc acttagaaaa
 660
 gctagc
 666

<210> 1342

<211> 209

<212> PRT

<213> Homo sapiens

<400> 1342

Met	Ser	Ser	Asp	Ser	Ile	Val	Leu	Gln	Ser	Phe	Leu	Pro	Cys	Phe	Asp
1			5						10					15	
His	Ile	Phe	Thr	Thr	Gly	Phe	Pro	Thr	Glu	Val	Trp	Gln	Ser	Val	Ile
			20					25					30		
Glu	Lys	Leu	Ala	Lys	Lys	Gly	Leu	Trp	His	Ser	Phe	Leu	Leu	Leu	Ser
		35					40				45				
Ala	Lys	Lys	Asp	Arg	Leu	Pro	Arg	Asn	Ile	His	Val	Pro	Glu	Leu	Ser
		50				55					60				
Leu	Lys	Ser	Leu	Phe	Glu	Lys	Tyr	Val	Phe	Ile	Gly	Leu	Tyr	Glu	Lys
65					70				75					80	
Met	Glu	Gln	Val	Pro	Lys	Leu	Val	Gln	Trp	Leu	Ile	Ser	Ile	Gly	Ala
			85					90						95	
Ser	Val	Glu	Thr	Ile	Gly	Pro	Tyr	Pro	Leu	His	Ala	Leu	Met	Arg	Leu
			100					105						110	
Cys	Ile	Gln	Ala	Arg	Glu	Asn	His	Leu	Phe	Arg	Trp	Leu	Met	Asp	His
		115				120						125			
Lys	Pro	Glu	Trp	Lys	Gly	Arg	Ile	Asn	Gln	Lys	Asp	Gly	Asp	Gly	Cys
		130				135					140				
Thr	Val	Leu	His	Val	Val	Ala	Ala	His	Ser	Pro	Gly	Tyr	Leu	Val	Lys
145				150					155					160	
Arg	Gln	Thr	Glu	Asp	Val	Gln	Met	Leu	Leu	Arg	Phe	Gly	Ala	Asp	Pro
			165						170					175	
Thr	Leu	Leu	Asp	Arg	Gln	Ser	Arg	Ser	Val	Val	Asp	Val	Leu	Lys	Arg
			180					185					190		
Asn	Lys	Asn	Phe	Lys	Ala	Ile	Glu	Lys	Ile	Asn	Ser	His	Leu	Glu	Lys
			195				200					205			
Leu															

<210> 1343

<211> 270

<212> DNA

<213> Homo sapiens

<400> 1343

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 60
 aaaagctgtg gaaaccgaaa tgagactcca tcggaccacg tcataattga cagattcttt
 120
 ttataatttt tcctcaagtg caatcagaat tgtttgaaaa cagcaggaaa cccaaggggc
 180
 atgagacggg ttcaggttgt gttgtcaaca acggtgaatg tggatggaca cgtcctggct
 240
 gtttctgaca acatgtttgt tcataacaac
 270

<210> 1344

<211> 90

<212> PRT

<213> Homo sapiens

<400> 1344

Pro	Glu	Met	Cys	Arg	Val	Leu	Leu	Thr	His	Glu	Val	Met	Cys	Ser	Arg
1				5				10					15		
Cys	Cys	Glu	Lys	Lys	Ser	Cys	Gly	Asn	Arg	Asn	Glu	Thr	Pro	Ser	Asp
			20				25					30			
Pro	Val	Ile	Asp	Arg	Phe	Phe	Leu	Lys	Phe	Phe	Leu	Lys	Cys	Asn	
	35				40		45								
Gln	Asn	Cys	Leu	Lys	Thr	Ala	Gly	Asn	Pro	Arg	Asp	Met	Arg	Arg	Phe
	50				55				60						
Gln	Val	Val	Leu	Ser	Thr	Thr	Val	Asn	Val	Asp	Gly	His	Val	Leu	Ala
	65				70				75					80	
Val	Ser	Asp	Asn	Met	Phe	Val	His	Asn	Asn						
			85					90							

<210> 1345

<211> 402

<212> DNA

<213> Homo sapiens

<400> 1345

acgcgtttga aaccaccga tgacttgtcg gtgatcctgg gtaccgcgt cagcaacttc
 60
 agcggcaccg acaacaccga cttctacgac ccgaccaagg ccgacaaccg tctcacctac
 120
 cgccagacgg gcgtcgctac gccctatgcc ggcatcgtct acgacctgaa tgacatctgg
 180
 tcggtgtaca ccagctacac caagatctac aagccgcaga acagcaagga cgccgaccgc
 240
 aagttgctcg atccgattga aggtgacacc tacgaagccg ggctcaaggc agcgtttttc
 300
 gacggccgcc tgaacgccag ttttgccgca ttccgcatcg aacaggacaa cgctgcacag
 360

tacgttttcg ggtttgagac cgactcgtgt atcgccatt gc
402

<210> 1346

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1346

Thr	Arg	Leu	Lys	Pro	Thr	Asp	Asp	Leu	Ser	Val	Ile	Leu	Gly	Thr	Arg
1				5					10					15	
Val	Ser	Asn	Phe	Ser	Gly	Thr	Asp	Asn	Thr	Asp	Phe	Tyr	Asp	Pro	Thr
			20				25						30		
Lys	Ala	Asp	Asn	Arg	Leu	Thr	Tyr	Arg	Gln	Thr	Gly	Val	Val	Thr	Pro
			35				40					45			
Tyr	Ala	Gly	Ile	Val	Tyr	Asp	Leu	Asn	Asp	Ile	Trp	Ser	Val	Tyr	Thr
			50			55					60				
Ser	Tyr	Thr	Lys	Ile	Tyr	Lys	Pro	Gln	Asn	Ser	Lys	Asp	Ala	Asp	Arg
			65			70				75				80	
Lys	Leu	Leu	Asp	Pro	Ile	Glu	Gly	Asp	Thr	Tyr	Glu	Ala	Gly	Leu	Lys
			85						90					95	
Ala	Ala	Phe	Phe	Asp	Gly	Arg	Leu	Asn	Ala	Ser	Phe	Ala	Ala	Phe	Arg
			100					105						110	
Ile	Glu	Gln	Asp	Asn	Val	Ala	Gln	Tyr	Val	Ser	Gly	Phe	Glu	Thr	Asp
			115				120						125		
Ser	Cys	Ile	Ala	His	Cys										
			130												

<210> 1347

<211> 415

<212> DNA

<213> Homo sapiens

<400> 1347

naccaccttc tgggcaggct ctcattcttt cattccaaga agcatttatt aaagactggc
60
tagggcgagg gaaccagct aggggctggg gataaaaaat aagaaataac tgaaggacct
120
tgctcttaag gaactccatc ttaactgggtg gagccaaacg agaaaagaga gtcggggagg
180
gcaccaaagc ggtcttgccg aaattgectg aggcagggga aggggcacgc tttctgaaaa
240
acccccccaa accgatteca ggaagcccaa agggcgggcc cctctgcccg agcactgcct
300
tcacgtttac ttccatcccg gcctcctcct tccctaagg cttggcatgc aacatccctg
360
cttctcacc accttttatt taagactcct attatctgca cacaatggaa gttag
415

<210> 1348

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1348

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Met Glu Val Asn Val Lys Ala Val Leu Arg Ala Glu Gly Pro Pro Phe
 1           5           10           15
Gly Leu Pro Gly Ile Gly Leu Gly Gly Phe Phe Arg Lys Arg Ala Pro
          20           25           30
Ser Pro Ala Ser Gly Asn Phe Gly Lys Thr Ala Leu Val Pro Ser Arg
          35           40           45
Ala Leu Phe Ser Arg Leu Ala Pro Pro Ser Lys Met Glu Phe Leu Lys
          50           55           60
Ser Lys Val Leu Gln Leu Phe Leu Ile Phe Tyr Pro Gln Pro Leu Ala
65           70           75           80
Gly Phe Pro Arg Pro Ser Gln Ser Leu Ile Asn Ala Ser Trp Asn Glu
          85           90           95
Arg Met Arg Ala Cys Pro Glu Gly Gly
          100          105

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<210> 1349

<211> 924

<212> DNA

<213> Homo sapiens

<400> 1349

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gccgggatcg tcacaccaca gcaggtcgcg ttaccccatg acgtcttccg tgagcttggc
60
gtcagacagg tcatgcgttc gatcgccgaa aagcttggcc ttccggtcat cgtaaagccg
120
gcacgtgggg gctcaagcct cggcgctaca aaagtcgatg gcgtcgacga tcttcctcag
180
gccgtcgcca acgcctatgc ctatgacgac atggtttag tagaggaatt cattgtgggc
240
aacgaactcg caataggcat gatcacgacg tctgaaggca cgcgtgtgct gccagccgctc
300
gagattcgcc ctgtcggtag tgtttatgat tattcagcga tgtacaccgg tggtagagaca
360
cgactaacag ctccctgcaga cattagcgat acggcgggccc aaaccgcgac ggcatggcc
420
cgagtcgtgc aaaaggagct cgatttctcc gggatatctc gtgtcgatgc gatcgtggac
480
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540
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 <212> PRT
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 35 40 45
 Val Thr Lys Val Asp Gly Val Asp Asp Leu Pro Gln Ala Val Ala Asn
 50 55 60
 Ala Tyr Ala Tyr Asp Asp Met Val Val Val Glu Glu Phe Ile Val Gly
 65 70 75 80
 Asn Glu Leu Ala Ile Gly Met Ile Thr Thr Ser Glu Gly Thr Arg Val
 85 90 95
 Leu Pro Ala Val Glu Ile Arg Pro Val Gly Gly Val Tyr Asp Tyr Ser
 100 105 110
 Ala Met Tyr Thr Gly Gly Glu Thr Arg Leu Thr Ala Pro Ala Asp Ile
 115 120 125
 Ser Asp Thr Ala Ala Gln Thr Ala Thr Ala Met Ala Arg Val Val Gln
 130 135 140
 Lys Glu Leu Asp Phe Ser Gly Ile Ser Arg Val Asp Ala Ile Val Asp
 145 150 155 160
 Glu Ser Gly Arg Pro Val Phe Leu Glu Ala Gly Ala Ala Pro Gly Met
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 Thr Ala Thr Ser Leu Val Pro Val Ala Met Lys Ala Ala Gly Leu Asp
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 Leu Gly Glu Val Cys Ser Arg Leu Val Asp Asp Val Ala Arg Asn His
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<210> 1351
 <211> 398
 <212> DNA
 <213> Homo sapiens

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<210> 1352
<211> 70
<212> PRT
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Leu His Pro Gly Leu Leu Ile Val Asp His Ile His Phe Gln Tyr Asn
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Gly Phe Leu Ile Arg Gly Pro Leu Tyr Arg Leu Gly Ala Arg Thr Asp
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Ala Ser Ala Leu Phe Leu
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<210> 1353
<211> 480
<212> DNA
<213> Homo sapiens

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<212> PRT
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Gly	Gly Ser Gly Arg Gln Ser Leu Ala Arg Leu Ala Ser Ser Ile Cys					
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Asp	Tyr Thr Thr Phe Gln Ile Glu Val Thr Lys His Tyr Arg Lys Gln					
	65		70		75	
Glu	Phe Arg Asp Asp Ile Lys Arg Leu Tyr Arg Gln Ala Gly Val Glu					
	85		90		95	
Leu	Lys Thr Thr Ser Phe Ile Phe Val Asp Thr Gln Ile Ala Asp Glu					
	100		105		110	
Ser	Phe Leu Glu Asp Ile Asn Asn Ile Leu Ser Ser Gly Glu Val Pro					
	115		120		125	
His	Leu Phe Arg Pro Asp Glu Phe Glu Glu Ile Gln Ser His Ile Ile					
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<210> 1355

<211> 1063

<212> DNA

<213> Homo sapiens

<400> 1355

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<210> 1356
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 <212> PRT
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<400> 1356
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 35 40 45
 Thr Ala Asn Ser Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His
 50 55 60
 Ala Thr Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser
 65 70 75 80
 Gln Ser Leu Asp Gly Thr Tyr Gln Gly Gly Val Cys Ile Asp Cys
 85 90 95
 Gln His His Thr Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe
 100 105 110
 Tyr Arg Ser Pro Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg
 115 120 125
 Cys Asn Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr
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 Gly Arg Cys Tyr Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val
 145 150 155 160
 Cys Ala Glu Gly Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser
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 Ser Ser Asn Asp Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val
 180 185 190
 Asn Cys Asp Cys Ser Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys
 195 200 205
 Asp Pro Arg Val Gly Arg Cys Phe Ala Asn Pro Asn Phe Gln Gly Thr
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 His Cys Glu Leu Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Pro Gly
 225 230 235 240
 Ser Leu His Ala

<210> 1357
 <211> 663
 <212> DNA
 <213> Homo sapiens

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<210> 1358

<211> 221

<212> PRT

<213> Homo sapiens

<400> 1358

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Cys	Gly	Phe	Gly	Thr	Glu	Val	Glu	Phe	Asn	Thr	Pro	Val	Leu
		35					40				45		Pro
Gly	Gly	Val	Arg	Pro	Val	Ile	Leu	Gln	Arg	Pro	Gly	Trp	Cys
		50				55				60			Pro
Val	Phe	Val	Gly	Leu	Pro	Asn	His	His	Leu	Asp	Gly	Val	Ala
				70					75				Met
Cys	Glu	Leu	Leu	Ala	Ala	Val	Phe	Cys	Ala	Arg	Ala	Cys	Leu
				85					90				Trp
Leu	Gln	Glu	Ser	Leu	Ala	His	Arg	Ala	Ser	Ala	Ser	Val	Lys
			100					105				110	Ser
Leu	Arg	Arg	Asp	Ile	Leu	Gln	Ala	Arg	Leu	Ser	Arg	Pro	Thr
			115				120					125	Asp
Thr	Met	Pro	Ser	Arg	Thr	Leu	Ile	Ser	Leu	Met	Thr	Thr	Gly
			130			135					140		Leu
Ala	Leu	Asp	Gly	Tyr	Tyr	Ser	Lys	Tyr	Leu	Pro	Gln	Leu	Val
				145			150			155			Ala
Val	Ile	Val	Pro	Ala	Val	Leu	Ala	Thr	Ala	Ile	Gly	Leu	Asn
				165				170					Asp
Thr	Ser	Leu	Val	Ile	Val	Val	Val	Thr	Ile	Pro	Leu	Ile	Pro
				180				185				190	Val
Met	Ala	Leu	Ile	Gly	Trp	Arg	Thr	Glu	Ala	Ala	Val	Ala	Lys
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210

215

220

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 <212> DNA
 <213> Homo sapiens

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<210> 1360
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 <212> PRT
 <213> Homo sapiens

<400> 1360
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 35 40 45
 Val Gly Tyr Trp Leu Ala Asp Tyr Thr Ser Leu Ser Ile Lys Gln Ile
 50 55 60
 Asp Lys Gln Pro Phe Val Ser Arg Thr Pro Cys Asp Ile Leu Glu Ser
 65 70 75 80
 Trp Asn Phe Ile Met Gln Lys Gln Gly Leu Ser Thr Asp Val Arg Ala
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<210> 1361
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 <212> DNA
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<210> 1362

<211> 1587

<212> PRT

<213> Homo sapiens

<400> 1362

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Ala	Ala	Gly	Ala	Gly	Met	Gly	Ala	Cys	Tyr	Asp	Gly	Ala	Gly	Arg	Pro
		20						25				30			
Gln	Arg	Cys	Leu	Pro	Val	Phe	Glu	Asn	Ala	Ala	Phe	Gly	Arg	Leu	Ala
		35					40					45			
Gln	Ala	Ser	His	Thr	Cys	Gly	Ser	Pro	Pro	Glu	Asp	Phe	Cys	Pro	His
		50				55					60				
Val	Gly	Ala	Ala	Gly	Ala	Gly	Ala	His	Cys	Gln	Arg	Cys	Asp	Ala	Ala
		65				70				75				80	
Asp	Pro	Gln	Arg	His	His	Asn	Ala	Ser	Tyr	Leu	Thr	Asp	Phe	His	Ser
				85					90					95	
Gln	Asp	Glu	Ser	Thr	Trp	Trp	Gln	Ser	Pro	Ser	Met	Ala	Phe	Gly	Val
		100						105					110		
Gln	Tyr	Pro	Thr	Ser	Val	Asn	Ile	Thr	Leu	Arg	Leu	Gly	Lys	Ala	Tyr
		115					120					125			
Glu	Ile	Thr	Tyr	Val	Arg	Leu	Lys	Phe	His	Thr	Ser	Arg	Pro	Glu	Ser
		130					135				140				
Phe	Ala	Ile	Tyr	Lys	Arg	Ser	Arg	Ala	Asp	Gly	Pro	Trp	Glu	Pro	Tyr
		145				150				155				160	
Gln	Phe	Tyr	Ser	Ala	Ser	Cys	Gln	Lys	Thr	Tyr	Gly	Arg	Pro	Glu	Gly
				165					170					175	
Gln	Tyr	Leu	Arg	Pro	Gly	Glu	Asp	Glu	Arg	Val	Ala	Phe	Cys	Thr	Ser
		180					185						190		
Glu	Phe	Ser	Asp	Ile	Ser	Pro	Leu	Ser	Gly	Gly	Asn	Val	Ala	Phe	Ser
		195					200					205			
Thr	Leu	Glu	Gly	Arg	Pro	Ser	Ala	Tyr	Asn	Phe	Glu	Glu	Ser	Pro	Gly
		210					215					220			
Leu	Gln	Glu	Trp	Val	Thr	Ser	Thr	Glu	Leu	Leu	Ile	Ser	Leu	Asp	Arg
		225					230				235			240	
Leu	Asn	Thr	Phe	Gly	Asp	Asp	Ile	Phe	Lys	Asp	Pro	Lys	Val	Leu	Gln
				245					250					255	
Ser	Tyr	Tyr	Tyr	Ala	Val	Ser	Asp	Phe	Ser	Val	Gly	Gly	Arg	Cys	Lys

[illegible]

690	695	700
Val Pro Cys Thr Cys Asn Gln His Gly Thr Cys Asp Pro Asn Thr Gly		
705	710	715
Ile Cys Val Cys Ser His His Thr Glu Gly Pro Ser Cys Glu Arg Cys		
	725	730
Leu Pro Gly Phe Tyr Gly Asn Pro Phe Ala Gly Gln Ala Asp Asp Cys		
	740	745
Gln Pro Cys Pro Cys Pro Gly Gln Ser Ala Cys Thr Thr Ile Pro Glu		
	755	760
Ser Gly Glu Val Val Cys Thr His Cys Pro Pro Gly Gln Arg Gly Arg		
	770	775
Arg Cys Glu Val Cys Asp Asp Gly Phe Phe Gly Asp Pro Leu Gly Leu		
785	790	795
Phe Gly His Pro Gln Pro Cys His Gln Cys Gln Cys Ser Gly Asn Val		
	805	810
Asp Pro Asn Ala Val Gly Asn Cys Asp Pro Leu Ser Gly His Cys Leu		
	820	825
Arg Cys Leu His Asn Thr Thr Gly Asp His Cys Glu His Cys Gln Glu		
	835	840
Gly Phe Tyr Gly Ser Ala Leu Ala Pro Arg Pro Ala Asp Lys Cys Met		
850	855	860
Pro Cys Ser Cys His Pro Gln Gly Ser Val Ser Glu Gln Met Pro Cys		
865	870	875
Asp Pro Val Thr Gly Gln Cys Ser Cys Leu Pro His Val Thr Ala Arg		
	885	890
Asp Cys Ser Arg Cys Tyr Pro Gly Phe Phe Asp Leu Gln Pro Gly Arg		
	900	905
Gly Cys Arg Ser Cys Lys Cys His Pro Leu Gly Ser Gln Glu Asp Gln		
	915	920
Cys His Pro Lys Thr Gly Gln Cys Thr Cys Arg Pro Gly Val Thr Gly		
	930	935
Gln Ala Cys Asp Arg Cys Gln Leu Gly Phe Phe Gly Ser Ser Ile Lys		
945	950	955
Gly Cys Arg Ala Cys Arg Cys Ser Pro Leu Gly Ala Ala Ser Ala Gln		
	965	970
Cys His Tyr Asn Gly Thr Cys Val Cys Arg Pro Gly Phe Glu Gly Tyr		
	980	985
Lys Cys Asp Arg Cys His Tyr Asn Phe Phe Leu Thr Ala Asp Gly Thr		
	995	1000
His Cys Gln Gln Cys Pro Ser Cys Tyr Ala Leu Val Lys Glu Glu Thr		
	1010	1015
Ala Lys Leu Lys Ala Arg Leu Thr Leu Thr Glu Gly Trp Leu Gln Gly		
1025	1030	1035
Ser Asp Cys Gly Ser Pro Trp Gly Pro Leu Asp Ile Leu Leu Gly Glu		
	1045	1050
Ala Pro Arg Gly Asp Val Tyr Gln Gly His His Leu Leu Pro Gly Ala		
	1060	1065
Arg Glu Ala Phe Leu Glu Gln Met Met Gly Leu Glu Gly Ala Val Lys		
	1075	1080
Ala Ala Arg Glu Gln Leu Gln Arg Leu Asn Lys Gly Ala Arg Cys Ala		
	1090	1095
Gln Ala Gly Ser Gln Lys Thr Cys Thr Gln Leu Ala Asp Leu Glu Ala		
1105	1110	1115
Val Leu Glu Ser Ser Glu Glu Glu Ile Leu His Ala Ala Ala Ile Leu		

	1125		1130		1135
Ala Ser Leu Glu Ile Pro Gln Glu Gly Pro Ser Gln Pro Thr Lys Trp					
	1140		1145		1150
Ser His Leu Ala Ile Glu Ala Arg Ala Leu Ala Arg Ser His Arg Asp					
	1155		1160		1165
Thr Ala Thr Lys Ile Ala Ala Thr Ala Trp Arg Ala Leu Leu Ala Ser					
	1170		1175		1180
Asn Thr Ser Tyr Ala Leu Leu Trp Asn Leu Leu Glu Gly Arg Val Ala					
	1185		1190		1195
Leu Glu Thr Gln Arg Asp Leu Glu Asp Arg Tyr Gln Glu Val Gln Ala					
	1205		1210		1215
Ala Gln Lys Ala Leu Arg Thr Ala Val Ala Glu Val Leu Pro Glu Ala					
	1220		1225		1230
Glu Ser Val Leu Ala Thr Val Arg Gln Val Gly Ala Asp Thr Ala Pro					
	1235		1240		1245
Tyr Leu Ala Leu Leu Ala Ser Pro Gly Ala Leu Pro Gln Lys Ser Arg					
	1250		1255		1260
Ala Glu Asp Leu Gly Leu Lys Ala Lys Ala Leu Glu Lys Thr Val Ala					
	1265		1270		1275
Ser Trp Gln His Met Ala Thr Glu Ala Ala Arg Thr Leu Gln Thr Ala					
	1285		1290		1295
Ala Gln Ala Thr Leu Arg Gln Thr Glu Pro Leu Thr Met Ala Arg Ser					
	1300		1305		1310
Arg Leu Thr Ala Thr Phe Ala Ser Gln Leu His Gln Glu Ala Arg Ala					
	1315		1320		1325
Ala Leu Thr Gln Ala Ser Ser Ser Val Gln Ala Ala Thr Val Thr Val					
	1330		1335		1340
Met Gly Ala Arg Thr Leu Leu Ala Asp Leu Glu Gly Met Lys Leu Gln					
	1345		1350		1355
Phe Pro Arg Pro Lys Asp Gln Ala Ala Leu Gln Arg Lys Ala Asp Ser					
	1365		1370		1375
Val Ser Asp Arg Leu Leu Ala Asp Thr Arg Lys Lys Thr Lys Gln Ala					
	1380		1385		1390
Glu Arg Met Leu Gly Asn Ala Ala Pro Leu Ser Ser Ser Ala Lys Lys					
	1395		1400		1405
Lys Gly Arg Glu Ala Glu Val Leu Ala Lys Asp Ser Ala Lys Leu Ala					
	1410		1415		1420
Lys Ala Leu Leu Arg Glu Arg Lys Gln Ala His Arg Arg Ala Ser Arg					
	1425		1430		1435
Leu Thr Ser Gln Thr Gln Ala Thr Leu Gln Gln Ala Ser Gln Gln Val					
	1445		1450		1455
Leu Ala Ser Glu Ala Arg Arg Gln Glu Leu Glu Glu Ala Glu Arg Val					
	1460		1465		1470
Gly Ala Gly Leu Ser Glu Met Glu Gln Gln Ile Arg Glu Ser Arg Ile					
	1475		1480		1485
Ser Leu Glu Lys Asp Ile Glu Thr Leu Ser Glu Leu Leu Ala Arg Leu					
	1490		1495		1500
Gly Ser Leu Asp Thr His Gln Ala Pro Ala Gln Ala Leu Asn Glu Thr					
	1505		1510		1515
Gln Trp Ala Leu Glu Arg Leu Arg Leu Gln Leu Gly Ser Pro Gly Ser					
	1525		1530		1535
Leu Gln Arg Lys Leu Ser Leu Leu Glu Gln Glu Ser Gln Gln Gln Glu					
	1540		1545		1550
Leu Gln Ile Gln Gly Phe Glu Ser Asp Leu Ala Glu Ile Arg Ala Asp					

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      1555              1560              1565
Lys Gln Asn Leu Glu Ala Ile Leu His Ser Leu Pro Glu Asn Cys Ala
      1570              1575              1580
Ser Trp Gln
1585

<210> 1363
<211> 392
<212> DNA
<213> Homo sapiens

<400> 1363
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60
gaaggcgcca ccgaagacaa ggacgtagag gaaagccgcg ctgtgctcga aggcgcagca
120
ggaatctcgc aaaccgacaa agatgcggct gtttgagtgg atgtgaagga agatgcaggt
180
gtctcatcgg cggggccacc atgaacaacc cttcttgatg ccccgtaggt gacgcgctca
240
cacacgacat gcacaacaaa taaatcgcaa agcacagagg gacaatcgaa tacaccttga
300
cccatgcact tgcgtgcctg gaggcattggc taccaggcaa tcccttcatt tccagaatga
360
gcctgttttt gaaagcgact aggggaagttc ag
392

<210> 1364
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1364
Met Arg Gly Leu Pro Gly Ser His Ala Ser Arg His Ala Ser Ala Trp
1      5      10      15
Val Lys Val Tyr Ser Ile Val Pro Leu Cys Phe Ala Ile Tyr Leu Leu
      20      25      30
Cys Met Ser Cys Val Ser Ala Ser Pro Thr Gly His Gln Glu Gly Leu
      35      40      45
Phe Met Val Ala Pro Pro Met Arg His Leu His Leu Pro Ser His Pro
      50      55      60
Leu Lys Gln Pro His Leu Cys Arg Phe Arg Arg Phe Leu Leu Arg Leu
      65      70      75      80
Arg Ala Gln Arg Gly Phe Pro Leu Arg Pro Cys Leu Arg Trp Arg Leu
      85      90      95
Arg Leu Gln Trp Arg Leu Tyr Pro
100

<210> 1365
<211> 451
<212> DNA
<213> Homo sapiens

<400> 1365

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nnacgcgtga gggagaagat ggatgacacc agcctctata atacgccctg tgcctcggac
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 ctacagcggg ccctggttca ggatcgccaa gaggcgcctt ggaatgaggt ggatgaggtc
 120
 tggcccaatg tcttcatagc tgagaagagt gtggctgtga acaaggggag gctgaagagg
 180
 ctgggaatca cccacattct gaatgctgcy catggcaccg gcgtttacac tggccccgaa
 240
 ttctacactg gcttgagat ccagtacctg ggtgtagagg tggatgactt tcctgaggtg
 300
 gacatttccc agcatttccg gaaggcgtct gagttcctgg atgaggcgct gctgacttac
 360
 agagggaag tcttggtcag cagcgaaatg ggcatcagcc ggtcagcagt gctggtggtc
 420
 gcctacctga tgatcttcca caacatggcc a
 451

<210> 1366

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1366

Xaa	Arg	Val	Arg	Glu	Lys	Met	Asp	Asp	Thr	Ser	Leu	Tyr	Asn	Thr	Pro
1				5					10					15	
Cys	Val	Leu	Asp	Leu	Gln	Arg	Ala	Leu	Val	Gln	Asp	Arg	Gln	Glu	Ala
		20						25					30		
Pro	Trp	Asn	Glu	Val	Asp	Glu	Val	Trp	Pro	Asn	Val	Phe	Ile	Ala	Glu
		35				40						45			
Lys	Ser	Val	Ala	Val	Asn	Lys	Gly	Arg	Leu	Lys	Arg	Leu	Gly	Ile	Thr
	50					55				60					
His	Ile	Leu	Asn	Ala	Ala	His	Gly	Thr	Gly	Val	Tyr	Thr	Gly	Pro	Glu
	65				70				75					80	
Phe	Thr	Thr	Gly	Leu	Glu	Ile	Gln	Tyr	Leu	Gly	Val	Glu	Val	Asp	Asp
			85					90						95	
Phe	Pro	Glu	Val	Asp	Ile	Ser	Gln	His	Phe	Arg	Lys	Ala	Ser	Glu	Phe
		100					105						110		
Leu	Asp	Glu	Ala	Leu	Leu	Thr	Tyr	Arg	Gly	Lys	Val	Leu	Val	Ser	Ser
		115				120						125			
Glu	Met	Gly	Ile	Ser	Arg	Ser	Ala	Val	Leu	Val	Val	Ala	Tyr	Leu	Met
	130					135					140				
Ile	Phe	His	Asn	Met	Ala										
145					150										

<210> 1367

<211> 330

<212> DNA

<213> Homo sapiens

<400> 1367

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 60
 cgccgatacy cgccaacgcc gtagaccgcy aacgctggct caccggcgcc gctgtactgc
 120

tcgtcgtcgc attgctgctg gtcctcgtcg cactgcccgt cagcgcactc gtcggccaga
 180
 gctttcttga ccgcgaaggc gccttcgtcg gcctcgccaa ctctcgtcgc tacctcgaca
 240
 accccgccct gggtccagtc gccttcaaca gcctctgggt ggccgcgac agcgccgtca
 300
 tctgcaccgc catcgcctac gtctacgcgt
 330

<210> 1368

<211> 82

<212> PRT

<213> Homo sapiens

<400> 1368

Thr	Ala	Asn	Ala	Gly	Ser	Pro	Ala	Pro	Leu	Tyr	Cys	Ser	Ser	Ser	His
1				5				10				15			
Cys	Cys	Trp	Ser	Ser	Ser	His	Cys	Pro	Ser	Ala	His	Ser	Ser	Ala	Arg
			20				25					30			
Ala	Ser	Ser	Thr	Ala	Lys	Ala	Pro	Ser	Ser	Ala	Ser	Pro	Thr	Ser	Leu
			35			40					45				
Ala	Thr	Ser	Thr	Thr	Pro	Pro	Trp	Ser	Ser	Pro	Pro	Ser	Thr	Ala	Ser
	50				55					60					
Gly	Trp	Pro	Arg	Ser	Ala	Pro	Ser	Ser	Ala	Pro	Pro	Ser	Pro	Thr	Ser
65				70					75					80	
Thr	Arg														

<210> 1369

<211> 356

<212> DNA

<213> Homo sapiens

<400> 1369

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 60
 catcacctgt acgtactgca ggctctcatg ctggggctgc tggagccgcg catgaggagc
 120
 cccctggacc cctacagcca ggagcagcgg gagcagctgc aggtcctacg ccaggctgcc
 180
 ttcgagggtg aggggggagtc ctccgggtgcc gggctaagtg ctgaccgtcg ccgttccctc
 240
 tgtgcccagc agttccgcaa actgggcttt tctaacagca acccagcaca ggacctggag
 300
 cgcgtgcccc ccggtctgct ggccctggac aacatgttgt acttctccag aaacgc
 356

<210> 1370

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1370

Met Gly Asp Glu Met Ala His His Leu Tyr Val Leu Gln Ala Leu Met

```

      1           5           10           15
Leu Gly Leu Leu Glu Pro Arg Met Arg Thr Pro Leu Asp Pro Tyr Ser
      20           25           30
Gln Glu Gln Arg Glu Gln Leu Gln Val Leu Arg Gln Ala Ala Phe Glu
      35           40           45
Val Glu Gly Glu Ser Ser Gly Ala Gly Leu Ser Ala Asp Arg Arg Arg
      50           55           60
Ser Leu Cys Ala Arg Glu Phe Arg Lys Leu Gly Phe Ser Asn Ser Asn
      65           70           75           80
Pro Ala Gln Asp Leu Glu Arg Val Pro Pro Gly Leu Leu Ala Leu Asp
      85           90           95
Asn Met Leu Tyr Phe Ser Arg Asn
      100

```

<210> 1371

<211> 648

<212> DNA

<213> Homo sapiens

<400> 1371

```

tcgcgagcac actccagcct ctgggctgcc ttttccaggt ttgcaaacct ggctatgaat
60
tggtcagcgg ttggattagc cagttctgca gactggctca caccagacc atctggaccg
120
cttatagaga agacatgttc caagtacctt ctttcttttg tctgcttttc tcattgggtac
180
tttgccctct aagaagccta ctttctcttt ttctctctct cctctcccta tttctctttg
240
ttgagagagc agtcagatta acccaacaac tcttggagtg ccttggctac ctgagagcat
300
ggaaaagtcca tgccctcacc agagtaatga ctaccatttc tccaaaactc tctctatgcc
360
atccgatagg cagtattgat cagaagggga aatctagtgt gttaaaattg ataaaccagc
420
ttaagtatta cctacaataa aagaccagc cttagcccat ggctgaatgt tgaatactgt
480
tgcattgaaa ttggggattt ctagttagag gctttataaa ggtagaatca tgcagacaca
540
tatacctgga aatattcgga acattctatt agcagaaatg caatgttaga agcttattgg
600
ttctagaaga atgtgtcatt gtcagtaatt ggaattactg acagatct
648

```

<210> 1372

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1372

```

Met Phe Gln Val Pro Ser Phe Leu Cys Leu Leu Phe Ser Trp Val Leu
      1           5           10           15
Cys Pro Leu Arg Ser Leu Leu Ser Ser Phe Pro Leu Leu Ser Leu
      20           25           30
Phe Leu Phe Val Glu Arg Ala Val Arg Leu Thr Gln Gln Leu Leu Glu

```



```

      35              40              45
Cys Leu Gly His Leu Arg Ala Trp Lys Val His Ala Leu Thr Arg Val
  50              55              60
Met Thr Thr Ile Ser Pro Lys Leu Ser Ser Cys His Pro Ile Gly Ser
  65              70              75              80
Ile Asp Gln Lys Gly Lys Ser Ser Val Leu Lys Leu Ile Asn Gln Leu
      85              90              95
Lys Leu Tyr Leu Gln
      100

```

```

<210> 1373
<211> 369
<212> DNA
<213> Homo sapiens

```

```

<400> 1373
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  60
tgcaggcgcc ctgcattgca gagaactttt tccaccacaa cttctgtgta acaggcagtt
 120
acatgggttt catgggtcga catgggttcc gtgtcctgct tgccgggcct gagctgtttg
 180
tcagggtgtac aaccgagaac cttgcagacc agaatccaag actccgcagc atgtgtgtgc
 240
cggggcgggga cagcagctgt tggaggagaa agccatcagt gtatttagag gcaaagggct
 300
tctaaatcg aggctgtgca ggcctcctga aagtccttac ccaagcttcc gaggtaaatc
 360
ctctccgca
 369

```

```

<210> 1374
<211> 98
<212> PRT
<213> Homo sapiens

```

```

<400> 1374
Met Ala Glu Asn Phe Phe His His Asn Leu Arg Val Thr Gly Ser Tyr
  1              5              10              15
Met Gly Phe Met Gly Arg His Gly Phe Arg Val Leu Leu Ala Gly Pro
  20              25              30
Glu Leu Phe Val Arg Cys Thr Thr Glu Asn Leu Ala Asp Gln Asn Pro
  35              40              45
Arg Leu Arg Ser Met Cys Val Pro Gly Arg Asp Thr Ser Cys Trp Arg
  50              55              60
Arg Lys Pro Ser Val Tyr Leu Glu Ala Lys Gly Phe Leu Asn Arg Gly
  65              70              75              80
Cys Ala Gly Leu Leu Lys Val Leu Thr Gln Ala Ser Glu Val Asn Pro
      85              90              95
Leu Arg

```

```

<210> 1375
<211> 282

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<212> DNA

<213> Homo sapiens

<400> 1375

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 60
 ggctggcact ggcgcgcctt caacatcgct gacatggcca tcgtgggcgg ggcgatcgcg
 120
 ctggtggccc agtcgttcat gagcgtggag aaccgggccg ccacaaagga gtcccagtga
 180
 cattgggacg atccggaat tcgcaatgca cacggtgcag gacaccaatc tgaagagaac
 240
 ggccccacg atgagcggcc gcggcttgcc cctcatgcta gc
 282

<210> 1376

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1376

Xaa	Ala	Phe	Asp	Arg	Ala	Thr	Arg	Gly	His	Val	Ile	Asp	Tyr	Ile	Asp
1			5					10				15			
Phe	His	Leu	His	Gly	Trp	His	Trp	Pro	Ala	Phe	Asn	Ile	Ala	Asp	Met
		20						25				30			
Ala	Ile	Val	Gly	Gly	Ala	Ile	Ala	Leu	Val	Ala	Gln	Ser	Phe	Met	Ser
		35					40					45			
Val	Glu	Asn	Pro	Ala	Ala	Thr	Lys	Glu	Ser	Gln					
	50						55								

<210> 1377

<211> 6306

<212> DNA

<213> Homo sapiens

<400> 1377

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 120
 atggcgctggg acatgtgcaa ccaggactct gagtctgtat ggagtgacat cgagtgtgtc
 180
 gctctggttg gtgaagacca gcctctttgc ccagatcttc ctgaacttga tctttctgaa
 240
 ctgatgtga acgacttga tacagacagc tttctgggtg gactcaagtg gtgcagtgac
 300
 caatcagaaa taatatccaa tcagtacaac aatgagcctt caaacatatt tgagaagata
 360
 gatgaagaga atgaggcaaa cttgctagca gtcctcacag agacactaga cagtctccct
 420
 gtggatgaag acggattgcc ctcatattgat gcgctgacag atggagacgt gaccactgac
 480
 aatgaggcta gtccttcttc catgcctgac ggcacccctc caccacagga ggcagaagag
 540

ccgtctctac ttaagaagct cttactggca ccagccaaca ctcagctaag ttataatgaa
600
tgcagtgggtc tcagtaccca gaaccatgca aatcacatc acaggatcag aacaaacctt
660
gcaattgtta agactgagaa ttcattggagc aataaagcga agagtatttg tcaacagcaa
720
aagccacaaa gacgtccctg ctctggagctt ctcaaatac tgaccacaaa cgatgacctt
780
cttcacacca aacccacaga gaacagaaac agcagcagag acaaatgcac ctccaaaaag
840
aagtcccaca cacagtgcga gtcacaacac ttacaagcca aaccaacaac tttatctctt
900
cctctgaccc cagagtcacc aatgacccc aagggtctcc catttgagaa caagactatt
960
gaacgcacct taagtgtgga actctctgga actgcaggcc taactccacc caccactcct
1020
cttcataaag ccaaccaaga taacctttt agggcttctc caaagctgaa gtcctcttgc
1080
aagactgttg tgccaccacc atcaaagaag cccaggtaca gtgagtcttc tggatcacaa
1140
ggcaataact ccaccaagaa agggccggag caatccgagt tgtatgcaca actcagcaag
1200
tcctcagtc tcaactggtg acacgaggaa aggaagacca agcggcccag tctgaggctg
1260
tttggtgacc atgactattg ccagtcattt aattccaaaa cggaataact cattaatata
1320
tcacaggagc tccaagactc tagacaacta gaaaataaag atgtctcttc tgattggcag
1380
gggcagattt gttcttccac agattcagac cagtgtctacc tgagagagac tttggaggca
1440
agcaagcagg tctctccttg cagcacaaga aacagctcc aagaccagga aatccgagcc
1500
gagctgaaca agcacttcgg tcatccagc caagctgttt ttgacgacga agcagacaa
1560
accggtgaac tgagggacag tgatttcagt aatgaacaat tctccaaact acctatgttt
1620
ataaattcag gactagccat ggatggcctg tttgatgaca gcgaagatga aagtataaa
1680
ctgagctacc cttgggatgg caccgaatcc tattcattgt tcaatgtgtc tcctctctgt
1740
tcttctttta actctccatg tagagattct gtgtcaccac ccaaatcctt atttctcaa
1800
agaccccaaa ggatgcgctc tcgttcaagg tcctttcttc gacacaggtc gtgttcccca
1860
tcaccatatt ccaggtcaag atcaaggtct ccaggcagta gatcctcttc aagatcctgc
1920
tattactatg agtcaagcca ctacagacac cgcacgcacc gaaattctcc cttgtatgtg
1980
agatcacgtt caagatcgcc ctacagccgt cggcccagggt atgacagcta cgaggaatat
2040
cagcacgaga ggctgaagag ggaagaatat cgcagagagt atgagaagcg agagtctgag
2100
agggccaagc aaaggagag gcagaggcag aaggcaattg aagagcgccg tgtgatttat
2160

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<210> 1378

<211> 798

<212> PRT

<213> Homo sapiens

<400> 1378

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 35 40 45
 Asp Ser Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile
 50 55 60
 Ile Ser Asn Gln Tyr Asn Asn Glu Pro Ser Asn Ile Phe Glu Lys Ile
 65 70 75 80
 Asp Glu Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu
 85 90 95
 Asp Ser Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu
 100 105 110
 Thr Asp Gly Asp Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met

115	120	125
Pro Asp Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu		
130	135	140
Lys Lys Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu		
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Cys Ser Gly Leu Ser Thr Gln Asn His Ala Asn His Asn His Arg Ile		
165	170	175
Arg Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys		
180	185	190
Ala Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser		
195	200	205
Glu Leu Leu Lys Tyr Leu Thr Asn Asp Asp Pro Pro His Thr Lys		
210	215	220
Pro Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Thr Ser Lys Lys		
225	230	235
Lys Ser His Thr Gln Ser Gln Ser Gln His Leu Gln Ala Lys Pro Thr		
245	250	255
Thr Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly		
260	265	270
Ser Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu		
275	280	285
Ser Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala		
290	295	300
Asn Gln Asp Asn Pro Phe Arg Ala Ser Pro Lys Leu Lys Ser Ser Cys		
305	310	315
Lys Thr Val Val Pro Pro Pro Ser Lys Lys Pro Arg Tyr Ser Glu Ser		
325	330	335
Ser Gly Thr Gln Gly Asn Asn Ser Thr Lys Lys Gly Pro Glu Gln Ser		
340	345	350
Glu Leu Tyr Ala Gln Leu Ser Lys Ser Ser Val Leu Thr Gly Gly His		
355	360	365
Glu Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His		
370	375	380
Asp Tyr Cys Gln Ser Ile Asn Ser Lys Thr Glu Ile Leu Ile Asn Ile		
385	390	395
Ser Gln Glu Leu Gln Asp Ser Arg Gln Leu Glu Asn Lys Asp Val Ser		
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Ser Asp Trp Gln Gly Gln Ile Cys Ser Ser Thr Asp Ser Asp Gln Cys		
420	425	430
Tyr Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser		
435	440	445
Thr Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys		
450	455	460
His Phe Gly His Pro Ser Gln Ala Val Phe Asp Asp Glu Ala Asp Lys		
465	470	475
Thr Gly Glu Leu Arg Asp Ser Asp Phe Ser Asn Glu Gln Phe Ser Lys		
485	490	495
Leu Pro Met Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp		
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Asp Ser Glu Asp Glu Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr		
515	520	525
Gln Ser Tyr Ser Leu Phe Asn Val Ser Pro Ser Cys Ser Ser Phe Asn		
530	535	540
Ser Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln		

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545          550          555          560
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          565          570          575
Ser Cys Ser Arg Ser Pro Tyr Ser Arg Ser Arg Ser Arg Ser Pro Gly
          580          585          590
Ser Arg Ser Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr
          595          600          605
Arg His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser
          610          615          620
Arg Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Glu Tyr
          625          630          635          640
Gln His Glu Arg Leu Lys Arg Glu Glu Tyr Arg Arg Glu Tyr Glu Lys
          645          650          655
Arg Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Arg Gln Lys Ala
          660          665          670
Ile Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr
          675          680          685
Thr Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu
          690          695          700
Glu Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile
          705          710          715          720
Thr Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr
          725          730          735
Thr Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly
          740          745          750
Arg Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Ser Asn Ser
          755          760          765
Asp Asp Phe Asp Pro Ala Ser Thr Lys Ser Lys Tyr Asp Ser Leu Asp
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<210> 1379

<211> 590

<212> DNA

<213> Homo sapiens

<400> 1379

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480

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tgtggccgcg tcnaccacc tctgccctcg gtgtccccgc cgtgtggccg cgtcnacca
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<210> 1380

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1380

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		20						25					30		
Cys	Pro	Cys	Arg	Val	Ala	Ala	Ser	Pro	Ile	Ser	Ala	Leu	Gly	Val	Pro
		35					40				45				
Ala	Leu	Trp	Pro	Arg	His	Pro	Ser	Leu	Pro	Ser	Glu	Ser	Leu	Pro	Cys
	50				55						60				
Gly	Arg	Val	Xaa	Pro	Ser	Leu	Pro	Ser	Glu	Ser	Leu	Pro	Cys	Gly	Arg
65			70						75				80		
Val	Xaa	Pro	Pro	Leu	Pro	Ser	Val	Ser	Leu	Pro	Cys	Gly	Arg	Val	Xaa
			85					90					95		
Pro	Pro	Leu	Pro	Ser	Val	Ser	Leu	Pro	Cys	Gly	Arg	Val	Xaa	Pro	Pro
		100					105					110			
Leu	Pro	Ser	Val	Ser	Pro	Pro	Cys	Gly	Arg	Val	Xaa	Pro	Ser	Leu	Pro
		115					120					125			
Ser	Val	Ser	Pro	Pro	Cys	Gly	Arg	Val	Thr	His	Leu	Cys			
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<210> 1381

<211> 433

<212> DNA

<213> Homo sapiens

<400> 1381

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 120
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<210> 1382

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1382

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Gly Arg Ser Thr Leu Thr Ala Leu Ala Lys His Ser Phe Pro Cys Pro
           35           40           45
Gly Cys His Gln Arg Gly Gly Arg Ser His Arg Ser Ala Leu Val Ser
           50           55           60
Ala Gly Leu Lys Trp Gly Phe Ser Phe Cys Val Glu Gln Phe Ile Arg
65           70           75           80
Gly Leu Ile Ser Lys Pro Arg His Trp Pro Cys Thr Cys Ser Ser Arg
           85           90           95
Lys Pro Asn Ser Cys Leu Trp Ala Pro Ala Tyr Arg Gln Pro Asn Gly
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Leu Ala Pro Ala Lys Gly Leu Phe Gly Asp Leu
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<210> 1383

<211> 906

<212> DNA

<213> Homo sapiens

<400> 1383

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<210> 1384
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 1384
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 35 40 45
 Thr Ala Ser Ser Leu Leu Pro Leu Thr Asn Thr Pro Gln Thr Pro His
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 Met Ser Ser Pro Thr Pro Pro Arg Ala Met Val Leu Thr Lys Gln Arg
 65 70 75 80
 Pro Ser Gln Thr Gln Ser Cys Gly Pro Arg Val Ser Arg Arg Ala Asp
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<210> 1385
 <211> 210
 <212> DNA
 <213> Homo sapiens

<400> 1385
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<210> 1386
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 1386
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 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Leu Cys Val Ala Cys Met His Gly Val Cys

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      35              40              45
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Thr Gly Gly Cys Val Cys
65              70

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<210> 1387

<211> 521

<212> DNA

<213> Homo sapiens

<400> 1387

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360
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420
cgatgagatc gatgttgccc ttggagtggtg aactcgggtc gaaggtgtac ccgatgaact
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<210> 1388

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1388

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20              25              30
Ser Pro Gly Gly Gln His Thr Glu Ala Gly Glu Asp Glu Gly Val Val
35              40              45
Ala Ala Asp Gly Ser Ser Asp Ser Thr Ala Gly Asp Gly Gly Lys Glu
50              55              60
Ser Glu Asp Glu Asp Ser Asp Arg Gly Gly Glu His Arg Cys Ser Phe
65              70              75              80
Val Arg Ala Gly Tyr Pro Ala Ile Cys His Pro His Ala Ala Thr Gly
85              90              95
Ala Ala Phe Ser Gly His Pro
100

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<210> 1389

<211> 4013

<212> DNA

<213> Homo sapiens

<400> 1389

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 120
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 180
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 420
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 480
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<210> 1390

<211> 1156

<212> PRT

<213> Homo sapiens

<400> 1390

Pro Leu Lys Met Glu Thr Ser Gly Met Thr Thr Pro Ser Leu Lys Thr
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Thr Ile Ile Ser Thr Ile Pro Ser Thr Ala Met His Thr Arg Ser Thr
35 40 45
Ala Ala Pro Ile Pro Ile Leu Pro Glu Arg Gly Val Ser Leu Phe Pro
50 55 60
Tyr Gly Ala Asp Ala Gly Asp Leu Glu Phe Val Arg Arg Thr Val Asp
65 70 75 80
Phe Thr Ser Pro Leu Phe Lys Pro Ala Thr Gly Phe Pro Leu Gly Ser
85 90 95
Ser Leu Arg Asp Ser Leu Tyr Phe Thr Asp Asn Gly Gln Ile Ile Phe
100 105 110
Pro Glu Ser Asp Tyr Gln Ile Phe Ser Tyr Pro Asn Pro Leu Pro Thr
115 120 125
Gly Phe Thr Gly Arg Asp Pro Val Ala Leu Val Ala Pro Phe Trp Asp

130					135					140				
Asp	Ala	Asp	Phe	Ser	Thr	Gly	Arg	Gly	Thr	Thr	Phe	Tyr	Gln	Glu
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Glu	Thr	Phe	Tyr	Gly	Glu	His	Ser	Leu	Leu	Val	Gln	Gln	Ala	Glu
				165					170					175
Trp	Ile	Arg	Lys	Ile	Thr	Asn	Asn	Gly	Gly	Tyr	Lys	Ala	Arg	Trp
			180					185					190	
Leu	Lys	Val	Thr	Trp	Val	Asn	Ala	His	Ala	Tyr	Pro	Ala	Gln	Trp
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Leu	Gly	Ser	Asn	Thr	Tyr	Gln	Ala	Ile	Leu	Ser	Thr	Asp	Gly	Ser
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Ser	Tyr	Ala	Leu	Phe	Leu	Tyr	Gln	Ser	Gly	Gly	Met	Gln	Trp	Asp
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Ala	Gln	Arg	Ser	Gly	Asn	Pro	Val	Leu	Met	Gly	Phe	Ser	Ser	Gly
				245					250					255
Gly	Tyr	Phe	Glu	Asn	Ser	Pro	Leu	Met	Ser	Gln	Pro	Val	Trp	Glu
			260					265					270	
Tyr	Arg	Pro	Asp	Arg	Phe	Leu	Asn	Ser	Asn	Ser	Gly	Leu	Gln	Gly
	275					280						285		
Gln	Phe	Tyr	Arg	Leu	His	Arg	Glu	Glu	Arg	Pro	Asn	Tyr	Arg	Leu
	290				295					300				
Cys	Leu	Gln	Trp	Leu	Lys	Ser	Gln	Pro	Arg	Trp	Pro	Ser	Trp	Gly
305					310					315				320
Asn	Gln	Val	Ser	Cys	Pro	Cys	Ser	Trp	Gln	Gln	Gly	Arg	Arg	Asp
				325					330					335
Arg	Phe	Gln	Pro	Val	Ser	Ile	Gly	Arg	Trp	Gly	Leu	Gly	Ser	Arg
			340				345					350		
Leu	Cys	Ser	Phe	Thr	Ser	Trp	Arg	Gly	Gly	Val	Cys	Cys	Ser	Tyr
	355					360					365			
Pro	Trp	Gly	Glu	Phe	Arg	Glu	Gly	Trp	His	Val	Gln	Arg	Pro	Trp
	370				375						380			
Leu	Ala	Gln	Glu	Leu	Glu	Pro	Gln	Ser	Trp	Cys	Cys	Arg	Trp	Asn
385					390					395				400
Lys	Pro	Tyr	Leu	Cys	Ala	Leu	Tyr	Gln	Gln	Arg	Arg	Pro	His	Val
			405					410					415	
Cys	Ala	Thr	Tyr	Arg	Pro	Pro	Gln	Pro	Ala	Trp	Met	Phe	Gly	Asp
			420				425					430		
His	Ile	Thr	Thr	Leu	Asp	Gly	Val	Ser	Tyr	Thr	Phe	Asn	Gly	Leu
	435				440						445			
Asp	Phe	Leu	Leu	Val	Gly	Ala	Gln	Asp	Gly	Asn	Ser	Ser	Phe	Leu
	450				455					460				
Gln	Gly	Arg	Thr	Ala	Gln	Thr	Gly	Ser	Ala	Gln	Ala	Thr	Asn	Phe
	465				470				475					480
Ala	Phe	Ala	Ala	Gln	Tyr	Arg	Ser	Ser	Ser	Leu	Gly	Pro	Val	Thr
			485						490				495	
Gln	Trp	Leu	Leu	Glu	Pro	His	Asp	Ala	Ile	Arg	Val	Leu	Leu	Asp
		500					505					510		
Gln	Thr	Val	Thr	Phe	Gln	Pro	Asp	His	Glu	Asp	Gly	Gly	Gly	Gln
	515					520					525			
Thr	Phe	Asn	Ala	Thr	Gly	Val	Leu	Leu	Ser	Arg	Asn	Gly	Ser	Glu
	530				535					540				
Ser	Ala	Ser	Phe	Asp	Gly	Trp	Ala	Thr	Val	Ser	Val	Ile	Ala	Leu
	545				550				555					560
Asn	Ile	Leu	His	Ala	Ser	Ala	Ser	Leu	Pro	Pro	Glu	Tyr	Gln	Asn

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580										585										590									
Arg	Met	Pro	Asn	Gly	Ser	Thr	Ile	Pro	Pro	Gly	Ser	Pro	Glu	Glu	Met														
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Leu	Phe	His	Phe	Gly	Met	Thr	Trp	Gln	Ile	Asn	Gly	Thr	Gly	Leu	Leu														
610										620										635									
Gly	Lys	Arg	Asn	Asp	Gln	Leu	Pro	Ser	Asn	Phe	Thr	Pro	Val	Phe	Tyr														
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Ser	Gln	Leu	Gln	Lys	Asn	Ser	Ser	Trp	Ala	Glu	His	Leu	Ile	Ser	Asn														
645										650										655									
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675										680										685									
Ala	Asn	Ala	Thr	Leu	Asn	Gln	Tyr	Pro	Pro	Ser	Ile	Asn	Gly	Gly	Arg														
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Pro Arg Arg Ser Glu Glu Pro Arg Asn Asp Val Val Phe Gln Pro Ile
  1010                1015                1020
Ser Gly Glu Asp Val Arg Asp Val Thr Ala Leu Asn Val Ser Thr Leu
  1025                1030                1035                1040
Lys Ala Tyr Phe Arg Cys Asp Gly Tyr Lys Gly Tyr Asp Leu Val Tyr
          1045                1050                1055
Ser Pro Gln Ser Gly Phe Thr Cys Val Ser Pro Cys Ser Arg Gly Tyr
          1060                1065                1070
Cys Asp His Gly Gly Gln Cys Gln His Leu Pro Ser Gly Pro Arg Cys
          1075                1080                1085
Ser Cys Val Ser Phe Ser Ile Tyr Thr Ala Trp Gly Glu His Cys Glu
          1090                1095                1100
His Leu Ser Met Lys Leu Asp Ala Phe Phe Gly Ile Phe Phe Gly Ala
  1105                1110                1115                1120
Leu Gly Gly Leu Leu Leu Leu Gly Val Gly Thr Phe Val Val Leu Arg
          1125                1130                1135
Phe Trp Gly Cys Ser Gly Ala Arg Phe Ser Tyr Phe Leu Asn Ser Ala
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Glu Ala Leu Pro
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<210> 1391
<211> 481
<212> DNA
<213> Homo sapiens

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120
ctggcgccgc gcaaggtgct cggtaaaagc aagcagaagg ccgaggagct ggcgggtccgg
180
caactgaccc acgtgggcct gacgcacaag ctcaagacct ttcccgcana gctttccggc
240
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<210> 1392
<211> 160
<212> PRT
<213> Homo sapiens

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<400> 1392
Val Asp Gly Ile Glu Val His Asp Lys Ala Thr Asp Leu Asn Arg Leu

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```

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Arg Gln Lys Ile Gly Ile Val Phe Gln Gln Trp Asn Ala Phe Pro His
      20           25           30
Leu Thr Val Leu Glu Asn Val Met Leu Ala Pro Arg Lys Val Leu Gly
      35           40           45
Lys Ser Lys Gln Lys Ala Glu Glu Leu Ala Val Arg Gln Leu Thr His
      50           55           60
Val Gly Leu Ser Asp Lys Leu Lys Thr Phe Pro Ala Xaa Leu Ser Gly
      65           70           75           80
Gly Gln Gln Gln Arg Met Ala Ile Ala Arg Ala Leu Ala Met Ser Pro
      85           90           95
Asp Tyr Met Leu Phe Asp Glu Ala Thr Ser Ala Leu Asp Pro Gln Leu
      100          105          110
Val Gly Glu Val Leu Asp Thr Met Arg Met Leu Ala Glu Asp Gly Met
      115          120          125
Thr Met Val Leu Val Thr His Glu Ile Arg Phe Ala Arg Asp Val Ser
      130          135          140
Asp Arg Val Ala Phe Phe Arg Asn Gly Leu Val His Glu Ile Gly Ala
      145          150          155          160

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<210> 1393

<211> 309

<212> DNA

<213> Homo sapiens

<400> 1393

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120
tgggcccttc tgcgcgctca gggcatcagg tggcccgcgtg cancggtgga ggcctcatg
180
cgggacaacc ggtggcgtgg ggtgacccgc cgtaagaagg ttncgcacca ccacgcgtga
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ccggctgccc gggcgagccc cggatctggt ggaccgccag ttccgcgtcg aggcgccccaa
300
caagttgct
309

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<210> 1394

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1394

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Arg Pro Pro Ser Ala Arg Ala Leu Trp Asp Met Ala Ile Thr Glu Val
      1           5           10           15
Leu Ala Gly Tyr Tyr Glu Pro Asp Glu His Gly His Arg Lys Pro Glu
      20           25           30
Ser Leu Tyr Gly Ala Val Lys Met Trp Ala Leu Leu Arg Arg Gln Gly
      35           40           45
Ile Arg Trp Pro Ala Ala Xaa Val Glu Arg Leu Met Arg Asp Asn Arg
      50           55           60
Trp Arg Gly Val Thr Arg Arg Lys Lys Val Xaa His His His Arg

```

65

70

75

<210> 1395

<211> 347

<212> DNA

<213> Homo sapiens

<400> 1395

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ccagattctt aaaggcggtc gcgatgttgc cggggcgaca agggccttgg ctggaggggt
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gtcgggtggg gagatcccct cagttgcact agagcacgtg gccgatgacg tggagggtatt
240
ggctcaggct aggggggctc atgcagtggg cggaagcgtt tccgacgcc tcattgccac
300
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347

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<210> 1396

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1396

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Met Thr Val Val Val Gly Glu Thr Val Leu Val Val Val Arg Arg Gln
1          5          10          15
Arg Arg Arg Ala Gln Ile Leu Lys Gly Gly Arg Asp Val Ala Arg Ala
20          25          30
Thr Arg Ala Leu Ala Gly Arg Val Ser Val Gly Glu Ile Pro Ser Val
35          40          45
Ala Leu Glu His Val Ala Asp Asp Val Glu Val Leu Ala Gln Ala Arg
50          55          60
Arg Ala His Ala Val Gly Gly Ser Val Ser Asp Ala Leu Ile Ala Thr
65          70          75          80
Ser Arg Gln Pro Gly Met Ala Gly Leu Val Pro Leu Ala His Ala
85          90          95

```

<210> 1397

<211> 308

<212> DNA

<213> Homo sapiens

<400> 1397

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ctggcccgcg tcgcgattgc cgccactatc cattctccgg aacgcgcgca agacatggtc
120
aaccgcctta gaaaacgcga agaaggcttc acgcaatggg tacgtgccgc acaggacgat
180
ggtcgactgt cctgcagcga ccggcgcttc gctgccacc agatacaaa cctgctcaag
240

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gcgttcgcct ttggccgca aatcaccttg ggccagccgg tgctggatgc cgccagccag
 300
 gccaacgt
 308

<210> 1398
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 1398
 Met Gln Met Met Ser Asp Thr Asn Phe Leu Asp Leu Ala Arg Val Ala
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 Ile Ala Ala Thr Ile His Ser Pro Glu Arg Ala Gln Asp Met Val Asn
 20 25 30
 Arg Leu Ser Lys Arg Glu Glu Gly Phe Thr Gln Trp Val Arg Ala Ala
 35 40 45
 Gln Asp Asp Gly Arg Leu Ser Cys Ser Asp Pro Ala Phe Ala Ala His
 50 55 60
 Gln Ile Gln Ser Leu Leu Lys Ala Phe Ala Phe Trp Pro Gln Ile Thr
 65 70 75 80
 Leu Gly Gln Pro Val Leu Asp Ala Ala Ser Gln Ala Asn
 85 90

<210> 1399
 <211> 539
 <212> DNA
 <213> Homo sapiens

<400> 1399
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 120
 ttgatatttt taacttcac agtactatct gtagtaggag gctgatttta ctaaaattag
 180
 ataattatat acatctgttc ctattccttt ggtaggacct ttaagaaagt catgctgaat
 240
 ctgagaatgc caggacattt cagctggtat gaatgtagga tattcattta cacatcgctg
 300
 cacagacagc ctctatataa cccaccctgt tgggggtattg aattttttct tttccgcgcc
 360
 tacttttaaa tcttgtcatg taatttcaac acataatttg tggcacttta gtttttttac
 420
 cctttatagt ttaataactt atacatgtac atgcttaaaa tgtcaaacaa tacaaatggg
 480
 aacaaagaaa attgcttcac catctgtgaa cccctccttt tgtagtcccc ttcacgcgt
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<210> 1400
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 1400

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Met Asn Val Gly Tyr Ser Phe Thr His Arg Cys Thr Asp Ser Leu Tyr
 1           5           10           15
Ile Thr His Pro Val Gly Val Leu Asn Phe Phe Phe Ser Arg Pro Thr
           20           25           30
Phe Lys Ser Cys His Val Ile Ser Thr His Asn Leu Trp His Phe Ser
           35           40           45
Phe Phe Thr Leu Tyr Ser Leu Ile Thr Tyr Thr Cys Thr Cys Leu Lys
           50           55           60
Cys Gln Thr Ile Gln Met Gly Thr Lys Lys Ile Ala Ser Pro Ser Val
65           70           75           80
Asn Pro Ser Phe Cys Ser Pro Leu His Ala
           85           90

```

<210> 1401

<211> 653

<212> DNA

<213> Homo sapiens

<400> 1401

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120
ncattggggt ttgatggcgc cgtttccctg ctgctgggcg cgatcctcat cgtcaccggc
180
ccaacgggtga ttaaccgat cctgcgtcag ttgcgtccta cccggcgagt gaggctctgc
240
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300
caggccataa ccagcatcga ccgatcttcc atcggacaag cgtctctgaa tctggggctc
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accctattgg tcgggctgct ctctcgtggc cccatcgggg ggatcgtcac cgcgatgatg
420
aaacggcacc tcatcccgga ctctctacaa ggcgtgattt tcgttggggt cgccgttggg
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540
ggcatctacc tggcgaacca gcgcaacctc gagcttgagc ccgtcatcga gttcaaggaa
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653

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<210> 1402

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1402

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Phe Glu Gly Ser Leu Gly Leu Lys Leu Arg Glu Val Arg Asp Leu Gly
 1           5           10           15
Arg Pro Ile Phe Arg Leu Cys Thr Val Thr Ala Arg Leu Ala Trp Val
           20           25           30
Xaa Ser Ser Pro Ala Arg Arg Trp Xaa Leu Gly Phe Asp Gly Arg Val

```

```

      35              40              45
Ser Leu Leu Leu Gly Ala Ile Leu Ile Val Thr Gly Pro Thr Val Ile
  50              55              60
Asn Pro Ile Leu Arg Gln Leu Arg Pro Thr Arg Arg Val Ser Ala Leu
  65              70              75              80
Leu Arg Trp Glu Gly Ile Val Val Asp Pro Leu Gly Ala Ile Leu Ala
      85              90              95
Leu Leu Val Tyr Gln Ala Ile Thr Ser Ile Asp Arg Ser Ser Ile Gly
      100              105              110
Gln Gly Val Leu Asn Leu Gly Leu Thr Leu Leu Val Gly Leu Leu Phe
      115              120              125
Ala Gly Pro Ile Gly Trp Ile Val Thr Ala Met Met Lys Arg His Leu
      130              135              140
Ile Pro Asp Phe Leu Gln Gly Val Ile Phe Val Gly Val Ala Val Gly
      145              150              155              160
Thr Cys Val Gly Ala Asn Val Ile Arg Glu Glu Ser Gly Leu Val Ala
      165              170              175
Val Thr Met Leu Gly Ile Tyr Leu Ala Asn Gln Arg Asn Leu Glu Leu
      180              185              190
Glu Pro Val Ile Glu Phe Lys Glu His Leu Gln Val Leu Leu Val Gly
      195              200              205
Val Leu Phe Ile Met Leu Ala Gly Arg
      210              215

```

<210> 1403

<211> 393

<212> DNA

<213> Homo sapiens

<400> 1403

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aagctttgca gtttcttggt atccaaatcc aggcgttctt ggtctttttc cacaacagtg
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  120
tggttccttg ggcatgatac tcacaaagtt gggcataatct cctttatcag ctgcttgcca
  180
gagcttcctt ccatactcttt cattatgacc tcaaaggag agtgccacgt agtcttgga
  240
gtcctagctt gtttccgaag ggctgtcaga gcctccctgt taccatttct tatcttatca
  300
ttttccacca actgatgtct agccagaaga actttttctg catcagtcct aatatcaacc
  360
agagcctctt gaagctgctt catgttgga tcc
  393

```

<210> 1404

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1404

```

Met Lys Gln Leu Gln Glu Ala Leu Val Asp Ile Glu Thr Asp Ala Glu
  1              5              10              15
Lys Val Leu Leu Ala Arg His Gln Leu Val Glu Asn Asp Lys Ile Arg

```

```

                20                25                30
Asn Gly Asn Arg Glu Ala Leu Thr Ala Leu Arg Lys Gln Ala Arg Thr
    35                40                45
Ser Lys Thr Ser Val Pro Ser Pro Phe Glu Val Ile Met Lys Glu Met
    50                55                60
Glu Gly Ser Ser Gly Lys Gln Leu Ile Lys Glu Ile Cys Pro Thr Cys
    65                70                75                80
Gly Asp His Asp Pro Lys Glu His Thr Trp Leu Met Phe Pro Gly Ser
    85                90                95
Asp Met Phe Ala Arg Val Pro Phe His Val Ala His Thr Val Val Glu
    100                105                110
Lys Asp Gln Glu Arg Leu Asp Leu Asp Thr Lys Lys Leu Gln Ser
    115                120                125

<210> 1405
<211> 421
<212> DNA
<213> Homo sapiens

<400> 1405
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120
gaagagttcg ccgccgagca aaacctgcgt gccgccctgg gcgagttgca tatccaggtc
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420
t
421

<210> 1406
<211> 140
<212> PRT
<213> Homo sapiens

<400> 1406
Xaa Arg Leu His Lys Ala Leu Gly Ile Glu Leu Pro Gly Ala Leu Gln
1 5 10 15
Val Ile Val Lys Gly Glu Thr Ser Leu Gln Trp Leu Gly Pro Asp Glu
20 25 30
Trp Leu Leu Ile Val Pro Ser Gly Glu Glu Phe Ala Ala Glu Gln Asn
35 40 45
Leu Arg Ala Ala Leu Gly Glu Leu His Ile Gln Val Val Asn Val Ser
50 55 60
Gly Gly Gln Gln Ile Leu Glu Leu Ser Gly Pro Asn Val Arg Asp Val
65 70 75 80
Leu Met Lys Ser Thr Ser Tyr Asp Val His Pro Asn Asn Phe Pro Val

```


	85		90		95										
Gly	Lys	Ala	Val	Gly	Thr	Val	Phe	Ala	Lys	Ser	Gln	Leu	Val	Ile	Arg
	100		105		110										
His	Thr	Ala	Glu	Asp	Thr	Trp	Glu	Leu	Leu	Ile	Arg	Arg	Ser	Phe	Ser
	115		120		125										
Asp	Tyr	Trp	Trp	Leu	Trp	Leu	Gln	Asp	Ala	Ala	Ala				
	130		135		140										

<210> 1407

<211> 1006

<212> DNA

<213> Homo sapiens

<400> 1407

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120
ctggaggcgg ccagcaagtt ccagttccac acctcttgca aagtetgegt gtcctttctt
180
gagaagcagc tgacggccag caactgcctg ggcgttgctg ccatggccga ggccatgcag
240
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840
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900
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<210> 1408

<211> 335

<212> PRT

<213> Homo sapiens

<400> 1408

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Xaa Gly Arg Glu Lys Leu Glu Leu Val Leu Ser Asn Leu Gln Ala Asp
 1           5           10           15
Val Leu Glu Leu Leu Leu Glu Phe Val Tyr Thr Gly Ser Leu Val Ile
           20           25           30
Asp Ser Ala Asn Ala Lys Thr Leu Leu Glu Ala Ala Ser Lys Phe Gln
           35           40           45
Phe His Thr Phe Cys Lys Val Cys Val Ser Phe Leu Glu Lys Gln Leu
           50           55           60
Thr Ala Ser Asn Cys Leu Gly Val Ala Ala Met Ala Glu Ala Met Gln
           65           70           75           80
Cys Ser Glu Leu Tyr His Xaa Ala Lys Ala Phe Ala Leu Gln Ile Phe
           85           90           95
Pro Glu Val Ala Ala Gln Glu Glu Ile Leu Ser Ile Ser Lys Asp Asp
           100          105          110
Phe Ile Ala Tyr Val Ser Asn Asp Ser Leu Asn Thr Lys Ala Glu Glu
           115          120          125
Leu Val Tyr Glu Thr Val Ile Lys Trp Ile Lys Lys Asp Pro Ala Thr
           130          135          140
Arg Thr Gln Tyr Ala Ala Glu Leu Leu Ala Val Val Arg Leu Pro Phe
           145          150          155          160
Ile His Pro Ser Tyr Leu Leu Asn Val Val Asp Asn Glu Glu Leu Ile
           165          170          175
Lys Ser Ser Glu Ala Cys Arg Asp Leu Val Asn Glu Ala Lys Arg Tyr
           180          185          190
His Met Leu Pro His Ala Arg Gln Glu Met Gln Thr Pro Arg Thr Arg
           195          200          205
Pro Arg Leu Ser Ala Gly Val Ala Glu Val Ile Val Leu Val Gly Gly
           210          215          220
Arg Gln Met Val Gly Met Thr Gln Arg Ser Leu Val Ala Val Thr Cys
           225          230          235          240
Trp Asn Pro Gln Asn Asn Lys Trp Tyr Pro Leu Ala Ser Val Pro Phe
           245          250          255
Leu Gly Pro Gly Phe Phe Ser Val Val Ser Ala Gly Ala Asn Ile Tyr
           260          265          270
Leu Ser Gly Gly Met Glu Ser Gly Val Pro Leu Ala Asp Val Trp Cys
           275          280          285
Tyr Met Ser Leu Leu Asp Asn Trp Asn Leu Val Ser Arg Met Pro Val
           290          295          300
Pro Arg Cys Arg Pro His Ser Leu Val Tyr Asp Gly Lys Ile Tyr Thr
           305          310          315          320
Leu Gly Gly Leu Gly Val Ala Gly Asn Val Asp His Val Glu Arg
           325          330          335

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<210> 1409

<211> 279

<212> DNA

<213> Homo sapiens

<400> 1409

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120

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cacgaccaac aggccgcaat cgctcgagcgc gcgctggagg ccggcgcttac gcaaatgctg
 180
 ctgacaggca ccagcctggc ggctcagcgaa caagccctgg aactgtgcc tcaactggat
 240
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 279

<210> 1410
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 1410
 Xaa Met Lys Phe Leu Val Phe Ser Glu Lys Arg Ala Phe Cys Tyr Ala
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 Gly Arg Pro Ala Ala Arg Asp Ser Thr Met Gln Leu Ile Asp Ile Gly
 20 25 30
 Val Asn Leu Thr Asn Ser Ser Phe His Asp Gln Gln Ala Ala Ile Val
 35 40 45
 Glu Arg Ala Leu Glu Ala Gly Val Thr Gln Met Leu Leu Thr Gly Thr
 50 55 60
 Ser Leu Ala Val Ser Glu Gln Ala Leu Glu Leu Cys His Gln Leu Asp
 65 70 75 80
 Ala Ser Gly Ala His Leu Phe Ala Thr Ala Gly Val His
 85 90

<210> 1411
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 1411
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 120
 gatttttcaat ctattttctta ctattccgcg ccaaaaagca tgaaggataa gcctaagtgc
 180
 ttagacgaag tcgatcctga attgttacgt acctatgaaa aactgggcat tcctctcata
 240
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 300
 actacttttc gtcaaaagct t
 321

<210> 1412
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 1412
 Xaa Arg Ile Ser Gly Met Lys Asn Glu Pro Glu Trp Met Leu Glu Trp
 1 5 10 15
 Arg Leu Ser Ala Phe Arg Glu Trp Leu Glu Met Glu Glu Pro Ser Trp

```

                20                25                30
Ala His Val Asp Tyr Pro Lys Ile Asp Phe Gln Ser Ile Ser Tyr Tyr
      35                40                45
Ser Ala Pro Lys Ser Met Lys Asp Lys Pro Lys Ser Leu Asp Glu Val
      50                55                60
Asp Pro Glu Leu Leu Arg Thr Tyr Glu Lys Leu Gly Ile Pro Leu Ile
      65                70                75                80
Glu Gln Gln Met Leu Ala Gly Ile Ala Val Asp Ala Val Phe Asp Ser
      85                90                95
Val Ser Val Val Thr Thr Phe Arg Gln Lys Leu
      100                105

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<210> 1413
 <211> 385
 <212> DNA
 <213> Homo sapiens

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<400> 1413
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120
cgccctggcg cgttggaagc cgaagtgata aaccgtgtgc tgcataaacc cngcacgaag
180
ccggaaccgc aacatgttaa accgctgcct acgaaattgc gttgggtcga ataaactcata
240
gaggaacacc atcatgacta taaaagccat caacgtgcgt aaccagttaa aaggcaccat
300
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360
cgtaacttct gtgatcacta cgcgt
385

```

<210> 1414
 <211> 55
 <212> PRT
 <213> Homo sapiens

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<400> 1414
Met Thr His Asp Val Ser Glu Ala Val Ala Ile Ala Asp Arg Val Ile
1      5      10      15
Leu Ile Glu Asp Gly Glu Ile Gly Leu Asp Leu Ile Ile Asp Leu Pro
      20      25      30
Arg Pro Arg Ala Arg Gly Ser His Arg Leu Ala Ala Leu Glu Ala Glu
      35      40      45
Val Ile Asn Arg Val Leu Ser
50      55

```

<210> 1415
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 1415

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 120
 tctgaggctg aagaggagga gaaagccctt gtgttgccag agagtacaga agggcgggag
 180
 ctgaccagg gcccggcaga gtctctctct ctctcaggt gtgggagctg gcagccccgg
 240
 aagctgccag tcttcaagtc cctccggcac atgaggcagg tcttgggtgc ccttcttttc
 300
 cgcattctgg cctggcacgt tctcatgggg aaccaggtga tctggaaaag cagagacgtg
 360
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 420

<210> 1416

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1416

Met	Arg	Leu	Phe	Val	Pro	Val	Thr	Val	Leu	Val	Ile	Cys	Leu	Ala	Asp
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Leu	Glu	Glu	Glu	Ser	Glu	Ser	Trp	Asp	Asn	Ser	Glu	Ala	Glu	Glu	Glu
			20					25					30		
Glu	Lys	Ala	Pro	Val	Leu	Pro	Glu	Ser	Thr	Glu	Gly	Arg	Glu	Leu	Thr
		35				40						45			
Gln	Gly	Pro	Ala	Glu	Ser	Ser	Ser	Leu	Ser	Gly	Cys	Gly	Ser	Trp	Gln
		50				55					60				
Pro	Arg	Lys	Leu	Pro	Val	Phe	Lys	Ser	Leu	Arg	His	Met	Arg	Gln	Val
				70						75				80	
Leu	Gly	Ala	Pro	Ser	Phe	Arg	Met	Leu	Ala	Trp	His	Val	Leu	Met	Gly
				85				90						95	
Asn	Gln	Val	Ile	Trp	Lys	Ser	Arg	Asp	Val	Asp	Leu	Val	Gln	Ser	Ala
			100					105					110		
Phe	Glu	Val	Leu	Arg	Val	Arg	Thr	Ser	Phe	Pro					
		115					120								

<210> 1417

<211> 5058

<212> DNA

<213> Homo sapiens

<400> 1417

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 120
 taggaggggt gccaccccat ttccagtgtg acctgttccc attcccccat gtctctctcc
 180
 atccctcccg ccaactcagct caggctgatg agaagcagag caacgggtgt atcggtgttt
 240
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 300

ccgccectct tttgtcctct tcccagggtc cctggccctc tcggagaaac gcacttggtt
360
cgggccagcc gcctgagggg acgggctcac gtctgtcctc cacactgcag ctgctggggc
420
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480
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540
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600
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720
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<210> 1418

<211> 1532

<212> PRT

<213> Homo sapiens

<400> 1418

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Leu Cys Leu Cys Leu Leu Pro His Val Val Pro Gly Thr Thr Glu Asp
           20           25           30
Thr Leu Ile Thr Gly Ser Lys Thr Pro Ala Pro Val Thr Ser Thr Gly
 35           40           45
Ser Thr Thr Ala Thr Leu Glu Gly Gln Ser Thr Ala Ala Ser Ser Arg
 50           55           60
Thr Ser Asn Gln Asp Ile Ser Ala Ser Ser Gln Asn His Gln Thr Lys
 65           70           75           80
Ser Thr Glu Thr Thr Ser Lys Ala Gln Thr Asp Thr Leu Thr Gln Met
           85           90           95
Met Thr Ser Thr Leu Phe Ser Ser Pro Ser Val His Asn Val Met Glu
 100           105           110
Thr Val Thr Gln Glu Thr Ala Pro Pro Asp Glu Met Thr Thr Ser Phe
 115           120           125
Pro Ser Ser Val Thr Asn Thr Leu Met Met Thr Ser Lys Thr Ile Thr
 130           135           140
Met Thr Thr Ser Thr Asp Ser Thr Leu Gly Asn Thr Glu Glu Thr Ser
 145           150           155           160
Thr Ala Gly Thr Glu Ser Ser Thr Pro Val Thr Ser Ala Val Ser Ile
           165           170           175
Thr Ala Gly Gln Glu Gly Gln Ser Arg Lys Thr Ser Trp Arg Thr Ser
 180           185           190
Ile Gln Asp Thr Ser Ala Ser Ser Gln Asn His Trp Thr Arg Ser Thr
 195           200           205
Gln Thr Thr Arg Glu Ser Gln Thr Ser Thr Leu Thr His Arg Thr Thr
 210           215           220
Ser Thr Pro Ser Phe Ser Pro Ser Val His Asn Val Thr Gly Thr Val
 225           230           235           240
Ser Gln Lys Thr Ser Pro Ser Gly Glu Thr Ala Thr Ser Ser Leu Cys
           245           250           255
Ser Val Thr Asn Thr Ser Met Met Thr Ser Glu Lys Ile Thr Val Thr
 260           265           270
Thr Ser Thr Gly Ser Thr Leu Gly Asn Pro Gly Glu Thr Ser Ser Val
 275           280           285
Pro Val Thr Gly Ser Leu Met Pro Val Thr Ser Ala Ala Leu Val Thr
 290           295           300
Val Asp Pro Glu Gly Gln Ser Pro Ala Thr Phe Ser Arg Thr Ser Thr
 305           310           315           320
Gln Asp Thr Thr Ala Phe Ser Lys Asn His Gln Thr Gln Ser val Glu
           325           330           335
Thr Thr Arg Val Ser Gln Ile Asn Thr Leu Asn Thr Leu Thr Pro Val
 340           345           350
Thr Thr Ser Thr val Leu Ser Ser Pro Ser Gly Phe Asn Pro Ser Gly
 355           360           365
Thr Val Ser Gln Glu Thr Phe Pro Ser Gly Glu Thr Thr Ile Ser Ser
 370           375           380
Pro Ser Ser Val Ser Asn Thr Phe Leu Val Thr Ser Lys Val Phe Arg

```

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385          390          395          400
Met Pro Ile Ser Arg Asp Ser Thr Leu Gly Asn Thr Glu Glu Thr Ser
          405          410          415
Leu Ser Val Ser Gly Thr Ile Ser Ala Ile Thr Ser Lys Val Ser Thr
          420          425          430
Ile Trp Trp Ser Asp Thr Leu Ser Thr Ala Leu Ser Pro Ser Ser Leu
          435          440          445
Pro Pro Lys Ile Ser Thr Ala Phe His Thr Gln Gln Ser Glu Gly Ala
          450          455          460
Glu Thr Thr Gly Arg Pro His Glu Arg Ser Ser Phe Ser Pro Gly Val
          465          470          475          480
Ser Gln Glu Ile Phe Thr Leu His Glu Thr Thr Trp Pro Ser Ser
          485          490          495
Phe Ser Ser Lys Gly His Thr Thr Trp Ser Gln Thr Glu Leu Pro Ser
          500          505          510
Thr Ser Thr Gly Ala Ala Thr Arg Leu Val Thr Gly Asn Pro Ser Thr
          515          520          525
Gly Ala Ala Gly Thr Ile Pro Arg Val Pro Ser Lys Val Ser Ala Ile
          530          535          540
Gly Glu Pro Gly Glu Pro Thr Thr Tyr Ser Ser His Ser Thr Thr Leu
          545          550          555          560
Pro Lys Thr Thr Gly Ala Gly Ala Gln Thr Gln Trp Thr Gln Glu Thr
          565          570          575
Gly Thr Thr Gly Glu Ala Leu Leu Ser Ser Pro Ser Tyr Ser Val Thr
          580          585          590
Gln Met Ile Lys Thr Ala Thr Ser Pro Ser Ser Pro Met Leu Asp
          595          600          605
Arg His Thr Ser Gln Gln Ile Thr Thr Ala Pro Ser Thr Asn His Ser
          610          615          620
Thr Ile His Ser Thr Ser Thr Ser Pro Gln Glu Ser Pro Ala Val Ser
          625          630          635          640
Gln Arg Gly His Thr Gln Ala Pro Gln Thr Thr Gln Glu Ser Gln Thr
          645          650          655
Thr Arg Ser Val Ser Pro Met Thr Asp Thr Lys Thr Val Thr Thr Pro
          660          665          670
Gly Ser Ser Phe Thr Ala Ser Gly His Ser Pro Ser Glu Ile Val Pro
          675          680          685
Gln Asp Ala Pro Thr Ile Ser Ala Ala Thr Thr Phe Ala Pro Ala Pro
          690          695          700
Thr Gly Asp Gly His Thr Thr Gln Ala Pro Thr Thr Ala Leu Gln Ala
          705          710          715          720
Thr Pro Ser Ser His Asp Ala Thr Leu Gly Pro Ser Gly Gly Thr Ser
          725          730          735
Leu Ser Lys Thr Gly Ala Leu Thr Leu Ala Asn Ser Val Val Ser Thr
          740          745          750
Pro Gly Gly Pro Glu Gly Gln Trp Thr Ser Ala Ser Ala Ser Thr Ser
          755          760          765
Pro Asp Thr Ala Ala Ala Met Thr His Thr His Gln Ala Glu Ser Thr
          770          775          780
Glu Ala Ser Gly Gln Thr Gln Thr Ser Glu Pro Ala Ser Ser Gly Ser
          785          790          795          800
Arg Thr Thr Ser Ala Gly Thr Ala Thr Pro Ser Ser Ser Gly Ala Ser
          805          810          815
Gly Thr Thr Pro Ser Gly Ser Glu Gly Ile Ser Thr Ser Gly Glu Thr

```

[illegible]

1250	1255	1260
Gly His Ala Thr Pro Leu His Val Thr Asp Ala Ser Ser Val Ser Thr		
1265	1270	1275
Gly Asp Thr Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Thr		1280
	1285	1290
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr		1295
	1300	1305
Gly Asp Thr Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Val Ser Thr		1310
	1315	1320
Ser His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr		1325
	1330	1335
Ser His Ala Thr Ser Leu Pro Val Thr Asp Pro Ser Ser Ala Ser Thr		1340
	1345	1350
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr		1355
	1365	1370
Gly His Ala Thr Ser Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1375
	1380	1385
Gly Asp Thr Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1390
	1395	1400
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1405
	1410	1415
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr		1420
	1425	1430
Gly His Thr Thr Pro Leu His Val Thr Ser Pro Ser Ser Ala Ser Thr		1435
	1445	1450
Gly His Ala Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Thr		1455
	1460	1465
Ser His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1470
	1475	1480
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr		1485
	1490	1495
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr		1500
	1505	1510
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser		1515
	1525	1530

<210> 1419

<211> 309

<212> DNA

<213> Homo sapiens

<400> 1419

aaggctatgg gaattcaaaa gtatgtgttc tattccatcc acaactgtga caagcagcct
60

gaggttccct tgatggaaat caagtattgt actggtaaat ttattcagga cagtggctgtg
120

gattatatca tcattccgttt gtgtgggttc atgcagggtc ttattgggca atatgtgttt
180

cctatactag aagagaagtc cgtctgggga actgatgctc caactcggat tgcttacatg
240

gatacccagg acgtagctcg actaacgttt atagctatgc ggaatagaga ggccaacaag
300

aaactcatg

309

<210> 1420

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1420

```

Lys Ala Met Gly Ile Gln Lys Tyr Val Phe Tyr Ser Ile His Asn Cys
 1             5             10             15
Asp Lys Gln Pro Glu Val Pro Leu Met Glu Ile Lys Tyr Cys Thr Gly
          20             25             30
Lys Phe Ile Gln Asp Ser Gly Leu Asp Tyr Ile Ile Arg Leu Cys
          35             40             45
Gly Phe Met Gln Gly Leu Ile Gly Gln Tyr Ala Val Pro Ile Leu Glu
          50             55             60
Glu Lys Ser Val Trp Gly Thr Asp Ala Pro Thr Arg Ile Ala Tyr Met
65             70             75             80
Asp Thr Gln Asp Val Ala Arg Leu Thr Phe Ile Ala Met Arg Asn Glu
          85             90             95
Lys Ala Asn Lys Lys Leu Met
          100

```

<210> 1421

<211> 385

<212> DNA

<213> Homo sapiens

<400> 1421

```

ccatggcggc atgggtggag agagaagctg gggagaagaa atgatgcaga gatctcgcca
60
ggccaggggag ctgggctggg cagccaggag tagagaaaca acgctcccag aggaggggag
120
gatgttagag caaagccgag cccagctgct ggcgaaatgca tctgtgatgc ccatgagcag
180
ccaggatttc agctccgctc tacttcttga ctgctgcaga actcagcacc agctccagtg
240
ccctcagagc cctgattttt cacaaaccga ctctccaag cctcccctgt gggcgggata
300
cacaagccag agtcgccttg tcacatctct tctctctcca ccaggtcatg ggcaaacctt
360
cctgacatac tttagacat tacag
385

```

<210> 1422

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1422

```

Met Gly Gly Glu Arg Ser Trp Gly Glu Glu Met Met Gln Arg Ser Arg
 1             5             10             15
Gln Ala Arg Glu Leu Gly Trp Ala Ala Arg Ser Arg Glu Thr Thr Leu
          20             25             30
Pro Glu Glu Gly Arg Met Leu Glu Gln Ser Arg Ala Gln Leu Leu Ala

```

```

          35              40              45
Asn Ala Ser Val Met Pro Met Ser Ser Gln Asp Phe Ser Ser Ala Leu
 50              55              60
Leu Leu Asp Cys Cys Arg Thr Gln His Gln Leu Gln Cys Pro Gln Ser
 65              70              75              80
Pro Asp Phe Ser Gln Thr Asp Ser Ser Lys Pro Pro Leu Trp Ala Gly
          85              90              95
Tyr Thr Ser Gln Ser Arg Leu Val Thr Ser Leu Leu Ser Pro Pro Gly
          100              105              110
His Gly Gln Thr Phe Leu Thr Tyr Phe Thr Thr Leu Gln
          115              120              125

```

<210> 1423

<211> 336

<212> DNA

<213> Homo sapiens

<400> 1423

```

nntattcttc aatccttcca caatgtgcaa caaatggcga ttgactggct cactcgaagt
 60
ctctattttg tggaccatgt cggtgaccgg atctttgttt gtaattccaa cggttctgta
 120
tgtgtcacc c tgattgatct ggagcttcac aatcctaaag caatagcagt agatccaata
 180
gcaggaaaac ttttctttac tgactacggg aatgtcgcca aagtggagag atgtgacatg
 240
gatgggatga accgaacaag gataattgat tcaaagacag agcagccagc tgcactggga
 300
ctagacctag tcaacaaatt ggtttactgg gtagat
 336

```

<210> 1424

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1424

```

Xaa Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp Trp
 1              5              10              15
Leu Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile Phe
          20              25              30
Val Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu Glu
          35              40              45
Leu His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys Leu
          50              55              60
Phe Phe Thr Asp Tyr Gly Asn Val Ala Lys Val Glu Arg Cys Asp Met
 65              70              75              80
Asp Gly Met Asn Arg Thr Arg Ile Ile Asp Ser Lys Thr Glu Gln Pro
          85              90              95
Ala Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val Asp
          100              105              110

```

<210> 1425

<211> 672

<212> DNA

<213> Homo sapiens

<400> 1425

accggtgttt tcgatcacct gggcgggttg agtgactatc gcagtcagat cgccccgatg
 60
 gcccgcatg tcgaagacct ggccttggcg ctacaggcca ttgccggtga agatggggtc
 120
 gatgccgggg tgattccgat gccgctgcgc cgtatgcaaa ctcaaagcct gaagggggttg
 180
 cgagtcgcct ggtacagcga tgggtggcatt gagcccggtg acgcgctcac gcacaccaca
 240
 ttgcaggcgg tcgccgatct attggacgct gaaggcgcct tgatccgccc ggccttcccc
 300
 tcggcggtga gcaatgcccg tgacattacc gaacgctatt gggcaatgag tcaaagctcc
 360
 ggcgcgcagt cgatccagct gttttcagat tgggatcagt tccgtacagc catgctgggg
 420
 ttcatggcgg actacgacat tatcctgtgc cctgtcagat ccgcgcgggc gacccaactg
 480
 ggagagagac gccaggggct gttcagttcc ccccttccta atggcttggc gggttggcct
 540
 tgtgtgggtg tccggggccg aacggatagc gcggggttgc cggttggcgt gcagattgtc
 600
 gcgcgacctt ggcacgagcc tgcgcggtg gcggcagcag cggccattga gcgcgcgctg
 660
 ccgttcacgc gt
 672

<210> 1426

<211> 224

<212> PRT

<213> Homo sapiens

<400> 1426

Thr Gly Val Phe Asp His Leu Gly Gly Leu Ser Asp Tyr Arg Ser Gln
 1 5 10 15
 Ile Gly Pro Met Ala Arg His Val Glu Asp Leu Ala Leu Ala Leu Gln
 20 25 30
 Val Ile Ala Gly Glu Asp Gly Val Asp Ala Gly Val Ile Pro Met Pro
 35 40 45
 Leu Arg Arg Met Gln Thr Gln Thr Leu Lys Gly Leu Arg Val Ala Trp
 50 55 60
 Tyr Ser Asp Gly Gly Ile Glu Pro Val Asp Ala Leu Thr His Thr Thr
 65 70 75 80
 Leu Gln Ala Val Ala Asp Leu Leu Asp Ala Glu Gly Ala Leu Ile Arg
 85 90 95
 Pro Ala Phe Pro Ser Ala Leu Ser Asn Ala Arg Asp Ile Thr Glu Arg
 100 105 110
 Tyr Trp Ala Met Ser Gln Ser Ser Gly Ala Gln Ser Ile Gln Leu Phe
 115 120 125
 Ser Asp Trp Asp Gln Phe Arg Thr Ala Met Leu Gly Phe Met Ala Asp
 130 135 140
 Tyr Asp Ile Ile Leu Cys Pro Val Asp Ala Ala Pro Ala Thr Gln Leu

```

145          150          155          160
Gly Glu Thr Arg Pro Gly Leu Phe Ser Ser Pro Leu Pro Asn Gly Leu
          165          170          175
Ala Gly Trp Pro Cys Val Val Val Arg Ala Gly Thr Asp Ser Ala Gly
          180          185          190
Leu Pro Val Gly Val Gln Ile Val Ala Arg Pro Trp His Glu Pro Val
          195          200          205
Ala Leu Ala Ala Ala Ala Ile Glu Arg Ala Leu Pro Phe Thr Arg
          210          215          220

```

<210> 1427

<211> 270

<212> DNA

<213> Homo sapiens

<400> 1427

```

atggcttgct atctgaagca ggtggctgcc accgtctgca taaatgggccc cagcgcgctc
60
tttgatgttc cactaagata cggggatctg gtggtgacac ccatgcgact ggcttcggaa
120
ttgatgcaag tccatccctc aggggctgta cgcttcgcgc actgttcagt tccccagaat
180
aaactcaact cacaaaagat acttcgggtg gaaaaggccc aagggaagat cctcttcatt
240
gcaggagaga atgacgaaa gcttgctagc
270

```

<210> 1428

<211> 90

<212> PRT

<213> Homo sapiens

<400> 1428

```

Met Ala Cys Tyr Leu Lys Gln Val Ala Ala Thr Val Cys Ile Asn Gly
1          5          10          15
Pro Ser Ala Val Phe Asp Val Pro Leu Arg Tyr Gly Asp Leu Val Val
20          25          30
Thr Pro Met Arg Leu Ala Ser Glu Leu Met Gln Val His Pro Ser Gly
35          40          45
Ala Val Arg Phe Arg His Cys Ser Val Pro Gln Asn Lys Leu Asn Ser
50          55          60
Gln Lys Ile Leu Pro Val Glu Lys Ala Gln Gly Lys Ile Leu Phe Ile
65          70          75          80
Ala Gly Glu Asn Asp Glu Ser Leu Ala Ser
85          90

```

<210> 1429

<211> 384

<212> DNA

<213> Homo sapiens

<400> 1429

```

ncctagggga ttatcgacat aaacgcgact gcgtaagggtt ggtgactcat cccccagcga
60

```


catgaggcaa acgccatgac atccgagaat gcaccgccgc gaggcaagat catcatgatg
 120
 gcggtgatgc ccggcgcggt ggtaaccaac atttactgca cccagccggt gctgccgttg
 180
 atcgccctcg acatgggctg cgagtgctgc acggtaacc tgggtggcagg cgcggccttg
 240
 ctgggggttg ccaccgggtt ggcgttttta ttgccatgg gcgaccgctt tgaccggcgc
 300
 aagctggtac tcgggcagat tgcgctggcg ttctgctttg ccttgccggc ggccttttgcg
 360
 ccgaggatct gggcggtgat cggc
 384

<210> 1430

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1430

Met	Thr	Ser	Glu	Asn	Ala	Pro	Pro	Arg	Gly	Lys	Ile	Ile	Met	Met	Ala
1			5					10					15		
Val	Ile	Ala	Gly	Ala	Val	Val	Thr	Asn	Ile	Tyr	Cys	Thr	Gln	Pro	Val
		20					25					30			
Leu	Pro	Leu	Ile	Ala	Ser	Asp	Met	Gly	Val	Ala	Val	Ser	Thr	Val	Asn
		35				40					45				
Leu	Val	Ala	Gly	Ala	Ala	Leu	Leu	Gly	Phe	Ala	Thr	Gly	Leu	Ala	Phe
	50				55				60						
Leu	Leu	Pro	Met	Gly	Asp	Arg	Phe	Asp	Arg	Arg	Lys	Leu	Val	Leu	Gly
65				70				75					80		
Gln	Ile	Ala	Leu	Ala	Phe	Cys	Phe	Ala	Leu	Ala	Ala	Ala	Phe	Ala	Pro
			85					90					95		
Arg	Ile	Trp	Ala	Leu	Ile	Gly									
					100										

<210> 1431

<211> 414

<212> DNA

<213> Homo sapiens

<400> 1431

aagcttcagg gcagggtgcc cctgaagtca agcctgattc tgcatactct tgcatagcac
 60
 aaactggcga cacctgtgac ttgaccttc ccagggtccc tgcctctccg tccaggtagg
 120
 ctcagcctga gggagggtgc ggcaggagcc tcggaggcag gaggggctgg cgtgcttcac
 180
 tccttcagct tgtcttggga gagctgtggg ctgcatcccc ctggctcctc gtccacagg
 240
 cagccccgct gtgtgtctgg tcttcagagt tggctgcagc ttctgggccc tgcttcacag
 300
 cccctctccc atgacctccc agccttgga ggtgtaatat ttcccatgt tgctgatctt
 360
 tagtttgctt cctctcctt ggcgtgtctt tctgctgttc cactctctgt gcac
 414

<210> 1432
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 1432
 Met Gly Asn Tyr Tyr Thr Phe Gln Gly Trp Arg Ile Met Gly Arg Gly
 1 5 10 15
 Ala Gly Ser Arg Ala Gln Lys Leu Gln Pro Thr Cys Lys Thr Arg His
 20 25 30
 Thr Ala Gly Leu Pro Val Gly Arg Gly Ala Arg Gly Met Gln Pro Thr
 35 40 45
 Ala Leu Pro Arg Gln Ala Glu Gly Val Lys His Ala Ser Pro Ser Cys
 50 55 60
 Leu Arg Gly Ser Cys Gln His Leu Pro Gln Ala Glu Pro Thr Trp Ser
 65 70 75 80
 Gly Glu Gln Gly Pro Trp Glu Arg Gln Ser His Arg Cys Arg Gln Phe
 85 90 95
 Val Leu Tyr Lys Met Met Gln Asn Gln Ala
 100 105

<210> 1433
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 1433
 aaattttcga tgggaactggg cggcaatgca ccgtttattg tatttgatga tgcggatgtg
 60
 gacgcggccg tcagcaatgc tgtggcttgc aagtccgct gtggtggaca aacgtgcatt
 120
 tcggccaacc gaatctacgt gcacgaacaa gtgcacgacg agtttgtctc taagtttggc
 180
 gagagagtca agaagcttcg cgtgggctac ggtctggacg aaaacatcaa cattggaccg
 240
 ctagtgaatg aggctagtca ggacaaagca gagtcacatg tccgtgcgat gcaa
 294

<210> 1434
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 1434
 Lys Phe Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Asp
 1 5 10 15
 Asp Ala Asp Val Asp Ala Ala Val Ser Asn Ala Val Ala Cys Lys Phe
 20 25 30
 Arg Cys Gly Gly Gln Thr Cys Ile Ser Ala Asn Arg Ile Tyr Val His
 35 40 45
 Glu Gln Val His Asp Glu Phe Val Ser Lys Phe Gly Glu Arg Val Lys
 50 55 60
 Lys Leu Arg Val Gly Tyr Gly Leu Asp Glu Asn Ile Asn Ile Gly Pro

65		70		75		80
Leu	Val	Asn	Glu	Ala	Ser	Gln
		85		90		95
Met	Gln					

<210> 1435

<211> 1772

<212> DNA

<213> Homo sapiens

<400> 1435

```

ntttctggct tatgtggttt ccccggtgtgt gaggtgggat ccactccccg catagtctct
60
cgtggcgatg ggacacctgg aaagtgtgtg gatgtctttg aatgtgttaa tgatacaaa
120
ccagcctgcg tatttaacaa tgtggaatat tatgatggag acatgtttcg aatggacaac
180
tgtcggttct gtcgatgcca agggggcggt gccatctgct tcaactgccc gtgtgtgtgag
240
ataaactgcg agaggtaacta cgtgcccgaa ggagagtgtc gccactgtgt tgaaatccag
300
tgtatccttt taataatccc gctggctgtc gccaatggcc tgatccttgc ccacggagac
360
cgggtggcgg aagacgactg cacattctgc cagtgcgtca acggtgaacg ccactgcgtt
420
gcgaccgtct gcggacagac ctgcacaaac cctgtgaaag tgccctggga gtgttgccct
480
gtgtgcgaag aaccaacccat catcacagtt gatccacctg catgtgggga gttatcaaac
540
tgcactctga caggaagga ctgcattaat ggtttcaaac gcgatcacia tggttgtcgg
600
acctgtcagt gcataaacac cgaggaacta tgttcagaac gtaaacaaag ctgcaccttg
660
aactgtccct tcgggtttcct tactgatgcc caaaactgtg agatctgtga gtgccgccca
720
aggcccaaga agtgcagacc cataatctgt gacaagtatt gtccacttgg attgtctgaa
780
aataagcacg gctgtgacat ctgtcgctgt aagaaatgtc cagagctctc atgcagtaag
840
natctgcccc ttgggttttc agcaggacag tcacggctgt cttatctgca agtgcagaga
900
ggcctctgtc tcagctgggg caccatcctc gtccgggact tgtctcaccg tggatggtca
960
tcatcataaa aatgaggaga gctggcacga tgggtgccgg gaatgctact gtctcaatgg
1020
acgggaaaatg tgtgccctga tcacctgccc ggtgcctgcc tgtggcaacc ccaccattca
1080
ccctggacag tgctgcccac catgtgcaga tgacttttgt gtgcagaagc cagagctcag
1140
tactcennct ccatttgcca cgcctctgga ggagaatact ttgtggaag agaaacgtgg
1200
aacattgact cctgtactca gtgcacctgc cacagcggac ggggtgctgtg tgagacagag
1260

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gtgtgcccac cgctgctctg ccagaacccc tcacgcaccc aggattcctg ctgcccacag
 1320
 tgtacagatc aaccttttcg gccttccttg tcccgcaata acagcgtacc taattactgc
 1380
 aaaaatgatg aaggggatat attcctggca gctgagtcct ggaagcctga cgtttgtacc
 1440
 agctgcacat gcattgatag cgtaattagc tgtttctctg agtcctgccc ttctgtatcc
 1500
 tgtgaaaaac ctgtcttgag aaaaggccag tgttgtccct actgcataga agacacaatt
 1560
 ccaaagaagg tgggtgtcca cttagctggg aaggcctatg ccgacgagga gcggtgggac
 1620
 cttgacagct gcacccactg ctactgcctg cagggccaga ccttctgctc gaccgtcagc
 1680
 tgcccccttc tgccctgtgt tgagcccatc aacgtggaag gaagtgtctg cccaatgtgt
 1740
 ccagaaatgt atgtcccagt cccctcacgc gt
 1772

<210> 1436

<211> 322

<212> PRT

<213> Homo sapiens

<400> 1436

Xaa	Ser	Gly	Leu	Cys	Gly	Phe	Pro	Val	Cys	Glu	Val	Gly	Ser	Thr	Pro
1				5					10					15	
Arg	Ile	Val	Ser	Arg	Gly	Asp	Gly	Thr	Pro	Gly	Lys	Cys	Cys	Asp	Val
			20				25						30		
Phe	Glu	Cys	Val	Asn	Asp	Thr	Lys	Pro	Ala	Cys	Val	Phe	Asn	Asn	Val
		35					40					45			
Glu	Tyr	Tyr	Asp	Gly	Asp	Met	Phe	Arg	Met	Asp	Asn	Cys	Arg	Phe	Cys
		50			55					60					
Arg	Cys	Gln	Gly	Gly	Val	Ala	Ile	Cys	Phe	Thr	Ala	Gln	Cys	Gly	Glu
65					70				75					80	
Ile	Asn	Cys	Glu	Arg	Tyr	Tyr	Val	Pro	Glu	Gly	Glu	Cys	Cys	Pro	Val
			85					90					95		
Cys	Glu	Ile	Gln	Cys	Ile	Leu	Leu	Ile	Ile	Pro	Leu	Ala	Ala	Ala	Asn
			100					105					110		
Gly	Leu	Ile	Leu	Ala	His	Gly	Asp	Arg	Trp	Arg	Glu	Asp	Asp	Cys	Thr
			115				120				125				
Phe	Cys	Gln	Cys	Val	Asn	Gly	Glu	Arg	His	Cys	Val	Ala	Thr	Val	Cys
		130				135					140				
Gly	Gln	Thr	Cys	Thr	Asn	Pro	Val	Lys	Val	Pro	Gly	Glu	Cys	Cys	Pro
145					150					155				160	
Val	Cys	Glu	Glu	Pro	Thr	Ile	Ile	Thr	Val	Asp	Pro	Pro	Ala	Cys	Gly
			165					170					175		
Glu	Leu	Ser	Asn	Cys	Thr	Leu	Thr	Gly	Lys	Asp	Cys	Ile	Asn	Gly	Phe
		180						185					190		
Lys	Arg	Asp	His	Asn	Gly	Cys	Arg	Thr	Cys	Gln	Cys	Ile	Asn	Thr	Glu
		195				200						205			
Glu	Leu	Cys	Ser	Glu	Arg	Lys	Gln	Gly	Cys	Thr	Leu	Asn	Cys	Pro	Phe
		210				215					220				
Gly	Phe	Leu	Thr	Asp	Ala	Gln	Asn	Cys	Glu	Ile	Cys	Glu	Cys	Arg	Pro

```

225          230          235          240
Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys Asp Lys Tyr Cys Pro Leu
          245          250          255
Gly Leu Leu Lys Asn Lys His Gly Cys Asp Ile Cys Arg Cys Lys Lys
          260          265          270
Cys Pro Glu Leu Ser Cys Ser Lys Xaa Leu Pro Leu Gly Phe Pro Ala
          275          280          285
Gly Gln Ser Arg Leu Ser Tyr Leu Gln Val Gln Arg Gly Leu Cys Phe
          290          295          300
Ser Trp Ala Thr His Pro Val Gly His Leu Ser His Arg Gly Trp Ser
305          310          315          320
Ser Ser

```

<210> 1437

<211> 372

<212> DNA

<213> Homo sapiens

<400> 1437

```

cggggaactgt gctcgccac catccggtga cgggtgtcgg gcagtggcaa ctcaacaccc
60
aggccatgac cggagccatc ccgagcagca ggtgcacggc ccgggccggt gactcgtgga
120
cccgtaccct catgacctcg atgcaacttc cagggtggtc caccgatcac atcgaccgct
180
cgggtccatgt cgatgctgag cagttcgacc ggttgcgcag cgagtctctg tcccgtagggc
240
acagttctgg ccctgccgca catgggggtcc tgggacttgg ccggggcctg ggtggccaga
300
cgcggttctt ccccgagttc cgtcgcggag aatcttccga gggcacagtt cgagttgttc
360
tgccgcacgc gt
372

```

<210> 1438

<211> 62

<212> PRT

<213> Homo sapiens

<400> 1438

```

Met Ser Met Leu Ser Ser Ser Thr Gly Cys Ala Ala Ser Ser Cys Pro
1          5          10          15
Val Gly Thr Val Leu Ala Leu Pro His Met Gly Ser Trp Asp Leu Ala
          20          25          30
Gly Ala Trp Val Ala Arg Arg Gly Phe Ser Pro Ser Ser Val Ala Glu
          35          40          45
Asn Leu Pro Arg Ala Gln Phe Glu Leu Phe Cys Arg Thr Arg
          50          55          60

```

<210> 1439

<211> 471

<212> DNA

<213> Homo sapiens

<400> 1439
 accggtttgc tttccacaag gagagctaaa atgccggttg ctaagcagca tacatgccgc
 60
 tgctttcttc cacaatgtag acttaaaaaa atcccggtaa acattttacc atatgattga
 120
 gtcagggtgtg gggagtcgca gtaaacattt taccatgtga ttgagtcagt ggtggggagt
 180
 cgcgaaata cacagggcag gcagttcgct atcacgatgt tctctctcat ttctgtcttt
 240
 ggtctgtctt cctgggtaat gtcacatgga gaccagggg atctgccatc agctgtgtgc
 300
 agtggggtta caagacgacg gggaaacttca gagtcaggc agtcctcatc tttggcagat
 360
 tctgtatttg cacattcacc cactcactga aatgcatttg taaccccaaa atcaatacag
 420
 cgggtttcaca gtcattttcc gacacgggca gaggggtgaa gatactgagt c
 471

<210> 1440
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 1440
 Met Gly Gly Glu Ser Arg Lys Tyr Thr Gly Gln Ala Val Arg Tyr His
 1 5 10 15
 Asp Val Leu Ser His Phe Cys Leu Trp Ser Val Phe Leu Gly Asn Val
 20 25 30
 Thr Trp Arg Pro Arg Gly Ser Ala Ile Ser Cys Val Gln Trp Val Asn
 35 40 45
 Lys Thr Thr Gly Asn Phe Arg Val Gln Ala Val Leu Ile Phe Gly Arg
 50 55 60
 Phe Cys Ile Cys Thr Phe Thr His Ser Leu Lys Cys Ile Cys Asn Pro
 65 70 75 80
 Lys Ile Asn Thr Ala Val Ser Gln Ser Phe Ser Asp Thr Gly Arg Gly
 85 90 95
 Val Lys Ile Leu Ser
 100

<210> 1441
 <211> 376
 <212> DNA
 <213> Homo sapiens

<400> 1441
 nnngagtgc ggggaccttc atggactctc tcgtgctccg tagetccacac tcaccgcacg
 60
 gcagctcaca ttcaccacac gggaaactcac tctcaccaca cggcagctca ctctctctgc
 120
 accgcagctc acactcaccg caggcagct cactctcacc gcacggcagc tcacactcac
 180
 cacacagcag ctactctta ccggacgggg aacctaaact taccggacgg gaagcctcac
 240

tctcaccgca cggaaagctc acactcaccg caccgcagcc actctcaccg cagcgagct
 300
 cactctcacc gcaccgcagc tcactctcac cggacgggag ctactctca ccacacggca
 360
 cctcactctc acgctg
 376

<210> 1442

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1442

Xaa	Glu	Ser	Arg	Gly	Pro	Ser	Trp	Thr	Leu	Ser	Cys	Ser	Val	Ala	His
1				5				10					15		
Thr	His	Arg	Thr	Ala	Ala	His	Ile	His	His	Thr	Gly	Thr	His	Ser	His
			20				25						30		
His	Thr	Ala	Ala	His	Ser	Leu	Cys	Thr	Ala	Ala	His	Thr	His	Arg	Thr
			35				40					45			
Ala	Ala	His	Ser	His	Arg	Thr	Ala	Ala	His	Thr	His	His	Thr	Ala	Ala
		50				55				60					
His	Ser	Tyr	Arg	Thr	Gly	Asn	Leu	Asn	Leu	Pro	Asp	Gly	Lys	Pro	His
				70						75				80	
Ser	His	Arg	Thr	Glu	Ser	Ser	His	Ser	Pro	His	Arg	Ser	His	Ser	His
				85					90					95	
Arg	Thr	Ala	Ala	His	Ser	His	Arg	Thr	Ala	Ala	His	Ser	His	Arg	Thr
			100					105						110	
Gly	Ala	His	Ser	His	His	Thr	Ala	Pro	His	Ser	His	Ala			
			115				120						125		

<210> 1443

<211> 286

<212> DNA

<213> Homo sapiens

<400> 1443

atggcagccc tgcgtcccaa ggagctgccca caactaatgg tcgccatcgg caatgcgagc
 60
 ataaaaacgga caacacgctg cctgatcgaa tggcaactcc acaccatgac cgtcctcgcg
 120
 gaagccgcta cgacttcctg ggctgacatc gactgcgaca agaaaacctg gacgatccca
 180
 gcggagcgta tgaaaaagcg acgtgcccac gtcataccgc taaccgagca cgcacttgcc
 240
 ttgcttgaga caatcaaacc ctacagcggg cagagagagt acgctg
 286

<210> 1444

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1444

Met Ala Ala Leu Arg Pro Lys Glu Leu Pro Gln Leu Met Val Ala Ile

```

      1           5           10           15
Gly Asn Ala Ser Ile Lys Arg Thr Thr Arg Cys Leu Ile Glu Trp Gln
      20           25           30
Leu His Thr Met Thr Arg Pro Ala Glu Ala Ala Thr Thr Ser Trp Ala
      35           40           45
Asp Ile Asp Cys Asp Lys Lys Thr Trp Thr Ile Pro Ala Glu Arg Met
      50           55           60
Lys Lys Arg Arg Ala His Val Ile Pro Leu Thr Glu His Ala Leu Ala
      65           70           75           80
Leu Leu Glu Thr Ile Lys Pro Tyr Ser Gly His Arg Glu Tyr Ala
      85           90           95

```

<210> 1445

<211> 294

<212> DNA

<213> Homo sapiens

<400> 1445

```

naccggttca cgggggaggc cttcgatggg ggcaaggtca gcatggttgg ccgattcccc
60
atgtacctgt atggcacctt cgctcgttccg gacttcgacg cattcatctc cggaagcag
120
actccctacc gggagacggt ctccaagcgg accactactt ggtttcttcc agccggctca
180
gaggtttatg agctggccnt cccccgagga gtcgtgttcc ccatgcaaag cgctcgttg
240
agggtggacc ccgacaacac cgctcgacaag ctgccaacac tcggcgagcg cctg
294

```

<210> 1446

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1446

```

Xaa Arg Phe Thr Gly Glu Ala Phe Asp Gly Gly Lys Val Ser Met Val
      1           5           10           15
Gly Pro Ile Pro Met Tyr Leu Tyr Gly Thr Phe Val Val Pro Asp Phe
      20           25           30
Asp Ala Phe Ile Ser Gly Lys Gln Thr Pro Tyr Arg Glu Thr Val Ser
      35           40           45
Lys Arg Thr Thr Thr Trp Phe Phe Arg Ala Gly Ser Glu Val Tyr Glu
      50           55           60
Leu Ala Xaa Pro Arg Gly Val Val Phe Ala Met Gln Ser Ala Ser Leu
      65           70           75           80
Arg Val Asp Pro Asp Asn Thr Val Asp Lys Leu Pro Thr Leu Gly Glu
      85           90           95
Arg Leu

```

<210> 1447

<211> 363

<212> DNA

<213> Homo sapiens

<400> 1447

nnncagaacc agaagatcaa cctgcatgac ggctcgttct ccgacgttgg cggcatggtg
 60
 ggtaatatct ccattgccca ggggtgtcacg atcgagaacg ccgtcggcgg ttcgggcaac
 120
 gacctgctga tcggcaacga tgcggccaac gaactgcgcg cgggtgccgg caacgatatc
 180
 ctctacgggg ctggcgggtgc cgaccagggt tgggttggtt cgggcaacaa taccttcgtg
 240
 ttcgcccggc tttccgactc ggcggccgaaa cgggccgacc ggatcatgga cttcaccagt
 300
 ggccaggaca agatcgatct gtccgggata acccatggtt cgggcctgac cttcgtcaac
 360
 gcg
 363

<210> 1448

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1448

Xaa	Gln	Asn	Gln	Lys	Ile	Asn	Leu	His	Asp	Gly	Ser	Phe	Ser	Asp	Val
1				5					10					15	
Gly	Gly	Met	Val	Gly	Asn	Ile	Ser	Ile	Ala	Gln	Gly	Val	Thr	Ile	Glu
			20					25					30		
Asn	Ala	Val	Gly	Gly	Ser	Gly	Asn	Asp	Leu	Leu	Ile	Gly	Asn	Asp	Ala
		35					40				45				
Ala	Asn	Glu	Leu	Arg	Gly	Gly	Ala	Gly	Asn	Asp	Ile	Leu	Tyr	Gly	Ala
	50				55						60				
Gly	Gly	Ala	Asp	Gln	Val	Trp	Val	Gly	Ser	Gly	Asn	Asn	Thr	Phe	Val
65				70					75				80		
Phe	Ala	Ala	Val	Ser	Asp	Ser	Ala	Pro	Lys	Ala	Ala	Asp	Arg	Ile	Met
			85						90				95		
Asp	Phe	Thr	Ser	Gly	Gln	Asp	Lys	Ile	Asp	Leu	Ser	Gly	Ile	Thr	His
			100				105						110		
Gly	Ser	Gly	Leu	Thr	Phe	Val	Asn	Ala							
			115				120								

<210> 1449

<211> 541

<212> DNA

<213> Homo sapiens

<400> 1449

aggcgctacc agattatggg ctgcccgacc tcaatgacat gcgcttgagc ctgcatgaat
 60
 cactcagcca atcgcgcttg gcgattgaac gctttatcca ggcgtacgag cctcggttgg
 120
 ggaatgtacg tgtcaggagg agggagggtg cctacaaccc ttgtgactg gcgtttgtga
 180
 ttgaggcaac cgctgctcgc gatggtgtca tccaacctgt ggtgtttaac gcacacctgg
 240

tggggggggg gacgggtcga gtgtgttacc tgatgttctt tgagctcttt taccagagtg
 300
 aactcagtgc attgcgcacg cttggggcggc gtttttctga acgcaatccc gccttggcag
 360
 cctttcttgc cgattccagg ccaggaccgg gacgtcgagg gtctattgaa agtctttgcc
 420
 ttttccccg ggcgcctgcg ccagaagctt gctgacgagc ttctgaggtt gacccattca
 480
 ttgatgcact tgggtgtggcc caattacatg cggccattgc cggccttcag tattttgcag
 540
 t
 541

<210> 1450

<211> 138

<212> PRT

<213> Homo sapiens

<400> 1450

Met	Arg	Leu	Ser	Leu	His	Glu	Ser	Leu	Ser	Gln	Ser	Arg	Leu	Ala	Ile
1			5					10					15		
Glu	Arg	Phe	Ile	Gln	Ala	Tyr	Glu	Pro	Arg	Leu	Gly	Asn	Val	Arg	Val
		20						25				30			
Arg	Arg	Arg	Glu	Gly	Ala	Tyr	Asn	Pro	Leu	Val	Leu	Ala	Phe	Val	Ile
		35					40				45				
Glu	Ala	Thr	Val	Val	Ile	Asp	Gly	Val	Ile	Gln	Pro	Val	Val	Phe	Asn
		50				55				60					
Ala	His	Leu	Val	Gly	Gly	Gly	Thr	Gly	Arg	Val	Cys	Tyr	Leu	Met	Phe
65				70					75				80		
Phe	Glu	Leu	Phe	Tyr	Gln	Ser	Glu	Leu	Ser	Ala	Leu	Arg	Thr	Leu	Gly
		85						90				95			
Arg	Arg	Phe	Ser	Glu	Arg	Asn	Pro	Ala	Leu	Ala	Pro	Phe	Leu	Ala	Asp
		100					105					110			
Ser	Arg	Pro	Gly	Pro	Gly	Arg	Arg	Gly	Ser	Ile	Glu	Ser	Leu	Cys	Leu
		115				120					125				
Ser	Pro	Arg	Ala	Pro	Ala	Pro	Glu	Ala	Cys						
		130				135									

<210> 1451

<211> 326

<212> DNA

<213> Homo sapiens

<400> 1451

aggcctctgg cgagttgatc tacagcttcg gacccgggtg tatggctact ggcgtcaagt
 60
 acacgaacac agtttgact cctgtgggag actacgaggt ggtgctgacg gattcttggg
 120
 gtgatggctg gaacccgggt tcttacctga acatgtacga cagctcggac aacttgatcc
 180
 aggagttcac gatggattac gacgcctctt ctcgtaacat taaggagaag cacggcttct
 240
 tcacgggtgc ttccaccacg agcagcggca ctgtctggaa gattatggcg aacaagaagg
 300

tggacaagga gtggaactct gtggac
326

<210> 1452

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1452

```
Met Ala Thr Gly Val Lys Tyr Thr Asn Thr Val Cys Thr Pro Val Gly
  1                               10                   15
Asp Tyr Glu Val Val Leu Thr Asp Ser Trp Gly Asp Gly Trp Asn Pro
      20                   25                   30
Gly Ser Tyr Leu Asn Met Tyr Asp Ser Ser Asp Asn Leu Ile Gln Glu
      35                   40                   45
Phe Thr Met Asp Tyr Asp Ala Ser Ser Arg Asn Ile Lys Glu Lys His
      50                   55                   60
Gly Phe Phe Thr Val Ala Ser Thr Thr Ser Ser Gly Thr Val Trp Lys
      65                   70                   75                   80
Ile Met Ala Asn Lys Lys Val Asp Lys Glu Trp Asn Ser Val Asp
      85                   90                   95
```

<210> 1453

<211> 326

<212> DNA

<213> Homo sapiens

<400> 1453

```
cgggcgcgcg gccccacgtg caccgcgtgc atggtccctc gaggacgcgc atctgcagcc
  60
cccgctcccc gcaaacctcc aggcgggaga gctccggcca aggccgctgc atcacatgat
 120
acaggaggggg catgcacacg ctcacgtgca cacagcctca aacacgctca tccgtacata
 180
caggagtgtg tgaacgcact gaggtgcaca ggacaaagac acagacacct gtttgcacac
 240
cgactcgcct atagaaatgt gcaaacacc cgtgcgcaca ggccctccca cccatgcagg
 300
cgtgtgcaca tcacccacac ggacac
 326
```

<210> 1454

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1454

```
Met Val Pro Arg Gly Arg Ala Ser Ala Ala Pro Ala Pro Arg Lys Pro
  1                               10                   15
Pro Gly Arg Arg Ala Pro Ala Lys Ala Ala Ala Ser His Asp Thr Gly
      20                   25                   30
Gly Ala Cys Thr Arg Ser Arg Ala His Ser Leu Lys His Ala His Pro
      35                   40                   45
Tyr Ile Gln Glu Cys Val Asn Ala Leu Arg Cys Thr Gly Gln Arg His
```

```

      50              55              60
Arg His Leu Phe Ala His Arg Leu Ala Tyr Arg Asn Val Gln Thr Thr
65              70              75              80
Arg Ala His Arg Pro Leu His Pro Cys Arg Arg Val His Ile Thr His
      85              90              95
Thr Asp

```

<210> 1455
 <211> 314
 <212> DNA
 <213> Homo sapiens

```

<400> 1455
gatccagtca aaaaagcatg tgggggttgct cacgctgggt ggaaaggtag tttgttgggt
60
gttgctatgg ctacagttaa tgctatgata gcagaatatg gctgccgttt ggaataactt
120
tgggtggacct tggacccttc agtggggacct ggctgtttta ctcttcagg ggaatcagca
180
gaggcatttc ataattctca tctgcatgt gtacaactat ttgattcacc aaatccctgt
240
atcgacatcc gtaaagccac aagatacttg actggatttt tgtataactg cttcctgcct
300
ccttccaaac tgac
314

```

<210> 1456
 <211> 104
 <212> PRT
 <213> Homo sapiens

```

<400> 1456
Asp Pro Val Lys Lys Ala Cys Gly Val Ala His Ala Gly Trp Lys Gly
1      5      10      15
Thr Leu Leu Gly Val Ala Met Ala Thr Val Asn Ala Met Ile Ala Glu
      20      25      30
Tyr Gly Cys Arg Leu Glu Lys Leu Trp Trp Thr Leu Asp Pro Ser Val
      35      40      45
Gly Pro Gly Cys Phe Thr Leu Pro Gly Glu Ser Ala Glu Ala Phe His
      50      55      60
Asn Leu His Pro Ala Cys Val Gln Leu Phe Asp Ser Pro Asn Pro Cys
      65      70      75      80
Ile Asp Ile Arg Lys Ala Thr Arg Tyr Leu Thr Gly Phe Leu Tyr Asn
      85      90      95
Cys Phe Leu Pro Pro Ser Lys Leu
      100

```

<210> 1457
 <211> 437
 <212> DNA
 <213> Homo sapiens

<400> 1457

nattcaccag aatccccaga atccccaaa tactacattg cactttaggg ttcctttcta
 60
 gcacatgcat tgctaaaatc ggcgcccaga accttctctg cccctctccc atgggatgca
 120
 atgtcagcgg agaacacagac caagtctgca ctagectgtc cctacacct cccaggaaa
 180
 aggtccccct gcgccaagtc aacagctccc agaggaagcc cactgactgc tctcttcagg
 240
 gtgggggaca caggaagtcc acgcttgca cggaggggacg ggcacaccta cgtgactgc
 300
 cagagcccat ttgaggagtc tgattggaat ttatacagca ggagcactgg gcaactcggc
 360
 aactccagcc cacaaccaag tcactgggct gcctaccac tgcccaagt cctcaagtca
 420
 acacattcct gcactgn
 437

<210> 1458

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1458

Met	Ser	Ala	Glu	Lys	Gln	Thr	Lys	Ser	Ala	Leu	Ala	Cys	Pro	Tyr	Thr
1				5					10					15	
Leu	Pro	Arg	Lys	Arg	Ser	Pro	Cys	Ala	Lys	Ser	Thr	Ala	Pro	Arg	Gly
		20						25					30		
Ser	Pro	Leu	Thr	Ala	Leu	Phe	Arg	Val	Gly	Asp	Thr	Gly	Ser	Pro	Arg
		35					40					45			
Leu	His	Gly	Gly	Asp	Gly	His	Thr	Tyr	Arg	Asp	Cys	Gln	Ser	Pro	Phe
		50				55				60					
Trp	Glu	Ser	Asp	Trp	Asn	Leu	Tyr	Ser	Arg	Ser	Thr	Gly	His	Ser	Asp
		65			70				75					80	
Asn	Ser	Ser	Pro	Gln	Pro	Ser	His	Trp	Ala	Ala	Tyr	Pro	Leu	Pro	Lys
			85					90						95	
Cys	Leu	Lys	Ser	Thr	His	Ser	Cys	Thr							
		100						105							

<210> 1459

<211> 295

<212> DNA

<213> Homo sapiens

<400> 1459

ngagaggtea cgggccacga gattcccgcg gaggtcgcgc cccgccgcgc gggcgaccgc
 60
 gccgtactca tcgcttcttc ggagaagatc aagcggggagc tgggctggaa cccgacgcgc
 120
 acggatctgc gccgcacgt cgaggacgcc tgggccttta cggctggggg ggcgaacgcg
 180
 taaacccttg gtaaggcgac gcagttatcc tcgatctcct cccagagcag gcggcagccc
 240
 gccactgcgc tgctcagcat gccctccac tccccgatcg ccatgagctg gcgan
 295

<210> 1460

<211> 60

<212> PRT

<213> Homo sapiens

<400> 1460

```

Xaa Glu Val Thr Gly His Glu Ile Pro Ala Glu Val Ala Pro Arg Arg
 1           5           10          15
Ala Gly Asp Pro Ala Val Leu Ile Ala Ser Ser Glu Lys Ile Lys Arg
          20           25          30
Glu Leu Gly Trp Asn Pro Thr Arg Thr Asp Leu Arg Arg Ile Val Glu
          35           40          45
Asp Ala Trp Ala Phe Thr Ala Gly Gly Ala Glu Arg
          50           55          60

```

<210> 1461

<211> 432

<212> DNA

<213> Homo sapiens

<400> 1461

```

nnaagcttac gtgaaatgaa acgtcaatgg caacaggcga caatcgtgcc agagaaattg
60
gttgaagcac agtcaattgc ggggttctaaa tgcgaacacg cctggcgctt acaacgttca
120
gaaaatgact gggtaggcct tgaaaaaaat tggaaaagagg ttgttgcatc atccccgtgaa
180
gaagcacaaa ttcgcgggtga agcgcttaat ctaacgcctt atgatgcgat gcttgataag
240
tttgaaccag gcacgacaac ggtttcgctc aatactttgt tttcaaaggc aaagacgtgg
300
ttacctacgt taattgaaaa agcgcttagaa aagcagcaat cagaatctat cattatgcca
360
tcaggcacct tttccacggc gaatcaaaaa gcccttgatg tagaaataat gaaattgtta
420
aaattcgact tt
432

```

<210> 1462

<211> 144

<212> PRT

<213> Homo sapiens

<400> 1462

```

Xaa Ser Leu Arg Glu Met Lys Arg Gln Trp Gln Gln Ala Thr Ile Val
 1           5           10          15
Pro Glu Lys Leu Val Glu Ala Gln Ser Ile Ala Gly Ser Lys Cys Glu
          20           25          30
His Ala Trp Arg Leu Gln Arg Ser Glu Asn Asp Trp Val Gly Phe Glu
          35           40          45
Lys Asn Trp Lys Glu Val Val Ala Leu Ser Arg Glu Glu Ala Gln Ile
          50           55          60
Arg Gly Glu Ala Leu Asn Leu Thr Pro Tyr Asp Ala Met Leu Asp Lys

```

```

65          70          75          80
Phe Glu Pro Gly Thr Thr Val Ser Leu Asn Thr Leu Phe Ser Lys
      85          90          95
Val Lys Thr Trp Leu Pro Thr Leu Ile Glu Lys Ala Leu Glu Lys Gln
      100        105        110
Gln Ser Glu Ser Ile Ile Met Pro Ser Gly Thr Phe Ser Thr Ala Asn
      115        120        125
Gln Lys Ala Leu Gly Leu Glu Ile Met Lys Leu Leu Lys Phe Asp Phe
      130        135        140

```

<210> 1463
 <211> 421
 <212> DNA
 <213> Homo sapiens

```

<400> 1463
nacgcgttcc agagcaagct ggacctgacc gccttcgaat tcttctccga caaggccctg
60
gccaaagtca tgggccgtgg cgacgtaccg gcaccgttcg aaaccgaatg cccgttctac
120
gcgctgctgg aattcgaagc caccaccgaa gaagtcgcca accacgccct ggaaccttc
180
gagcactcgc ttgagcaggg ctgggtgctg gacggcgtga tgagccagag cgaaacccaa
240
ctgcacaacc tgtggaaact gcgcgagtag atctcggaga ctatttccca ctggagcggc
300
tacaagaacg acatctccgt gaccgtttcc aaagtcctcc cgttcttgaa ggaattgac
360
gcgatcgtcg tgagcattac ccggacttcg aaattgttgg tcggccacat cggcgacgca
420
a
421

```

<210> 1464
 <211> 140
 <212> PRT
 <213> Homo sapiens

```

<400> 1464
Xaa Ala Phe Gln Ser Lys Leu Asp Leu Thr Ala Phe Glu Phe Phe Ser
1      5      10      15
Asp Lys Ala Leu Ala Lys Val Met Gly Arg Gly Asp Val Pro Ala Pro
20     25     30
Phe Glu Thr Glu Cys Pro Phe Tyr Ala Leu Leu Glu Phe Glu Ala Thr
35     40     45
Thr Glu Glu Val Ala Asn His Ala Leu Glu Thr Phe Glu His Cys Val
50     55     60
Glu Gln Gly Trp Val Leu Asp Gly Val Met Ser Gln Ser Glu Thr Gln
65     70     75     80
Leu His Asn Leu Trp Lys Leu Arg Glu Tyr Ile Ser Glu Thr Ile Ser
85     90     95
His Trp Thr Pro Tyr Lys Asn Asp Ile Ser Val Thr Val Ser Lys Val
100    105    110
Pro Ala Phe Leu Lys Glu Ile Asp Ala Ile Val Val Ser Ile Thr Arg

```

	115		120		125						
Thr	Ser	Lys	Leu	Leu	Val	Gly	His	Ile	Gly	Asp	Ala
	130			135						140	

<210> 1465

<211> 424

<212> DNA

<213> Homo sapiens

<400> 1465

gtgcacggtc tttgagctgc aattcccagg aatcaggggc cataggcggg agatggcatg
 60
 cagcctctcg ggcggaag tggtctacag tgcctgcttg cccgggcagg cagctcgtag
 120
 gcttatatgc ttagtggtta tggccctac cactgttttt gaccgcgcta ccattcgcca
 180
 caacctcacc gaattcaaac tccggtgat ttcccacgcc gagcagtga agcgga
 240
 ccgtcctgca acagagtcta aagccgctga gacggactgc tcagtacatg gggatctctg
 300
 gaccttggcc acggaagttt tcggtcaagc acccgaattc gacttcccat atatgaaat
 360
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 420
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<210> 1466

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1466

Met	Ala	Cys	Ser	Leu	Ser	Gly	Gly	Lys	Val	Val	Tyr	Ser	Ala	Cys	Leu
1				5					10					15	
Pro	Gly	Gln	Ala	Ala	Arg	Arg	Leu	Ile	Cys	Leu	Val	Val	Met	Ala	Pro
			20				25						30		
Thr	Thr	Val	Phe	Asp	Arg	Ala	Thr	Ile	Arg	His	Asn	Leu	Thr	Glu	Phe
		35					40					45			
Lys	Leu	Arg	Trp	Ile	Ser	His	Ala	Glu	Gln	Trp	Lys	Ala	Glu	Asn	Arg
		50				55				60					
Pro	Ala	Thr	Glu	Ser	Lys	Ala	Ala	Glu	Thr	Asp	Cys	Ser	Val	His	Gly
65					70				75					80	
Asp	Leu	Trp	Thr	Leu	Ala	Thr	Glu	Val	Phe	Gly	Gln	Ala	Pro	Glu	Phe
			85					90					95		
Asp	Phe	Pro	Tyr	Met	Lys	Leu	Thr	Arg	Gln	Glu	Cys	Arg	Phe	Leu	Phe
			100				105						110		
Leu	Pro	Arg	Asn	Asp	Ile	Ser	Leu	Ser	Cys	Phe	Thr				
			115				120								

<210> 1467

<211> 441

<212> DNA

<213> Homo sapiens

<400> 1467

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 gtgccgtgca tcatggctca agtgccgcgc aactttcggc tgctcgagga gctggagaaa
 120
 ggcgaaaagg ggctaggaaa tggctcgtgc tcttacggcc ttgcgaacag tgatgacatt
 180
 cgtacgtatg cgcctgtgct gatggctcatg acaacgtgga atggccacgat cctaggcccc
 240
 gccaaactcg tgcatgagaa ccgcataatac tgccctgcgc tcgtgtgtgg cgactcgtac
 300
 cctcttgtgc cgcctgagat ttggttccag acgcgcacatc acttgccgtg cgtcgatggc
 360
 cacacggggc gcgtcatgcc cgatcagttc tcgccccctct tgcattggcg tgatgagtac
 420
 actatggaaa gctgctgcat g
 441

<210> 1468

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1468

Met	Ala	Gln	Val	Pro	Arg	Asn	Phe	Arg	Leu	Leu	Glu	Glu	Leu	Glu	Lys
1				5					10				15		
Gly	Glu	Lys	Gly	Leu	Gly	Asn	Gly	Ser	Cys	Ser	Tyr	Gly	Leu	Ala	Asn
			20					25					30		
Ser	Asp	Asp	Ile	Arg	Thr	Tyr	Ala	Pro	Val	Leu	Met	Val	Met	Thr	Thr
			35					40				45			
Trp	Asn	Ala	Thr	Ile	Leu	Gly	Pro	Ala	Asn	Ser	Val	His	Glu	Asn	Arg
			50			55					60				
Ile	Tyr	Cys	Leu	Arg	Leu	Val	Cys	Gly	Asp	Ser	Tyr	Pro	Leu	Val	Pro
					70					75				80	
Pro	Glu	Ile	Trp	Phe	Gln	Thr	Arg	Ile	Asn	Leu	Pro	Cys	Val	Asp	Ala
				85					90					95	
His	Thr	Gly	Arg	Val	Met	Pro	Asp	Gln	Phe	Ser	Pro	Leu	Leu	His	Trp
			100					105					110		
Arg	Asp	Glu	Tyr	Thr	Met	Glu	Ser	Cys	Cys	Met					
				115				120							

<210> 1469

<211> 468

<212> DNA

<213> Homo sapiens

<400> 1469

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 60
 gcgcttcaac atcttttagc gatttttagt ccaattgtca ccnctggatt attgatttgc
 120
 ttggcattag gcgtgtctcg cgaagacacc aatatgattc tttctatgac attaatatt
 180

tcagggatcg cgactttctt gcaatgtaaa aaagttggtc catttggcgc tggattactt
 240
 attgttcaag gaactagctt taatttcatt ggtcctatca ttggtatagg tagctcaatg
 300
 gtggctgctg gcacacctgt cgaacaagtt atggctgcga tttttggtgt cgtaaatcgca
 360
 gggttcattta tcgaaatggg cgtatctcaa attttacctt gggtaaaaaa gctgattact
 420
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 468

<210> 1470

<211> 156

<212> PRT

<213> Homo sapiens

<400> 1470

Xaa	Leu	Asp	Leu	Val	Tyr	Gly	Leu	Asn	Asp	Arg	Pro	Asn	Pro	Phe	Ile
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Ala	Phe	Leu	Ala	Ala	Leu	Gln	His	Leu	Leu	Ala	Ile	Leu	Val	Pro	Ile
		20					25					30			
Val	Thr	Xaa	Gly	Leu	Leu	Ile	Cys	Leu	Ala	Leu	Gly	Val	Ser	Arg	Glu
	35					40					45				
Asp	Thr	Asn	Met	Ile	Leu	Ser	Met	Ser	Leu	Ile	Ile	Ser	Gly	Ile	Ala
	50				55					60					
Thr	Phe	Leu	Gln	Cys	Lys	Lys	Val	Gly	Pro	Phe	Gly	Ala	Gly	Leu	Leu
65					70				75					80	
Ile	Val	Gln	Gly	Thr	Ser	Phe	Asn	Phe	Ile	Gly	Pro	Ile	Ile	Gly	Ile
			85					90					95		
Gly	Ser	Ser	Met	Val	Ala	Ala	Gly	Thr	Pro	Val	Glu	Gln	Val	Met	Ala
			100					105					110		
Ala	Ile	Phe	Gly	Val	Val	Ile	Ala	Gly	Ser	Phe	Ile	Glu	Met	Gly	Val
			115				120					125			
Ser	Gln	Ile	Leu	Pro	Trp	Val	Lys	Lys	Leu	Ile	Thr	Pro	Leu	Val	Thr
	130					135					140				
Gly	Ile	Val	Val	Leu	Leu	Ile	Gly	Leu	Pro	Leu	Met				
145					150					155					

<210> 1471

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1471

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 gttatcgatc agccgctgac gattttgcac accaatctgg cggtgtatat cggcattgtg
 120
 tacgcttata tgccgcttat ggtactgccc atttatacgg cgctgacgcg cattgattac
 180
 tcgctggtgg aggcctcact ggatctcggt gcccgctccg tgaaaacggt tttcaatgtg
 240
 attgtccgcg tcaccaaagg cggcattatc gcggggctga tgctgggtgtt tatcccggcg
 300

gtcgggtgagt ttgttatccc ggaactgctc ggcgggcggcc g
341

<210> 1472

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1472

Ala	Trp	Met	Gly	Ile	Leu	Lys	Asn	Asn	Gly	Val	Leu	Asn	Asn	Phe	Leu
1			5						10					15	
Leu	Trp	Leu	Gly	Val	Ile	Asp	Gln	Pro	Leu	Thr	Ile	Leu	His	Thr	Asn
			20				25					30			
Leu	Ala	Val	Tyr	Ile	Gly	Ile	Val	Tyr	Ala	Tyr	Leu	Pro	Phe	Met	Val
	35						40				45				
Leu	Pro	Ile	Tyr	Thr	Ala	Leu	Thr	Arg	Ile	Asp	Tyr	Ser	Leu	Val	Glu
	50				55				60						
Ala	Ser	Leu	Asp	Leu	Gly	Ala	Arg	Pro	Leu	Lys	Thr	Phe	Phe	Asn	Val
65					70				75					80	
Ile	Val	Pro	Leu	Thr	Lys	Gly	Gly	Ile	Ile	Ala	Gly	Ser	Met	Leu	Val
			85					90					95		
Phe	Ile	Pro	Ala	Val	Gly	Glu	Phe	Val	Ile	Pro	Glu	Leu	Leu	Gly	Gly
			100					105					110		

Gly

<210> 1473

<211> 352

<212> DNA

<213> Homo sapiens

<400> 1473

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60
gaaactgacg gaaatgttca aactccagtt tgttggttaag cagatcacta aacttaaaaat
120
gcttggtattc tgcaggaaca ttatcccaat attctgttcg tttagagacg ttagagagtg
180
ataaaatgcc agttccaatt tcacaagtgg tgccttcagc tttcttggaa aatgtctctt
240
tatgcaaagc ctgtagcttt ctgaagtatg tggagtctaa ctgtcgagtt tcttccacca
300
gtccacacct tttataagca atttggtccg attttaccat ctttgtccat gg
352

<210> 1474

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1474

Met	Val	Lys	Ser	Asp	Gln	Ile	Ala	Tyr	Lys	Lys	Val	Glu	Leu	Val	Glu
1					5				10					15	
Glu	Thr	Arg	Gln	Leu	Asp	Ser	Thr	Tyr	Phe	Arg	Lys	Leu	Gln	Ala	Leu


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145                               150                               155                               160
Asp Trp Asn Gly Lys Arg
                               165

<210> 1479
<211> 421
<212> DNA
<213> Homo sapiens

<400> 1479
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60
ttaagtatgt tctttacatt gaaacagaaa ggaagaaga taggaaaaat ggtgccagca
120
cgctggggtt tttttgttt ctgttttggg tggggtgtgc tagtgcatgt tccgggtgat
180
gcttttgtcc tcaaacaggc ttgttcccg gtcagagttt cattattgtt gctggtaaac
240
aaatgccaaag ttgacaaaa aacagtgaag taaagcaaaa gattttgaaa aatgcttcac
300
catgtcagaa ggaagaacc cttttcacgg gtgcctgccc acatttcctt gcccgacctg
360
agaccctatt gactttgaat tatcttttgc tgttttattt ctatgaaaaa tatatacgcg
420
t
421

<210> 1480
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1480
Met Lys Ala Arg Cys Ala Ser Leu Ile Glu Ala Gly Thr Leu Lys Tyr
1 5 10 15
Val Leu Tyr Ile Glu Thr Glu Arg Lys Glu Asp Arg Lys Asn Gly Ala
20 25 30
Ser Thr Leu Gly Phe Phe Cys Leu Leu Phe Trp Val Gly Cys Ala Ser
35 40 45
Ala Val Ser Gly Val Arg Phe Cys Pro Gln Thr Gly Leu Phe Pro Gly
50 55 60
Gln Ser Phe Ile Ile Val Ala Gly Lys Gln Met Pro Ser Leu Thr Lys
65 70 75 80
Asn Ser Glu Ile Lys Gln Lys Ile Leu Lys Asn Ala Ser Ser Cys Gln
85 90 95
Lys Glu Arg Thr Leu Phe Thr Gly Ala Cys Pro His Phe Leu Ala Gln
100 105 110
Pro Glu Thr Leu Leu Thr Leu Asn Tyr Leu Leu Leu Phe Tyr Phe Tyr
115 120 125
Glu Asn Tyr Ile Arg
130

<210> 1481
<211> 545

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<212> DNA

<213> Homo sapiens

<400> 1481

gtcgggtcgc cgccagctct cgtgccgaca tgcagttcct ggccccggag gtcgcatcca
 60
 tccggatgca gatgggcgag ttggccacgc gcgattattt gcgctcggag ctacgcgacg
 120
 agtttgcgctc cctgctcgag gagatcgagg cctcaccggc ctccactaa ctgacccggt
 180
 tcgcgacgag cgagttgtcg catcggggcca acggtgtgta gacaagttag catgagcacc
 240
 gagaacccagc tgggtaaggc cattgccgat gcgttgtcgc acgtcaatga ccccgagatc
 300
 aaacgcccc ttaccgatct caacatgatt gatgagatta ccgtcgacga gcaaggacgc
 360
 gctttctgctc gcctcctgct gaccgtcgcc ggggtgtccc tcaagaccga gctgcgtgag
 420
 caggccacgc aggtgtgtcg cagcgttgac ggggtgacca gtgtttccgt cgaactcggc
 480
 accatgacgc acgaacagcg cgatgctctc aaagttcagc tgcgcggtga cgtccccgaa
 540
 cgcgt
 545

<210> 1482

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1482

Met Ser Thr Glu Asn Pro Val Val Lys Ala Ile Ala Asp Ala Leu Ser
 1 5 10 15
 His Val Asn Asp Pro Glu Ile Lys Arg Pro Ile Thr Asp Leu Asn Met
 20 25 30
 Ile Asp Glu Ile Thr Val Asp Glu Gln Gly Arg Ala Phe Val Arg Ile
 35 40 45
 Leu Leu Thr Val Ala Gly Cys Pro Leu Lys Thr Glu Leu Arg Glu Gln
 50 55 60
 Ala Thr Glu Ala Val Arg Ser Val Asp Gly Val Thr Ser Val Ser Val
 65 70 75 80
 Glu Leu Gly Thr Met Thr Asp Glu Gln Arg Asp Ala Leu Lys Val Gln
 85 90 95
 Leu Arg Gly Asp Val Pro Glu Arg
 100

<210> 1483

<211> 625

<212> DNA

<213> Homo sapiens

<400> 1483

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 60

ttggaggtaa agctgggtgct gctgtggaaa cacaacatgc gcattgagta tgtggctatg
 120
 gcatcctggc ccctggagcc tgagggccct cgagtaaacac ggggtgaagt gacgatggaa
 180
 ggccggctacg acattttgca tgatgtgtcc tgtgcactaa ggcagcccatc tcgttcattg
 240
 tatcgtaccc atgttatccg gcgtttcttg aacacgctgc agagcatcaa ccagacagac
 300
 cagatgcttg ccacacttca gtccttctcc tcagtgcctg agcatttcac gcttctcgac
 360
 agcaccaaga gcgagtgcc actcttctac atccctccag gctccaccac cccgggtgctc
 420
 tccctccagc ccagtgggtc tgactcatcc catgccagc ttgctgccta ctggaagccc
 480
 agtgcgtgcc atggatgcaa attcctggca gcgatggctg cacatgcacg gcctgggtgt
 540
 aatcctggag catgacacac caatcccca gcaattgcac accccgggca gcaatgggag
 600
 ctactacgga gagaagacaa cgcgt
 625

<210> 1484

<211> 184

<212> PRT

<213> Homo sapiens

<400> 1484

Val	Arg	Leu	Arg	Glu	Gly	Tyr	Ser	Val	Arg	Glu	Val	Thr	Leu	Ala	Lys
1				5					10					15	
Gly	Gly	Ser	Gln	Leu	Glu	Val	Lys	Leu	Val	Leu	Leu	Trp	Lys	His	Asn
			20				25						30		
Met	Arg	Ile	Glu	Tyr	Val	Ala	Met	Ala	Ser	Trp	Pro	Leu	Glu	Pro	Glu
		35					40					45			
Gly	Pro	Arg	Val	Thr	Arg	Val	Glu	Val	Thr	Met	Glu	Gly	Gly	Tyr	Asp
		50				55				60					
Ile	Leu	His	Asp	Val	Ser	Cys	Ala	Leu	Arg	Gln	Pro	Ile	Arg	Ser	Leu
65				70					75					80	
Tyr	Arg	Thr	His	Val	Ile	Arg	Arg	Phe	Trp	Asn	Thr	Leu	Gln	Ser	Ile
			85						90					95	
Asn	Gln	Thr	Asp	Gln	Met	Leu	Ala	His	Leu	Gln	Ser	Phe	Ser	Ser	Val
			100					105						110	
Pro	Glu	His	Phe	Thr	Leu	Pro	Asp	Ser	Thr	Lys	Ser	Gly	Val	Pro	Leu
			115				120					125			
Phe	Tyr	Ile	Pro	Pro	Gly	Ser	Thr	Thr	Pro	Val	Leu	Ser	Leu	Gln	Pro
		130				135					140				
Ser	Gly	Ser	Asp	Ser	Ser	His	Ala	Gln	Phe	Ala	Ala	Tyr	Trp	Lys	Pro
145				150					155					160	
Ser	Ala	Val	His	Gly	Cys	Lys	Phe	Leu	Ala	Ala	Met	Ala	Ala	His	Ala
				165				170						175	
Ser	Pro	Gly	Ala	Asn	Pro	Gly	Ala								
				180											

<210> 1485

<211> 2058

<212> DNA

<213> Homo sapiens

<400> 1485

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120
gttggcgata ttacttctga atcaccgtct aaaatgtggc ataccagaac tttattgaat
180
gcctacagca atctgaaaga tgatgccaaag tccaattggg tatgggtggga ccttcctatg
240
ccagcccaga gaaaaatctgc tttcgccgat ttgattgaag aaaaatcctag cagcgtaaag
300
tgccataccc ggaaggaaac acagcagctc ttggatatga tgactgatgt taacttagct
360
aaggttgagg ctgcaaaaaa gctatcgatc gagtctaagg aaaatgttgt agggacaatt
420
tataaaagaa ctgcgaccga tagctttgga gttaaagcgc agcgtgctga agtgcggttt
480
gatgatgttg cgggttgtct tcgcaccctc ggaggggggt caagtcggga agtcataatg
540
gtcgttgata acgggactgt aaaaacgagg ttgatctcaa gtagagaaac tgcaaggctt
600
atgggggttac ccgacgaata catattgcc aaaaattata atgaggcgta tcacttaacg
660
ggtgatgggt ttgtagtgcc gggtgtatcc cacatagcca ctcatatTTT tgaccagtg
720
atggagcgtg tgtttgagga tgcggcgga ctgcttaagc aaatcgcata gcactgtttt
780
ggcaggaaga tatgagcgtt attccgtgta aaaaggacct tcagctaaaa aaattgattg
840
aatcctatgc agaagccttg aaagttaggg ccataagct aggagagcat ggattaactg
900
aagctgaatt ttatgatagc ggcctcttct ggggggctat cgagcgaatt caggagacgt
960
tctccgcgac catgcgggag aaaagaaatt tcgttaagca tgttttaaat tacatgcagg
1020
ataacgacta cattgctgat tgggagtcgg ctgggtgaatc gaatcgccat gattatatgg
1080
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1260
ctgaaatcat ttcacgggag caaaggattg atggaatggt cttttgggac tgggcttgtg
1320
gaacagtcgg aaggccatgc ccaaaaatag caactgaacc tgagcgggct gtaacatttg
1380
ggccgttcaa attgccgcca ccatgtttgt atctttttacc ttcgacgatt ccaagcccaa
1440
gaaacaaccc gtctccaaga gctcagcaga tgaagacgt gcagctaact aaagcgtttc
1500

acgattgttt tgggtgccgg tctgaagaag ttaatttcgt taactttgat gttggttatc
 1560
 atgggtaaaga taccgctccgt aaaacgacta tcattcgaaa cggcgatggtg gaggctgaat
 1620
 cggaatgac ggcaataagg cggctctaat ttgtgcatgc ctatgctgca tgaatccgca
 1680
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 1740
 catgcacctg catgaaaacc gctacataaa gcgggcaggc gtggcgggga tacgagcgcg
 1800
 cgcaacgggg tgaatgggtg aatatcaggg gcaatctccg gcacgctggc ggcttgaatc
 1860
 gggtaggggtg agtgagaggc agcaataaag aagcgccccg cagaatgctg ctggggcgct
 1920
 gtgagaggtg gtcttgttgt cgcgggtgcgg tgggtcagtc gtagcgattg tcttctgtca
 1980
 gccccagcgt gtacggctca aagcggatca cttcttcgcc cagccagtc taaagctccc
 2040
 gcagtcgctt ctgcaggc
 2058

<210> 1486

<211> 256

<212> PRT

<213> Homo sapiens

<400> 1486

Xaa Cys Ser Ala Phe Asn Asp Ile Gly Tyr His Tyr Gly Ala Met Val
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 20 25 30
 Ile Gly Val Arg Asn Asp Ile Phe Val Gly Asp Ile Thr Ser Glu Ser
 35 40 45
 Pro Ser Lys Met Trp His Thr Arg Thr Leu Leu Asn Ala Tyr Ser Asn
 50 55 60
 Leu Lys Asp Asp Ala Lys Ser Asn Trp Val Trp Asp Leu Pro Met
 65 70 75 80
 Pro Ala Gln Arg Lys Ser Ala Phe Ala Asp Leu Ile Glu Glu Asn Pro
 85 90 95
 Ser Ser Val Lys Trp His Thr Arg Lys Glu Thr Gln Gln Leu Leu Asp
 100 105 110
 Met Met Thr Asp Val Asn Leu Ala Lys Val Glu Ala Ala Lys Lys Leu
 115 120 125
 Ser Ile Glu Ser Lys Glu Asn Val Val Gly Thr Ile Tyr Lys Arg Thr
 130 135 140
 Arg Thr Asp Ser Phe Gly Val Lys Ala Gln Arg Ala Glu Val Arg Phe
 145 150 155 160
 Asp Asp Val Ala Gly Cys Leu Arg Thr Pro Gly Gly Gly Ser Ser Arg
 165 170 175
 Gln Val Ile Met Val Val Asp Asn Gly Thr Val Lys Thr Arg Leu Ile
 180 185 190
 Ser Ser Arg Glu Thr Ala Arg Leu Met Gly Leu Pro Asp Glu Tyr Ile
 195 200 205
 Leu Pro Lys Asn Tyr Asn Glu Ala Tyr His Leu Thr Gly Asp Gly Val

210	215	220
Val Val Pro Val Val Ser His Ile Ala Thr His Ile Phe Asp Pro Val		
225	230	235
Met Glu Arg Val Phe Glu Asp Ala Ala Gly Leu Leu Lys Gln Ile Ala		240
	245	250
		255

<210> 1487

<211> 823

<212> DNA

<213> Homo sapiens

<400> 1487

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120
catcagggaa tgctggggaa aaaaagcact ccaggcccag ggatcagcaa agcacaggat
180
gcctggggga acacacagcc tcagagcatt tgaggaacag aaaaggcaac gtgactaagc
240
ttcctggggc ggtgaggtca ggcagggagg tgggtgcgag gtcatggggc cgcaggcaaa
300
cggccctccc tcccagtgcc ccacatgcag gccctggagc accaggagcg gggaggctcc
360
gtggtgtgtc ttctgtcaag tggcctgcct ttgggagcat cagccctttc tctctgggac
420
tggtgagagg cggtcagtgc ggaagaatgg ccctcgtcgc tgcgtagaga atgtagggga
480
cacagggcct ctcacggacc cagatcctga tcttgtcaga tctgcacgcc cgtgggaggg
540
tgctggcggc agaaacgcgt tgccataagc cttctcccca ctgcaggcag gtgtggtcag
600
gggacctcct tggagaacaa ggtgggggaa tttggcagct ttctcagcat ggcgtccatc
660
cccctacat tcttggggca cccactgtag gccaggccct gtgccggatc tgatgataca
720
gtgatgacta agtcacagtc cctgcctctg agggccccat gatgtgcogg gacagccaag
780
caaccaata tgttaaaatc cagtgtcagg acccnaggag aag
823

<210> 1488

<211> 149

<212> PRT

<213> Homo sapiens

<400> 1488

Met Leu Gly Arg Ser Cys Glu Gly Lys Phe Arg Lys Asp Leu Ser Glu	
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Gln Val Thr Phe Gln Leu Arg Leu Gly Arg Met Arg Arg Ser Gln Glu	
20	30
Leu Gln Ala Ser Gly Asn Ala Gly Glu Lys Lys His Ser Arg Pro Arg	
35	45
Asp Gln Gln Ser Thr Gly Cys Leu Gly Glu His Thr Ala Ser Glu His	

```

      50              55              60
Leu Arg Asn Arg Lys Gly Asn Val Thr Lys Leu Pro Gly Ala Val Arg
65              70              75              80
Ser Gly Arg Glu Val Gly Ala Arg Ser Trp Gly Arg Arg Gln Thr Ala
      85              90              95
Leu Pro Pro Ser Ala Pro His Ala Gly Pro Gly Ala Pro Gly Ala Gly
      100              105              110
Arg Leu Arg Gly Val Ser Ser Cys Lys Trp Pro Ala Phe Gly Ser Ile
      115              120              125
Ser Pro Phe Ser Trp Gly Leu Gly Glu Ala Gly Ser Glu Gly Arg Met
      130              135              140
Ala Leu Gly Arg Ala
145

<210> 1489
<211> 342
<212> DNA
<213> Homo sapiens

<400> 1489
nnccagttca ccgtcaagct ggccgcggcc gccgaacaca atgtgcgcaa tgcgctggcc
60
gcgattgect gcgcgctggg tgccggcacc aaccaggacg ccacgtgtcg cgccctcgaa
120
gccttcgccc cggtcggcgg acgtttgcag cgcaagcagg ccgccagcgg cgcgcccgtc
180
attgacgaca cccacaaccc caatcccaat tcaatgcgcc cggcgatcga cgtgctggcc
240
cgcgtaaccg cgccgcgcat cctggtggtg gccgacatgg gcgaagtcgg cgcacaggga
300
aaagaatttc acgaagaaat cggggcttac gcacacacgc gt
342

<210> 1490
<211> 114
<212> PRT
<213> Homo sapiens

<400> 1490
Xaa Gln Phe Thr Val Lys Leu Ala Ala Ala Gly Glu His Asn Val Arg
1              5              10              15
Asn Ala Leu Ala Ala Ile Ala Cys Ala Val Gly Ala Gly Ile Asn Gln
      20              25              30
Asp Ala Ile Val Arg Gly Leu Glu Ala Phe Ala Pro Val Gly Gly Arg
      35              40              45
Leu Gln Arg Lys Gln Ala Ala Ser Gly Ala Pro Val Ile Asp Asp Thr
      50              55              60
His Asn Pro Asn Pro Asn Ser Met Arg Pro Ala Ile Asp Val Leu Ala
65              70              75              80
Arg Val Pro Ala Pro Arg Ile Leu Val Val Gly Asp Met Gly Glu Val
      85              90              95
Gly Ala Gln Gly Lys Glu Phe His Glu Glu Ile Gly Ala Tyr Ala His
      100              105              110
Thr Arg

```

<210> 1491
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 1491
 ncctcggtgt tctcatagag ggctacggca tcgcgtttga actgttcgga gtacctggac
 60
 atgggggtag attacctttc ttcccagctc gactgggctg gatatcaggt gtccaccaca
 120
 tggggggtcag gtccactcc caaaggagta gccatcaccc acgagtcggc ggtcaatacag
 180
 attgtcgatg tcaacgaacg cctcgggggtg actccgaccg accggatatt ggggatttca
 240
 gagctaaact tcgatctatc ggtatacgac atcttcggga tggtcgcgcg ggggtgctacc
 300
 ttgggtgttc catctccagc agacaaacgt gat
 333

<210> 1492
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1492
 Met Gly Val Asp Tyr Leu Ser Ser Gln Leu Asp Trp Ala Gly Tyr Gln
 1 5 10 15
 Val Ser Thr Thr Trp Gly Ser Gly Pro Thr Pro Lys Gly Val Ala Ile
 20 25 30
 Thr His Glu Ser Ala Val Asn Thr Ile Val Asp Val Asn Glu Arg Leu
 35 40 45
 Gly Val Thr Pro Thr Asp Arg Ile Leu Gly Ile Ser Glu Leu Asn Phe
 50 55 60
 Asp Leu Ser Val Tyr Asp Ile Phe Gly Met Phe Ala Arg Gly Ala Thr
 65 70 75 80
 Leu Val Leu Pro Ser Pro Ala Asp Lys Arg Asp
 85 90

<210> 1493
 <211> 1316
 <212> DNA
 <213> Homo sapiens

<400> 1493
 nggtaccagg gcaaagaagg ctggggcccc gcctcctacc taaagaagaa cagtggggag
 60
 cccttgcccc cgaagccagg ccctggctca ccctcccacc cgggtgacct tgacttgat
 120
 ggtgtttccc ggcagcagaa cgcggtgggc agggagaagg agctgctcag cagccagagg
 180
 gacgggcggt ttgaaggccg ccggtgcccc gacggtgacg ccaagcagag atcaccaaag
 240

atgaggcaga gacccccctcc tcgcccggac atgaccattc ctcgaggcct caacctgccg
 300
 aagccgcccc tcccgcccc aagtggaggaa gaggattaca ccatcgccga attccagaca
 360
 accatcccag acggcatcag cttccaggca ggccctgaagg tcgagggtgat cgagaaaaac
 420
 ttgagtggtt ggtggtacat tcagattgaa gataaggaag ggtgggcccc ggccaccttc
 480
 attgacaagt acaagaagac gagcaacgcg tcgagaccca actttctggc tcccctgcc
 540
 cagcagggtga cccagctccg gctgggggaa gcagcagcgc tggagaacaa caggggcagc
 600
 gaagccacgg gccctcccg gccctcgct gacgcaccgc atggtgtcat ggactcgggg
 660
 ttgccatggt ctaaagactg gaagggcagt aaggatgtcc tgagggaagg atcttcagac
 720
 atgtctcgct cagcaggcta cgaggagatc tcagaccccc acatggagga gaagccagc
 780
 ctccctccgc ggaagaatc catcatcaag tcggaggggg agctgtctgga gcgggagcgg
 840
 gagcggcaga ggacggagca gctccggggc cccactccca agcctccggg cgtgattttg
 900
 ccgatgatgc cagccaaaca catccctcca gcccgggaca gcaggaggcc agagcccaaa
 960
 cctgacaaaa gcagactgtt ccagctgaaa aatgacatgg ggctggagtg tggccacaa
 1020
 gtcttgccca aggaagtga gaagcccaac ctccggccca tctccaaatc caaaactgac
 1080
 ctgccagagg agaagccaga tgccactccc cagaatccct tcttgaagtc cagacctcag
 1140
 gttaggccaa aaccagctcc ttcccccaaa acggagccac ctcagggcga agaccaagtc
 1200
 gacatctgca acctcaggag taagctcagg cctgccaagt cccaagacaa gtccttgtt
 1260
 gatggggagg gcccccaggc agtagggggc caagacgttg ctttcagccg aagcct
 1316

<210> 1494

<211> 438

<212> PRT

<213> Homo sapiens

<400> 1494

Xaa Tyr Gln Gly Lys Glu Gly Trp Ala Pro Ala Ser Tyr Leu Lys Lys
 1 5 10 15
 Asn Ser Gly Glu Pro Leu Pro Pro Lys Pro Gly Pro Gly Ser Pro Ser
 20 25 30
 His Pro Gly Ala Leu Asp Leu Asp Gly Val Ser Arg Gln Gln Asn Ala
 35 40 45
 Val Gly Arg Glu Lys Glu Leu Leu Ser Ser Gln Arg Asp Gly Arg Phe
 50 55 60
 Glu Gly Arg Pro Val Pro Asp Gly Asp Ala Lys Gln Arg Ser Pro Lys
 65 70 75 80
 Met Arg Gln Arg Pro Pro Pro Arg Arg Asp Met Thr Ile Pro Arg Gly

[illegible]

<210> 1495

<211> 329

<212> DNA

<213> Homo sapiens

<400> 1495

agatctctgt cccgtagagg tgccacctca tcttccatga gagctgtgct ttgctttctt
60

ctggaggctg caaggaggat ggccccatc acggcggacc tacatgctgg gagtcggga
 120
 gagggcaggc cgcggacatg gggcatgtgg cgatgtgttt caccacccac tcccgctga
 180
 agtgccactg tgagcccaac ccacgggtgcc aggtctgggt gcactccagg ctccctgcagc
 240
 agaccacact cctcagcctc cttccctga aggtctggga tggctcggac aaaggggtgc
 300
 ctctctgtgt gtgccatgt gacgtggca
 329

<210> 1496

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1496

Met Ala Gln Gln Arg Arg Thr Pro Phe Val Gln Ala Met Pro Ser Leu
 1 5 10 15
 Gln Gly Lys Glu Ala Glu Glu Val Gly Leu Leu Gln Glu Pro Gly Val
 20 25 30
 Gln Pro Ser Leu Ala Pro Trp Val Gly Leu Thr Val Ala Leu Gln Ala
 35 40 45
 Gly Val Gly Gly Glu Thr His Arg His Met Pro His Val Arg Gly Leu
 50 55 60
 Pro Ser Pro Gly Leu Pro Ala Cys Arg Ser Ala Val Met Gly Ala Ile
 65 70 75 80
 Leu Leu Ala Ala Ser Arg Arg Lys Gln Ser Thr Ala Leu Met Glu Asp
 85 90 95
 Glu Val Ala Pro Leu Arg Asp Arg Asp
 100 105

<210> 1497

<211> 345

<212> DNA

<213> Homo sapiens

<400> 1497

naactcttg cactcactca ggcgacgggt tggcggccga cttggaagcc gctgcagcac
 60
 ttgacgctgg gcatctcga agcgttcgggt cttggcctga cggctgatgg ctgcggcggtg
 120
 ccgttgatcg cgcgaatcg acgggtgggg caggggcgtgc ggccgacacc acogcaagaa
 180
 cgcaactcac ggcagatgaa tctgttttga aacgcaagga agggtaatga caggcaccga
 240
 caagaagcgg atccccgagc tgctgcgtgt tgagctcact gaacttaccg gcccgatcga
 300
 gcagccttac ggcggcgatg cagctcattc ttccggggcca cgcgt
 345

<210> 1498

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1498

```

Met Thr Cys Ile Gly Arg Val Arg Leu Leu Asp Arg Ala Gly Lys Phe
 1             5             10             15
Ser Glu Leu Asn Thr Gln Gln Leu Arg Asp Pro Leu Leu Val Gly Ala
      20             25             30
Cys His Tyr Pro Ser Leu Arg Phe Lys Thr Asp Ser Ser Ala Val Ser
      35             40             45
Cys Val Leu Ala Val Val Ser Ala Ala Arg Pro Ala Pro Pro Val Ala
      50             55             60
Phe Ala Arg Ser Thr Ala Arg Arg Ser His Arg Pro Ser Gly Gln Asp
65             70             75             80
Arg Thr Leu Arg Asp Arg Pro Ala Ser Ser Ala Ala Ala Ala Ser Lys
      85             90             95
Ser Ala Ala Asn Arg Ala Pro Glu
100

```

<210> 1499

<211> 402

<212> DNA

<213> Homo sapiens

<400> 1499

```

aaatatattc tgccagagtt tgaacacgac accatgctct ggcatattggg catgtcgggg
60
agtttccgct tatgcgagag caatgaagaa ttacgcaaac atgaccatct aatcattcag
120
tttgaagata tcgaactgcg ttatcatgat cctcgccggt ttggttgcat tctttggctg
180
gatgcacaat cacaaagcaa attaatagat acgctggggc cagaaccctt aagcgagaac
240
tttaatgcgg agtatttatt tgaaaaattg aagaataaaa aggttggcac caaagttgca
300
attatggata accatgtggt ggtgggcgta ggcaatatat atgcgaccga aagtctgttt
360
aatctgggga ttcattccagc acaaccggcc tcgactttaa gc
402

```

<210> 1500

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1500

```

Lys Tyr Ile Leu Pro Glu Phe Glu His Asp Thr Met Leu Trp His Leu
 1             5             10             15
Gly Met Ser Gly Ser Phe Arg Leu Cys Glu Ser Asn Glu Glu Leu Arg
      20             25             30
Lys His Asp His Leu Ile Ile Gln Phe Glu Asp Ile Glu Leu Arg Tyr
      35             40             45
His Asp Pro Arg Arg Phe Gly Cys Ile Leu Trp Leu Asp Ala Gln Ser
      50             55             60
Gln Ser Lys Leu Ile Asp Thr Leu Gly Pro Glu Pro Leu Ser Glu Asn

```

```

65          70          75          80
Phe Asn Ala Glu Tyr Leu Phe Glu Lys Leu Lys Asn Lys Lys Val Gly
      85          90          95
Thr Lys Val Ala Ile Met Asp Asn His Val Val Val Gly Val Gly Asn
      100         105         110
Ile Tyr Ala Thr Glu Ser Leu Phe Asn Leu Gly Ile His Pro Ala Gln
      115         120         125
Pro Ala Ser Thr Leu Ser
      130

```

```

<210> 1501
<211> 362
<212> DNA
<213> Homo sapiens

```

```

<400> 1501
nnacgcggtgc atgctgcagg catcatccat cgcgatctga agccccaaaa catcttctctg
60
gtgccgagcg cgcgcgagcg cgacttcgtg aagatcttcg acttcggcgc atgccagatg
120
gtcacaccga aggtatcgaa cggcgtgccc gagctgaaga cgagcgcggg aaatctcttc
180
ggcacgggtgc cgtacatggc gccggagtgc ttcgaggacg gctcgaccg gctggatgcg
240
cgcgcgggaca tctactccac gggcatcatc atgtaccgct gcgtgacggg gacgctcccc
300
ttcaaggcga acaccgtctt cgagatgctc atccatctgc gcgaggggccg cccatcaagc
360
tt
362

```

```

<210> 1502
<211> 120
<212> PRT
<213> Homo sapiens

```

```

<400> 1502
Xaa Arg Val His Ala Ala Gly Ile Ile His Arg Asp Leu Lys Pro Gln
1          5          10          15
Asn Ile Phe Leu Val Pro Ser Ala Arg Glu Arg Asp Phe Val Lys Ile
      20          25          30
Phe Asp Phe Gly Ala Cys Gln Met Val Thr Pro Lys Val Ser Asn Gly
      35          40          45
Val Pro Glu Leu Lys Thr Ser Ala Gly Asn Leu Phe Gly Thr Val Pro
      50          55          60
Tyr Met Ala Pro Glu Cys Phe Glu Asp Gly Ser His Arg Leu Asp Ala
65          70          75          80
Arg Ala Asp Ile Tyr Ser Thr Gly Ile Ile Met Tyr Arg Cys Val Thr
      85          90          95
Gly Thr Leu Pro Phe Lys Ala Asn Thr Val Phe Glu Met Leu Ile His
      100         105         110
Leu Arg Glu Gly Arg Pro Ser Ser
      115         120

```

<210> 1503

<211> 623

<212> DNA

<213> Homo sapiens

<400> 1503

gccggcggtga ggcagagaaa cgtcctcgcc ctgtcattcc accctgaaga gactgacgac
 60
 gaccgggtac accgcacctg gttgcgccag gtgtctgagg aggtctgaca gttaccgcaa
 120
 gggctcatga cgaccctcc tgaacctgt tcaaagggcg acggcttacc attcctcgct
 180
 gtgagtcctg aacagcagct tctcgaatat gaccgacgtc atgtctggca ccctacgcc
 240
 ccgacgatcg gggcagacc aatgcttgca gtgacggctg ccaacggagt ctggctgcag
 300
 ctgcatgatg ggaacaccg ccacgaggtc atcgatgcga tggcctcggt gtggtgccag
 360
 attcacgggt accgaaaccc ggtcctcgac gaggcctca accgtcaaag ctcccagttc
 420
 agtcacgtca tgtttgccgg actcaccat aagcccgcg ttgacccgt catatcccta
 480
 gtgcgcctgg ccccggggcc cctcgaccgg atcttccttg ctgattccgg gtctgtcggc
 540
 gtcgagggtg gtctcaaat ggctcgtcag gtgcaaatc ctgcaccgc agcgcgccgg
 600
 ggcactttga cgaggacacg cgt
 623

<210> 1504

<211> 165

<212> PRT

<213> Homo sapiens

<400> 1504

Met Thr Thr Pro Pro Glu His Cys Ser Lys Gly Asp Gly Leu Pro Phe
 1 5 10 15
 Leu Ala Val Ser Pro Glu Gln Gln Leu Leu Tyr Asp Arg Arg His
 20 25 30
 Val Trp His Pro Tyr Ala Pro Thr Ile Gly Ala Asp Pro Met Leu Ala
 35 40 45
 Val Thr Ala Ala Asn Gly Val Trp Leu Gln Leu His Asp Gly Glu His
 50 55 60
 Arg His Glu Val Ile Asp Ala Met Ala Ser Trp Trp Cys Gln Ile His
 65 70 75 80
 Gly Tyr Arg Asn Pro Val Leu Asp Glu Ala Leu Asn Arg Gln Ser Ser
 85 90 95
 Gln Phe Ser His Val Met Phe Gly Gly Leu Thr His Lys Ala Ala Val
 100 105 110
 Asp Ala Val Ile Ser Leu Val Arg Leu Ala Pro Gly Pro Leu Asp Arg
 115 120 125
 Ile Phe Leu Ala Asp Ser Gly Ser Val Gly Val Glu Val Ser Leu Lys
 130 135 140
 Leu Ala Arg Gln Val Gln Ile Ala Arg Thr Ala Ala Arg Gly Gly Thr

```

145                               150                               155                               160
Leu Thr Arg Thr Arg
      165

<210> 1505
<211> 556
<212> DNA
<213> Homo sapiens

<400> 1505
nngcgcgcgc gtcctctcaac accaccctga cttcgaaata tctggagaat gtctacgttg
60
gttttcaatcg gttttgccgaa cagatggcca ggatggcccg cgctctggcg aaactggacg
120
acggggggccc cgaaaactcgc tgacggcact aaaccttctt ccccggggcg aaccaccttg
180
gcttcncngca tgacgaagct cagcggggga gctcagcggt tgtcagctaa cggcggcaag
240
ctcaccgcagc gtgtctccca gctctccgga gggctcacia cttgtctca caagggccag
300
cagctcagccc aagggggcca tgggctggcg agcgggttgg cgacctacac cgatggcaca
360
gggaaggctcg tcgacggcat cgggcagctg tcggctggtt tgacgacgat ggatgagaag
420
atcgctgcgcg ctaccgggaa aatcgatccc tcccagctcg acaaaactcg cggtggggcc
480
ggacagcttgc ctgatggcat cgaccagttc accggcaatc tggttgggtta tcgtactgag
540
atccgccagt acgcgt
556

<210> 1506
<211> 169
<212> PRT
<213> Homo sapiens

<400> 1506
Met Ser Thr Leu Val Ser Ile Gly Leu Pro Asn Arg Trp Pro Gly Trp
1 5 10 15
Pro Ala Pro Arg Arg Asn Trp Thr Thr Gly Ala Pro Lys Leu Ala Asp
20 25 30
Gly Thr Lys Pro Ser Ser Pro Gly Ala Thr Thr Leu Ala Ser Xaa Met
35 40 45
Thr Lys Leu Ser Gly Gly Ala Gln Arg Leu Ser Ala Asn Gly Gly Lys
50 55 60
Leu Thr Asp Gly Val Ser Gln Leu Ser Gly Gly Leu Thr Thr Leu Ser
65 70 75 80
His Lys Gly Gln Gln Leu Ser Gln Gly Ala Asp Gly Leu Ala Ser Gly
85 90 95
Val Ala Thr Tyr Thr Asp Gly Thr Gly Lys Val Val Asp Gly Ile Gly
100 105 110
Gln Leu Ser Ala Gly Leu Thr Thr Met Asp Glu Lys Ile Ala Ala Ala
115 120 125
Thr Gly Lys Ile Asp Pro Ser Gln Leu Asp Lys Leu Ala Gly Gly Ala

```

```

      130                      135                      140
Gly Gln Leu Ala Asp Gly Ile Asp Gln Phe Thr Gly Asn Leu Val Gly
145                      150                      155                      160
Tyr Arg Thr Glu Ile Arg Gln Tyr Ala
      165

```

<210> 1507

<211> 667

<212> DNA

<213> Homo sapiens

<400> 1507

```

agatctctta agatgtgctc attatcatga gaacagcgtg gaggaaccca cccccaggat
60
ccagttacct ccacttgctc tgcccttggc acgtggggct tatggggatt acaattcaag
120
gtgagacttg ggtggggaca cagtgaaca tgaagtgtgc cagcgtgggt ggatgacgcc
180
ctctccccc cgccaccgag agctgcaggc cacatgattc cttttgggta gcaactcggga
240
aagggcagaa tgtacaggaa cagagtgaaga ttgcgagggc ctggggctga gggaggggac
300
gcactagagg aaggcaagg ggagcctcct ggggtgtggg agcactttct gtcttggttt
360
tggttggtgc tgcacagtgg cccacacccg tcagagctca cctgcctgca cccaggccct
420
ccgtgcaccc tggcagccca gatgactgca ccagcccagg ggaggtggag gaatgccaca
480
cgcacccgga cctggggacc ggggggtcctc ggtgatcatc ccgagctcca agacagaagc
540
tggactacag ccgtgctgag tggaggggtt tgggtgctgg gtgccgcct cctattgctc
600
ctgcagactc tgggggtctc ggcgccccca gtggggcaat gtgggtgct gcagggaact
660
cacgcgt
667

```

<210> 1508

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1508

```

Met Tyr Arg Asn Arg Val Arg Phe Ala Gly Pro Gly Ala Glu Gly Gly
1      5      10      15
Asp Ala Leu Glu Glu Gly Lys Gly Glu Pro Pro Gly Cys Gly Glu His
20      25      30
Phe Leu Ser Trp Phe Trp Trp Trp Leu His Ser Gly Pro His Pro Ser
35      40      45
Glu Leu Thr Cys Leu His Pro Gly Pro Pro Cys Thr Leu Ala Ala Gln
50      55      60
Met Thr Ala Pro Ala Gln Gly Arg Trp Arg Asn Ala Thr Arg Thr Gly
65      70      75      80
Thr Trp Gly Pro Gly Val Leu Gly Asp His Pro Glu Leu Gln Asp Arg

```

```

      85              90              95
Ser Trp Thr Thr Ala Val Leu Ser Gly Gly Val Trp Trp Leu Gly Ala
      100              105              110
Arg Leu Leu Leu Leu Gln Thr Leu Gly Ser Arg Ala Pro Pro Val
      115              120              125
Gly Gln Cys Gly Leu Leu Gln Gly Thr His Ala
      130              135

```

<210> 1509

<211> 463

<212> DNA

<213> Homo sapiens

<400> 1509

```

tgatcagagt ggctgagcaa cttgctcaag atcacagttt cagaagtacg ctctaagctg
60
ggctctggctg actccaaagt tgtggctttt gttggttttc ttgttctgtc gcgttttaga
120
aagggtctagg aaccgagcac tgggcgttgg gcttactctc ctctatgtgt gacctgggag
180
tggtgcccaa ggcgctctct tcccagcacc tcagggtcct cactggtaaa ggagggagtg
240
attggaatgt cgccaaagtt acttggctctt ggaattctgt ggctattcac gtggactctg
300
gatggcggctc accaagtaga agagggggccc tgggatagag agaagtctcc tctcctgctc
360
ctgatttccc aggcctctcc ctctcctggc cctccctcct ttcttcact tccccggatt
420
cccttcgagt ttggttgcaa ctttaatttt nngttcogat tca
463

```

<210> 1510

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1510

```

Met Val Thr Trp Glu Trp Cys Pro Arg Ser Leu Pro Ser Thr Ser
1      5      10      15
Gly Ser Ser Leu Val Lys Glu Gly Val Ile Gly Met Ser Pro Lys Leu
20      25      30
Leu Gly Ser Gly Ile Leu Trp Leu Phe Thr Trp Thr Leu Asp Gly Gly
35      40      45
His Gln Val Glu Glu Gly Pro Trp Asp Arg Glu Lys Ser Pro Leu Leu
50      55      60
Leu Leu Ile Ser Gln Ala Ser Pro Ser Pro Gly Pro Pro Ser Phe Leu
65      70      75      80
Pro Leu Pro Arg Ile Pro Phe Glu Phe Gly Cys Asn Phe Asn Phe Xaa
85      90      95
Phe Arg Phe

```

<210> 1511

<211> 633

<212> DNA

<213> Homo sapiens

<400> 1511

gccggcaccg gcgtcaaggc catggcgctg gggccgggat ggggtacacac cgaattccac
 60
 tcacgcgcga acgtcaccgg caaccatctg cgggactttt tctggatcga cgccgaagtt
 120
 ctggtacgcg aggtctctcaa cgaccttgac catgacaagg tagtatccat tcctaccccg
 180
 ctctggaagt tcttcacgcg agtggccaca cataccccac gttccgctat gagattcctg
 240
 tcacgaactc tgtcctcgtc tcgagacaag gacgaccatc ctcgacacac tccgggaggc
 300
 gaggcctgag atggccagcg tcaaaccac taaggaccgg ggccggtaca ccaatgatct
 360
 gtccgccgcg acgcggcagg cagcgaacat gcttctgctg cgctcctttg tgtggaaagt
 420
 cgtaaaagt agcgtccacg gagccgacaa cctcgacggg ctcgacgggt ccttacgctg
 480
 cgcgcgctaa ccattcctcc cacctcgacg cgccgctcgt ttttggggcc cttccaagc
 540
 ggctgtcaaa gtacctagct accggggcgc ctgctgacta tttcttcacc gtctggtgga
 600
 aggccatcgc tccggtgctc ttcttcaacg cgt
 633

<210> 1512

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1512

Ala Gly Thr Gly Val Lys Ala Met Ala Leu Gly Pro Gly Trp Val His
 1 5 10 15
 Thr Glu Phe His Ser Arg Ala Asn Val Thr Gly Asn His Leu Pro Asp
 20 25 30
 Phe Phe Trp Ile Asp Ala Glu Val Leu Val Arg Glu Ala Leu Asn Asp
 35 40 45
 Leu Asp His Asp Lys Val Val Ser Ile Pro Thr Pro Leu Trp Lys Phe
 50 55 60
 Phe Ile Ala Val Ala Thr His Thr Pro Arg Ser Ala Met Arg Phe Leu
 65 70 75 80
 Ser Arg Thr Leu Ser Ser Ser Arg Asp Lys Asp Asp His Pro Arg His
 85 90 95
 Thr Pro Gly Gly Glu Ala
 100

<210> 1513

<211> 401

<212> DNA

<213> Homo sapiens

<400> 1513

acgcgtgaag ggggtgaatt tcaccacaga ggggacgccg gggttcctgt tcagaaatat
 60
 ttggtcgtcc aatctcgtaa tgccttctg aatgacttgc tgggctgcc tcctgacacg
 120
 gctgtttcgc aggaaccgcc actcccgctc cttgcggtac tgactctcca ggtcgtgctc
 180
 ttctggggtc ttcacgacgg gctgggtaaa atagccgggc gctccagtcg cagaaccccg
 240
 tctgcaccgt ggcggagatg aaacttttgt gtccagcagc atcgctccgcg tcgtccgcag
 300
 tctgctctgg gcccttctg aacatcttcc gtgtccgggg gaactgggtg gagtgagggg
 360
 tgtactgcgc cccagcgggg cctgtggtgc ccggccggcc g
 401

<210> 1514

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1514

Met	Phe	Asp	Lys	Gly	Pro	Glu	Gln	Thr	Ala	Asp	Asp	Ala	Asp	Asp	Ala
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Ala	Gly	His	Lys	Ser	Phe	Ile	Ser	Ala	Thr	Val	Gln	Thr	Gly	Phe	Cys
			20				25				30				
Asp	Trp	Ser	Ala	Arg	Leu	Phe	Tyr	Pro	Ala	Arg	His	Glu	Asp	Pro	Arg
		35				40					45				
Arg	Ala	Arg	Pro	Gly	Glu	Ser	Asp	Pro	Gln	Gly	Ala	Gly	Val	Ala	Val
		50				55					60				
Pro	Ala	Lys	Gln	Pro	Cys	Gln	Glu	Ala	Gly	Pro	Ala	Ser	His	Ser	Glu
			70						75					80	
Gly	His	Tyr	Glu	Ile	Gly	Arg	Pro	Asn	Ile	Ser	Glu	Gln	Glu	Pro	Arg
			85					90					95		
Arg	Pro	Leu	Cys	Gly	Glu	Ile	Pro	Pro	Leu	His	Ala				
			100					105							

<210> 1515

<211> 720

<212> DNA

<213> Homo sapiens

<400> 1515

nnngatcctg accgcggcat gaggttcaac cctgccaaagc tattgctcga cccttatgcc
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 120
 aactacgagc ctgacctgac cgacgatgag acgtcgggtc cgtctgccgt cgtcattgac
 180
 gatccccggc cgccctacgc tattgcgcgc cgccacgaca tcagcgaatc gggcatctat
 240
 gagaccatg tcaaaagggt aaccgcgctt caccccctcg ttcttgagca tcttcgcagc
 300
 acctatgcgc ggcttgccca tccggctggt atcgaacacc tcaagtcaat cggagtaaca
 360

gccatcgaaac tactaccgcgt ccagcagttc gtctccgaac cattcatcgt tgggcgcggc
 420
 ttatccgatt actgggggta caacaccctg ggggtctttg cgccgcatgc tgcctactgc
 480
 tccgtcggct cgatgggaac ccagggtgcg gagttcaagg acatgggtgac gtctttccac
 540
 gaagccggca tcgaggtttt cctcgatgtc gtctacaacc acactgggtga gggcggccat
 600
 gaaggaccga ctctgtcttt ccgcggcacc gatcacgagt cttattaccg cctcaccaac
 660
 gatcaccgca atgactatga cgtcaccggt tgtggcaatt ctgtcgacac ctcccatccg
 720

<210> 1516

<211> 240

<212> PRT

<213> Homo sapiens

<400> 1516

Xaa	Asp	Pro	Asp	Arg	Gly	Met	Arg	Phe	Asn	Pro	Ala	Lys	Leu	Leu	Leu
1			5						10				15		
Asp	Pro	Tyr	Ala	Arg	Ala	Ile	Thr	Ala	Gly	Val	Asp	Tyr	His	Gly	Pro
		20						25					30		
Ile	Met	Asp	His	Thr	Pro	Glu	Ser	Asn	Tyr	Glu	Pro	Asp	Leu	Thr	Asp
		35					40					45			
Asp	Ala	Thr	Ser	Val	Pro	Leu	Ala	Val	Val	Ile	Asp	Asp	Pro	Gly	Pro
	50					55					60				
Pro	Thr	Pro	Ile	Ala	Arg	Arg	His	Asp	Ile	Ser	Glu	Ser	Gly	Ile	Tyr
	65				70				75					80	
Glu	Thr	His	Val	Lys	Gly	Leu	Thr	Arg	Leu	His	Pro	Leu	Val	Pro	Glu
			85						90				95		
His	Leu	Arg	Ser	Thr	Tyr	Ala	Gly	Leu	Ala	Tyr	Pro	Ala	Val	Ile	Glu
			100				105						110		
His	Leu	Lys	Ser	Ile	Gly	Val	Thr	Ala	Ile	Glu	Leu	Leu	Pro	Val	Gln
		115					120					125			
Gln	Phe	Val	Ser	Glu	Pro	Phe	Ile	Val	Gly	Arg	Gly	Leu	Ser	Asp	Tyr
	130					135					140				
Trp	Gly	Tyr	Asn	Thr	Leu	Gly	Phe	Phe	Ala	Pro	His	Ala	Ala	Tyr	Cys
	145				150					155				160	
Ser	Val	Gly	Ser	Met	Gly	Thr	Gln	Val	Arg	Glu	Phe	Lys	Asp	Met	Val
			165						170				175		
Thr	Ser	Phe	His	Glu	Ala	Gly	Ile	Glu	Val	Phe	Leu	Asp	Val	Val	Tyr
			180					185					190		
Asn	His	Thr	Gly	Glu	Gly	Gly	His	Glu	Gly	Pro	Thr	Leu	Ser	Phe	Arg
		195				200						205			
Gly	Ile	Asp	His	Glu	Ser	Tyr	Tyr	Arg	Leu	Thr	Asn	Asp	His	Arg	Asn
	210					215					220				
Asp	Tyr	Asp	Val	Thr	Gly	Cys	Gly	Asn	Ser	Val	Asp	Thr	Ser	His	Pro
	225				230						235				240

<210> 1517

<211> 497

<212> DNA

<213> Homo sapiens

<400> 1517
 nnacgcgtga aggggggttcg ggaggaggac gccctgctgg agaacgggag ccagagcaac
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 gaaagtgcag acgtcagcac agaccgtggc cctgcgccac cttccccgct caaggagacc
 120
 tccttttcca tcggggtgca agtactgttt ccattcctcc tggcaggctt tgggaccgtg
 180
 gctgctggca tgggtttgga catcgtgcag cactgggaag tcttcagaa ggtgacagag
 240
 gtcttcaccc tagtgctgc gctgctgggg ctcaaaggga acctgaaat gaccctggca
 300
 tcaaggcttt ccactgcagc caacattgga cacatggaca caccgaagga gctctggcgg
 360
 atgatcactg ggaacatggc cctcatccag gtgcaggccc cggtggtggg cttcctggcg
 420
 tccatcgcag ccgtcgtctt tggctggatc cctgatggcc acttcagtat tccgcacggc
 480
 ttcctgctct gtggtag
 497

<210> 1518
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 1518
 Xaa Arg Val Lys Gly Val Arg Glu Glu Asp Ala Leu Leu Glu Asn Gly
 1 5 10 15
 Ser Gln Ser Asn Glu Ser Asp Asp Val Ser Thr Asp Arg Gly Pro Ala
 20 25 30
 Pro Pro Ser Pro Leu Lys Glu Thr Ser Phe Ser Ile Gly Leu Gln Val
 35 40 45
 Leu Phe Pro Phe Leu Leu Ala Gly Phe Gly Thr Val Ala Ala Gly Met
 50 55 60
 Val Leu Asp Ile Val Gln His Trp Glu Val Phe Gln Lys Val Thr Glu
 65 70 75 80
 Val Phe Ile Leu Val Pro Ala Leu Leu Gly Leu Lys Gly Asn Leu Glu
 85 90 95
 Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala Asn Ile Gly His Met
 100 105 110
 Asp Thr Pro Lys Glu Leu Trp Arg Met Ile Thr Gly Asn Met Ala Leu
 115 120 125
 Ile Gln Val Gln Ala Pro Val Val Gly Phe Leu Ala Ser Ile Ala Ala
 130 135 140
 Val Val Phe Gly Trp Ile Pro Asp Gly His Phe Ser Ile Pro His Ala
 145 150 155 160
 Phe Leu Leu Cys Gly
 165

<210> 1519
 <211> 2076
 <212> DNA
 <213> Homo sapiens

<400> 1519
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gtgtgcaatg agatgttggt aaaatcccag tttgttgctt gtatggctac ttgtcattca
120
cttacaaaaa ttgaaggagt gctctctggt gatccacttg atctgaaaaa gtttggaggct
180
attggatgga ttctggaaga agcaactgaa gaagaaacag cacttcataa tcgaattatg
240
cccacagtgg ttctgctctcc caaacaactg cttctctgaat ctaccctctgc agggaaaccaa
300
gaaatggagc tgtttgaact tccagctact tatgagatag gaattgttcg ccagttccca
360
ttttcttctg ctttgcaacg tatgagtgtg gttgccaggg tgctggggga taggaaaaatg
420
gacgcctaca tgaagggagc gcccgaggcc attgccggtc tctgtaaacc tgaacagtt
480
cctgtcgatt ttcaaaacgt tttggaagac ttactaaac agggcttccg tgtgattgct
540
cttgacaca gaaaattgga gtcaaaactg acatggcata aagtacagaa tattagcaga
600
gatgcaattg agaacaacat ggattttatg ggattaatta taatgcagaa caaattaaag
660
caagaaaccc ctgcagtact tgaagatttg cataaaacca acattcgcac cgctcatggtc
720
acaggtgaca gtatgttgac tgctgtctct gtggccagag attgtggaat gattctacct
780
caggataaag tgattattgc tgaagcatta cctccaaagg atgggaaagt tgccaaaaata
840
aattggcatt atgcagactc cctcacgcag tgcagtcac catcagcaat tgaccagag
900
gctattccgg ttaaattggt ccatgatagc tttagaggatc ttcaaatgac tcgttatcat
960
tttgcaatga atggaaaac attctcagt atactggagc attttcaaga ctttgttcc
1020
aagtgtgatg tgcattggcac cgtgtttgcc cgtatggcac ctgacatgaa gacacagttg
1080
atagaagcat tgcaaaatgt tgattatttt gttgggatgt gtggtgatgg cgcaaatgat
1140
tgtggtgctt tgaagagggc acacggaggc atttccttat cggagctcga agcttcagtg
1200
gcatctccct ttacctctaa gactcctagt atttcctgtg tgccaaacct tatcagggaa
1260
ggccgtgctg ctttaataac ttcttctgtg gtgtttaaat tcatggcatt gtacagcatt
1320
atccagtact tcagtgttac tctgctgtat tctatcttaa gtaacctagg agacttccag
1380
tttctcttca ttgatctggc aatcattttg gtatgggat ttacaatgag tttaaatcct
1440
gcctgggaaa aacttgtggc acaaagacca ccttcgggtc ttatatcttg ggcccttctc
1500
ttctccgttt tgtctcagat tatcatctgc attggatttc aatctttggg ttttttttgg
1560

gtcaaacacg aaccttggtg tgaagtgtgg catccaaaat cagatgcttg taatacaaca
 1620
 ggaagcgggt tttggaattc ttcacacgta gacaatgaaa ccgaacttga tgaacataat
 1680
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 1740
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 1800
 gttttttctg tgattttttt atatattttt atattattca tcatgttgta tccagttgcc
 1860
 tctgttgacc aggtttcttc gatagtgtgt gtaccataac agtggcgtgt aactatgctc
 1920
 atcattgttc ttgtcaatgc ctttgtgtct atcacagtg agaacttctt ccttgacatg
 1980
 gtcctttgga aagtgtgtgt caaccgagac aaacaaggag agtatcggtt cagcaccaca
 2040
 cagccaccgc aggagtcagt ggatcggtgg ggaaaa
 2076

<210> 1520

<211> 692

<212> PRT

<213> Homo sapiens

<400> 1520

Xaa	Asp	Leu	Trp	Gly	Ile	Gln	Arg	Val	Glu	Asn	Ala	Arg	Phe	Leu	Ser
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Pro	Glu	Glu	Asn	Val	Cys	Asn	Glu	Met	Leu	Val	Lys	Ser	Gln	Phe	Val
			20					25					30		
Ala	Cys	Met	Ala	Thr	Cys	His	Ser	Leu	Thr	Lys	Ile	Glu	Gly	Val	Leu
		35					40					45			
Ser	Gly	Asp	Pro	Leu	Asp	Leu	Lys	Met	Phe	Glu	Ala	Ile	Gly	Trp	Ile
		50				55				60					
Leu	Glu	Glu	Ala	Thr	Glu	Glu	Glu	Thr	Ala	Leu	His	Asn	Arg	Ile	Met
65					70					75				80	
Pro	Thr	Val	Val	Arg	Pro	Pro	Lys	Gln	Leu	Pro	Glu	Ser	Thr	Pro	
			85					90					95		
Ala	Gly	Asn	Gln	Glu	Met	Glu	Leu	Phe	Glu	Leu	Pro	Ala	Thr	Tyr	Glu
			100					105					110		
Ile	Gly	Ile	Val	Arg	Gln	Phe	Pro	Phe	Ser	Ser	Ala	Leu	Gln	Arg	Met
			115				120					125			
Ser	Val	Val	Ala	Arg	Val	Leu	Gly	Asp	Arg	Lys	Met	Asp	Ala	Tyr	Met
		130				135					140				
Lys	Gly	Ala	Pro	Glu	Ala	Ile	Ala	Gly	Leu	Cys	Lys	Pro	Glu	Thr	Val
145					150					155				160	
Pro	Val	Asp	Phe	Gln	Asn	Val	Leu	Glu	Asp	Phe	Thr	Lys	Gln	Gly	Phe
				165					170					175	
Arg	Val	Ile	Ala	Leu	Ala	His	Arg	Lys	Leu	Glu	Ser	Lys	Leu	Thr	Trp
			180					185					190		
His	Lys	Val	Gln	Asn	Ile	Ser	Arg	Asp	Ala	Ile	Glu	Asn	Asn	Met	Asp
			195				200					205			
Phe	Met	Gly	Leu	Ile	Ile	Met	Gln	Asn	Lys	Leu	Lys	Gln	Glu	Thr	Pro
		210				215						220			
Ala	Val	Leu	Glu	Asp	Leu	His	Lys	Ala	Asn	Ile	Arg	Thr	Val	Met	Val

225					230					235				240
Thr	Gly	Asp	Ser	Met	Leu	Thr	Ala	Val	Ser	Val	Ala	Arg	Asp	Cys Gly
				245						250				255
Met	Ile	Leu	Pro	Gln	Asp	Lys	Val	Ile	Ile	Ala	Glu	Ala	Leu	Pro Pro
			260					265					270	
Lys	Asp	Gly	Lys	Val	Ala	Lys	Ile	Asn	Trp	His	Tyr	Ala	Asp	Ser Leu
		275					280					285		
Thr	Gln	Cys	Ser	His	Pro	Ser	Ala	Ile	Asp	Pro	Glu	Ala	Ile	Pro Val
	290					295					300			
Lys	Leu	Val	His	Asp	Ser	Leu	Glu	Asp	Leu	Gln	Met	Thr	Arg	Tyr His
305					310					315				320
Phe	Ala	Met	Asn	Gly	Lys	Ser	Phe	Ser	Val	Ile	Leu	Glu	His	Phe Gln
			325						330					335
Asp	Leu	Val	Pro	Lys	Leu	Met	Leu	His	Gly	Thr	Val	Phe	Ala	Arg Met
			340					345					350	
Ala	Pro	Asp	Gln	Lys	Thr	Gln	Leu	Ile	Glu	Ala	Leu	Gln	Asn	Val Asp
	355					360						365		
Tyr	Phe	Val	Gly	Met	Cys	Gly	Asp	Gly	Ala	Asn	Asp	Cys	Gly	Ala Leu
	370					375					380			
Lys	Arg	Ala	His	Gly	Gly	Ile	Ser	Leu	Ser	Glu	Leu	Glu	Ala	Ser Val
385					390					395				400
Ala	Ser	Pro	Phe	Thr	Ser	Lys	Thr	Pro	Ser	Ile	Ser	Cys	Val	Pro Asn
			405						410					415
Leu	Ile	Arg	Glu	Gly	Arg	Ala	Ala	Leu	Ile	Thr	Ser	Phe	Cys	Val Phe
			420				425						430	
Lys	Phe	Met	Ala	Leu	Tyr	Ser	Ile	Ile	Gln	Tyr	Phe	Ser	Val	Thr Leu
	435					440					445			
Leu	Tyr	Ser	Ile	Leu	Ser	Asn	Leu	Gly	Asp	Phe	Gln	Phe	Leu	Phe Ile
	450				455					460				
Asp	Leu	Ala	Ile	Ile	Leu	Val	Val	Val	Phe	Thr	Met	Ser	Leu	Asn Pro
465					470				475					480
Ala	Trp	Lys	Glu	Leu	Val	Ala	Gln	Arg	Pro	Pro	Ser	Gly	Leu	Ile Ser
			485					490					495	
Gly	Ala	Leu	Leu	Phe	Ser	Val	Leu	Ser	Gln	Ile	Ile	Ile	Cys	Ile Gly
		500					505						510	
Phe	Gln	Ser	Leu	Gly	Phe	Phe	Trp	Val	Lys	Gln	Gln	Pro	Trp	Tyr Glu
	515					520					525			
Val	Trp	His	Pro	Lys	Ser	Asp	Ala	Cys	Asn	Thr	Thr	Gly	Ser	Gly Phe
	530				535					540				
Trp	Asn	Ser	Ser	His	Val	Asp	Asn	Glu	Thr	Glu	Leu	Asp	Glu	His Asn
545				550					555					560
Ile	Gln	Asn	Tyr	Glu	Asn	Thr	Thr	Val	Phe	Phe	Ile	Ser	Ser	Phe Gln
			565					570					575	
Tyr	Leu	Ile	Val	Ala	Ile	Ala	Phe	Ser	Lys	Gly	Lys	Pro	Phe	Arg Gln
	580					585						590		
Pro	Cys	Tyr	Lys	Asn	Tyr	Phe	Phe	Val	Phe	Ser	Val	Ile	Phe	Leu Tyr
	595					600					605			
Ile	Phe	Ile	Leu	Phe	Ile	Met	Leu	Tyr	Pro	Val	Ala	Ser	Val	Asp Gln
	610				615					620				
Val	Leu	Gln	Ile	Val	Cys	Val	Pro	Tyr	Gln	Trp	Arg	Val	Thr	Met Leu
625					630				635					640
Ile	Ile	Val	Leu	Val	Asn	Ala	Phe	Val	Ser	Ile	Thr	Val	Glu	Asn Phe
			645					650					655	
Phe	Leu	Asp	Met	Val	Leu	Trp	Lys	Val	Val	Phe	Asn	Arg	Asp	Lys Gln

660 665 670
 Gly Glu Tyr Arg Phe Ser Thr Thr Gln Pro Pro Gln Glu Ser Val Asp
 675 680 685
 Arg Trp Gly Lys
 690

<210> 1521
 <211> 373
 <212> DNA
 <213> Homo sapiens

<400> 1521
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 tctgcacgcg ctgggacctca acgagtagtt cagcaaaagt aggcggaaca ggcgcaacga
 120
 gcgtaccatc cgatacacgc cagccttgac tgctgatata cccagccac tgcgcatcag
 180
 tgatttcaat ggcgggttaca cagtctggta tcggactgtc gatattatcg taataggcga
 240
 tcacattccc atttgcacgc tatgctgcga acttttgacc catgattatt atttcccgaa
 300
 tgcaaaccaa taaacagtgt tggcgcttga tgaatagccg ttctgcacca cggcggtaga
 360
 gagtggcgtc gac
 373

<210> 1522
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 1522
 Met Gly Gln Lys Phe Ala Ala Tyr Asp Ala Asn Gly Asn Val Ile Ala
 1 5 10 15
 Tyr Tyr Asp Asp Ile Asp Ser Pro Ile Pro Asp Cys Val Thr Ala Ile
 20 25 30
 Glu Ile Thr Asp Ala Gln Trp Leu Gly Cys Ile Ser Ser Gln Gly Trp
 35 40 45
 Arg Val Ser Asp Gly Thr Leu Val Ala Pro Val Pro Pro Thr Phe Ala
 50 55 60
 Glu Leu Leu Val Glu Ala Gln Arg Val Gln Thr Gln Val Ile Asp Ser
 65 70 75 80
 Ala Cys Ala Ser Ala Ile Thr Ala Gly Phe Ser Cys Asp Ala
 85 90

<210> 1523
 <211> 525
 <212> DNA
 <213> Homo sapiens

<400> 1523
 nnacgcgtgc ggtcaatatg ccgccattcc cataagcgtc tgggtggcatg tttccagggc
 60

cagcatggca cggatgccga gaggagacac aaaaaactgc ctctgacagc tcttgctcaa
 120
 aatattgcaag aagcatcgac tcagctggaa gactctctcc tggggaagat gctggagagc
 180
 tgtggagatg ctgagaatca gctggctctc gagctctccc agcacgaagt ctttgttgag
 240
 aaggagatcg tggacctctc gtacggcata gctgaggtgg agattcccaa catccagaag
 300
 cagaggaagc agcttgcaag attggtgtta gactgggatt cagtcagagc caggtggaac
 360
 caagctcaca aatctcagg aaccaacttt caggggcttc catcaaaaaa agatactcta
 420
 aaggaaggga tggatgaagc tggaaaataa gtagaacagt gcaaggatca acttcgagca
 480
 gacatgtaca actttatggc caaagaaggg gagtatggca aattt
 525

<210> 1524

<211> 175

<212> PRT

<213> Homo sapiens

<400> 1524

Xaa	Arg	Val	Arg	Ser	Ile	Cys	Arg	His	Ser	His	Lys	Arg	Leu	Val	Ala
1				5					10				15		
Cys	Phe	Gln	Gly	Gln	His	Gly	Thr	Asp	Ala	Glu	Arg	Arg	His	Lys	Lys
			20					25					30		
Leu	Pro	Leu	Thr	Ala	Leu	Ala	Gln	Asn	Met	Gln	Glu	Ala	Ser	Thr	Gln
		35					40				45				
Leu	Glu	Asp	Ser	Leu	Leu	Gly	Lys	Met	Leu	Glu	Thr	Cys	Gly	Asp	Ala
	50				55					60					
Glu	Asn	Gln	Leu	Ala	Leu	Glu	Leu	Ser	Gln	His	Glu	Val	Phe	Val	Glu
65				70					75					80	
Lys	Glu	Ile	Val	Asp	Pro	Leu	Tyr	Gly	Ile	Ala	Glu	Val	Glu	Ile	Pro
			85					90						95	
Asn	Ile	Gln	Lys	Gln	Arg	Lys	Gln	Leu	Ala	Arg	Leu	Val	Leu	Asp	Trp
			100				105							110	
Asp	Ser	Val	Arg	Ala	Arg	Trp	Asn	Gln	Ala	His	Lys	Ser	Ser	Gly	Thr
		115				120					125				
Asn	Phe	Gln	Gly	Leu	Pro	Ser	Lys	Ile	Asp	Thr	Leu	Lys	Glu	Gly	Met
	130					135				140					
Asp	Glu	Ala	Gly	Asn	Lys	Val	Glu	Gln	Cys	Lys	Asp	Gln	Leu	Ala	Ala
145				150					155					160	
Asp	Met	Tyr	Asn	Phe	Met	Ala	Lys	Glu	Gly	Glu	Tyr	Gly	Lys	Phe	
			165					170						175	

<210> 1525

<211> 294

<212> DNA

<213> Homo sapiens

<400> 1525

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 120
 ctgctgtttt ccctggacta tgaatatgaa ctgccgatgg cccagatgaa cggcggttta
 180
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 240
 ctgtgcaaac aggtcgcgca attcggcggt gaggtcaccg ggatgcttcg gatc
 294

<210> 1526

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1526

Val	His	Glu	Arg	Met	Asp	Leu	Ile	Arg	Gln	Ser	Val	Asp	Ala	Arg	Ile
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Asn	Val	Asp	Tyr	Trp	Ser	Gly	Leu	Leu	Val	Asp	Tyr	Thr	Ser	Gln	His
			20					25					30		
Gly	Val	Asp	Val	Leu	Val	Lys	Gly	Leu	Arg	Ser	Ser	Leu	Asp	Tyr	Glu
			35				40					45			
Tyr	Glu	Leu	Pro	Met	Ala	Gln	Met	Asn	Arg	Arg	Leu	Ser	Gly	Ile	Asp
			50			55					60				
Thr	Val	Phe	Leu	Leu	Thr	Asp	Glu	Lys	Tyr	Gly	Tyr	Ile	Ser	Ser	Ser
			65			70				75				80	
Leu	Cys	Lys	Gln	Val	Ala	Gln	Phe	Gly	Gly	Glu	Val	Thr	Gly	Met	Leu
			85						90					95	

Arg Ile

<210> 1527

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1527

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 60
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 120
 acttcgacct ggtgcacggg gttggcatga cggcgagta cccttgggtg gtgcaccgag
 180
 aagacattga cgcgtgggt tacgacgggt tggtcgaggc cggcgatgacc atctgtgtgg
 240
 aaagctacat cggccacgac gacggcggcg aaggcgtgaa gctcgaagaa cagatctaca
 300
 tccacgaaca cagcatcgag ttgctctccg attatccgtt cgaccacgcg ctgttgccgc
 360
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 371

<210> 1528

<211> 109

<212> PRT

<213> Homo sapiens

<400> 1528

```
Met Glu Met Leu Lys Ala Gly Arg Ser Phe Lys Glu Tyr Ala Glu Met
 1           5           10           15
Ala Trp Lys Ile Pro Glu His Tyr Lys Asn Arg Tyr Phe Ala Leu
 20           25           30
Val His Gly Val Gly Met Thr Gly Glu Tyr Pro Trp Val Val His Arg
 35           40           45
Glu Asp Ile Asp Ala Leu Gly Tyr Asp Gly Val Phe Glu Ala Gly Met
 50           55           60
Thr Ile Cys Val Glu Ser Tyr Ile Gly His Asp Asp Gly Gly Glu Gly
 65           70           75           80
Val Lys Leu Glu Glu Gln Ile Tyr Ile His Glu His Ser Ile Glu Leu
 85           90           95
Leu Ser Asp Tyr Pro Phe Asp Pro Arg Leu Leu Pro Arg
100           105
```

<210> 1529

<211> 609

<212> DNA

<213> Homo sapiens

<400> 1529

```
nacgcgtggg gctcaccctc cgtgtgactc gcgctctgtc cggtcaggg ctcgccctcc
 60
gtgggacttg cgctctgtcc ggctcagggc tcgccctccg tgggacttgc gctctgtccg
120
gctcagggct cgcctccgt gggacttgcg ctctgtccgg ctcagggctc gccctccgtg
180
ggacttgccg tctgtccggc tcagggctcg cctcctgtgg gacttgccgt ctgtccggct
240
cagggctcgc cctccgtggg acttgccgctc tgccggctc agggctcgcc ctccgtggga
300
tttgcgtctc gtctggctca ggctgcgcag ggcaatggag gaacctcccg agcaggccca
360
gcggctctct ccaccagcc cccatctccg gcgggccatt tgtgaggccc tctgccactg
420
aggtgcactg ttccaattc ctcattcaca agctctacct tccacagacc cagagcatga
480
acgcattccg ccatggctct caccactctg cgaggagcac agcctcttct ccaccgtcca
540
atagcgtggt cctcctttcc caggcctcac agaatgctct gtcgcgatcc tcccagcatt
600
ccattcacg
609
```

<210> 1530

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1530

```
Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala Leu
```

```

      1           5           10           15
Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala Leu Cys Pro Ala
      20           25           30
Gln Gly Ser Pro Ser Val Gly Leu Ala Leu Cys Pro Ala Gln Gly Ser
      35           40           45
Pro Ser Val Gly Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val
      50           55           60
Gly Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala
      65           70           75           80
Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Phe Ala Leu Cys Leu
      85           90           95
Ala Gln Ala Ala Gln Gly Asn Gly Gly Thr Ser Arg Ala Gly Pro Ala
      100          105          110
Ala Pro Ser Thr Gln Pro Pro Ser Pro Ala Gly His Leu
      115          120          125

```

<210> 1531

<211> 726

<212> DNA

<213> Homo sapiens

<400> 1531

```

accggtcgcc ggcttgctga gggtaacctt ctggccacag ttggtgatgg tgataggtcc
60
agcgttggac tgggacgccg acgctgaaaa agaagctgac gagtccttgg gggcgcccg
120
acattcgcca agcatgagga cggggagcat cgagaccgag acagctcgcc gaaggaattt
180
cggggtggca ggcattggca aactagcttt ctgtgatcgg cgtgcgcggc cgggcaacaa
240
cagggcgctg tcaggtggtc ttcgggctcg acttcgtctc cgttcccgcc accttcccg
300
tgccgatggc caggtggttc aagtcggggc ggatcagtc taccgctgag ctcagctccg
360
gcttttcacc ggattccagc gctgggttgg tcaccagcaa cctgacgcga ggatttttagc
420
acccttctcg cataccgcta tccagggcct ccacgacagc ggcaccgatg acgatcgctg
480
tcaccagcgc cggcgttttc ggcagcttcc acatggggat cagaccatat tgatgcactg
540
gcgatccctt catacgcgag ccgccgatat ggcccccgag tgagggccct cagttcgcgc
600
tgacgcacgc cgctctgcgc agcctgccaa cgctttcccg caacctcacc acacgtttgc
660
cggggttcggg gctggcgacg tgagccgtgt cacaagttca cgagctggct caccgctccg
720
cgagag
726

```

<210> 1532

<211> 178

<212> PRT

<213> Homo sapiens

<400> 1532

```

Met Val Ile Gly Pro Ala Leu Asp Trp Asp Ala Asp Ala Glu Lys Glu
 1           5           10           15
Ala Asp Glu Ser Leu Gly Ala Pro Ala His Ser Ala Ser Met Arg Thr
          20           25           30
Gly Ser Ile Glu Thr Ala Thr Ala Arg Arg Arg Asn Phe Gly Val Ala
          35           40           45
Gly Met Ala Lys Leu Ala Phe Cys Asp Arg Arg Ala Arg Pro Gly Asn
          50           55           60
Asn Arg Ala Ser Ser Gly Gly Leu Arg Ala Arg Leu Arg Leu Arg Ser
65          70          75          80
Arg His Leu Pro Ser Ala His Gly Gln Val Val Gln Val Gly Ala Asp
          85          90          95
Gln Ser Tyr Arg Cys Ala Gln Leu Arg Leu Phe Thr Gly Phe Gln Arg
          100          105          110
Trp Cys Gly His Gln Gln Pro Asp Ala Arg Ile Leu Ala Pro Pro Ser
          115          120          125
His Thr Ala Ile Gln Gly Leu His Asp Ser Gly Thr Asp Asp Asp Arg
          130          135          140
Val His Arg Ala Arg Arg Phe Arg Gln Leu Pro His Gly Asp Gln Thr
          145          150          155          160
Ile Leu Met His Trp Arg Ser Leu His Thr Arg Ala Ala Asp Met Ala
          165          170          175

Pro Glu

```

<210> 1533

<211> 364

<212> DNA

<213> Homo sapiens

<400> 1533

```

natatgctgg togatcatgt gcatcagatc gtccagtggc cggagcgcgg ctggctggcg
60
gagattattc acagcgaacg ggcgaccggc ggtgcgccgc ttaacgtcct gctgacgctg
120
gttaaaatgc acgtcggtt gccgttgacg gcggtcggtc ttatcggcga agacacgcgt
180
ggcgattaca ttatggcgat gctcgaccag taccacgtca atcggccagc ggtacagcgc
240
accacgtttg cccccacgtc gatgtcgacg gtgatgaccg atcccactgg gcagcgcacc
300
tttttcatt cgcctgccgc caatgcctg ctcgatctcc cgcctttga tcgactcgac
360
gcgt
364

```

<210> 1534

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1534

```

Xaa Met Leu Val Asp His Val His Gln Ile Val Gln Trp Pro Glu Arg

```

```

      1             5             10             15
Gly Trp Leu Ala Glu Ile Ile His Ser Glu Arg Ala Thr Gly Gly Ala
      20             25             30
Pro Leu Asn Val Leu Leu Thr Leu Val Lys Met His Val Gly Leu Pro
      35             40             45
Leu Gln Ala Val Gly Leu Ile Gly Glu Asp Ser Asp Gly Asp Tyr Ile
      50             55             60
Met Ala Met Leu Asp Gln Tyr His Val Asn Arg Gln Arg Val Gln Arg
      65             70             75             80
Thr Thr Phe Ala Pro Thr Ser Met Ser Gln Val Met Thr Asp Pro Thr
      85             90             95
Gly Gln Arg Thr Phe Phe His Ser Pro Ala Ala Asn Arg Leu Leu Asp
      100             105             110
Leu Pro Ala Phe Asp Arg Leu Asp Ala
      115             120

```

<210> 1535

<211> 369

<212> DNA

<213> Homo sapiens

<400> 1535

```

gaattcgggg ggctccggga atgaagtttc catttcgcaa gccttctgaa gcaaatccgc
60
caatccctcg ggcccgcggt gcgtgccgcg cagcggccag tcctggcccc gaatgatcca
120
ctcgatatct tcggcagaca acgccagcag accgggccta tcgcccgccg ccatggctgc
180
aaaaaaaaactc ttcacagtct ggacattccc ttgtgtgctc atcgaaatct ctccatgtcc
240
tttacctggg atcgtgtccg atctcatcgg acgcgttgag gacctgctgg tgaggacggg
300
gtgtcgggtga ttcagccgat atcgactttg catggcgatg tcccagctgc cggagccggt
360
actggccac
369

```

<210> 1536

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1536

```

Met Gln Ser Arg Tyr Arg Leu Asn His Arg His Pro Val Leu Thr Ser
      1             5             10             15
Arg Ser Ser Thr Arg Pro Met Arg Ser Asp Thr Ile Pro Gly Lys Gly
      20             25             30
His Gly Glu Ile Ser Met Ser Thr Gln Gly Asn Val Gln Thr Val Lys
      35             40             45
Ser Phe Phe Ala Ala Met Gly Arg Gly Asp Arg Pro Gly Leu Leu Ala
      50             55             60
Leu Ser Ala Glu Asp Ile Glu Trp Ile Ile Pro Gly Gln Asp Trp Pro
      65             70             75             80
Leu Ala Gly Thr His Arg Gly Pro Gln Gly Leu Ala Asp Leu Leu Gln

```

[illegible]

caggctgctc agccagggtc aggagaaggt gggtcaggct ccccggggac ctccaggccct
 240
 gacgcaccc taggcctcct ctgtcggggc agcctggctc agcagagccc
 300
 gggacacacg gctgaggcca cccaggctgg gccatcttgc cctgttttg tggccctac
 360
 tcagttctcc ttctgtctcg gctcaggctc aggccagtc agaggggtgc tgagaagcag
 420
 gaggagcctc agagaccctc cctcgaaag cactggggct tccacctcac aagcggcagg
 480
 ttcgctttgg gagctgctgg tccatcgccc aggcctggcc aggggcaggc gaggatcctg
 540
 gttgccgac catcgccag gctggccca ggagccggg aggaacctgg ggctgtgtg
 600
 caggggtcgc cgtctccagc tctctgccgt ggtgagggga ttgtgctgtg tgcacaccac
 660
 ctggctgcat cgaatccac catggccag aggggtggacc tgtggctcct tggggggcca
 720
 gcatccccc tctaattggg gccctgccca ctctcctgag ttccctgca gagctcccc
 780
 caacacctca gccttcacct ttctcagta atcaaaagat tccaaaaaaa gcaaacccat
 840
 cagaacggct tcctccaccg agtggttcagg ataaataatc atgtccagtc aagccagag
 900
 cagcccgat gatcatctat gaacagggtt taggtgggtg acagggcact gagcccgact
 960
 gccttggtg tcagccacat ctgttgagat gcgtgtgcct gacgccgaa cgcgt
 1015

<210> 1540

<211> 89

<212> PRT

<213> Homo sapiens

<400> 1540

His	Pro	Arg	Gln	Ser	Ala	Ser	Val	Pro	Cys	His	Pro	Pro	Arg	Thr	Cys
1				5				10					15		
Ser	Gln	His	Val	Ile	Arg	Ala	Ala	Leu	Ala	Leu	Thr	Gly	His	Asp	Tyr
			20				25					30			
Leu	Ser	Leu	His	Thr	Val	Ala	Ala	Leu	Gln	Ala	Lys	Lys	Gln	Ala	Ala
			35				40				45				
Gln	Pro	Gly	Ser	Gly	Glu	Gly	Gly	Ser	Gly	Ser	Pro	Gly	Thr	Ser	Gly
			50			55				60					
Pro	Asp	Ala	Ser	Trp	Pro	His	Pro	Arg	Pro	Pro	Leu	Ser	Gly	Gln	Pro
					70				75					80	
Gly	Ser	Ala	Glu	Pro	Gly	Thr	His	Gly							
					85										

<210> 1541

<211> 1482

<212> DNA

<213> Homo sapiens

<400> 1541

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cccgccgctg ccgcctccga gcagcccgc aggactcttg ctactggaga tgggcccgcg
120
gctatcgcg cgacgggtgc cggcggaccc gtccttgcc ctggacgcgc tgccccggga
180
gctgtgtggt caggtgtga gccacgtgcc ggccaacgtc cttggacacg cgatgcgcgc
240
cagtggtgccc cgcctggcgc gacatagtgg acgggcccac tgggaggctg ctgcaactgg
300
cccgcgaccg cagcgccgag gcccgagcac tctacgcagt ggctcaacgc tgccctgccca
360
acaacgaaga caaagaggag ttcccgctgt gcgccctggc gcgctactga ctgcgcgcgc
420
ccttcggccc caatctcatc ttcaactcct gcggagagca gggcttcaga ggctggaggg
480
tggagcatgg cgggaacggc tgggccatag aaaagaacct aacaccgggt cctggggctc
540
cttcgcagac ctgcttcgtg acctctttcg aatggtgctc caagaggcag cttgtggacc
600
tgggtgatgga aggggtgtgg caggagctgc tggacagcgc ccagatttag atctgtgtgg
660
ctgactggtg gggcgctcga gagaactgcg gctgcgtcta ccagctccgg gtccgccttc
720
tggatgtgta tgaaaaggaa gtggtcaagt tctcagctc acctgacctg gtccttcagt
780
ggactgagag gggctgccga caggtctccc acgtcttcac caactttggc aagggcatcc
840
gctacgtatc ttttgagcag tacgggagag acgtgagttc ctgggtgggg cactatggcg
900
cccttgtgac ccactccagt gtgaggggtca ggatccgctc gtcctagcga ctggactact
960
gcctgacgtt gtcagtcaag accagccttg cagccagggt cagtggctca cacctgtggg
1020
atccctccca tttggccttc caaaatgttg cgattatagg cgtgagccac tgtggctggc
1080
ctgaaatttt ctagtatcca cattcataaa gtaaaaagaa aataaaaagg catagaatgt
1140
caagctaacc aggcgtccgc tacttcagaa gagtgtactg tcgcatgggg agtctgtaac
1200
catgcttttc acttcactg catctctcgc tggctcaaaa cagcacaggt gtgtccattg
1260
gacaacagag agtgggaatt ccaaaagtat gggcactagg aaaagacttc ttccatcaag
1320
cttaattgtt ttgttattca tttaatgact ttccctgctg ttacctaat acaaattgga
1380
tggaaactgt tttttttctg ctttgttttt tcagtttgtg gtttctgtag ccatattgta
1440
ttctgtgtca aataaagtcc agttggattc tggaaaaaaa aa
1482

<210> 1542

<211> 57

<212> PRT

<213> Homo sapiens

<400> 1542

Lys Gly Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu
 1 5 10 15
 Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His Phe His Cys
 20 25 30
 Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg
 35 40 45
 Glu Trp Glu Phe Gln Lys Tyr Gly His
 50 55

<210> 1543

<211> 311

<212> DNA

<213> Homo sapiens

<400> 1543

gctagcgatg ctactttaag gtatgcgaag ttggatgctg acgttgccct ctatcggttg
 60
 gagtcaaacg gacgaacaag cgctcgaggt agctttaaat gcggcgacg ccagaaaagt
 120
 accaaagtgc gtgcgcgcgc ttatgtttct cgaatggctc acgcgcgcgag gctacttgct
 180
 ccacgggctcg agccgagccg acctcgcttg ttttgaacct cgagcaccca aagacttcag
 240
 ccctgacgag ttcagcaaac gcaccgcctg tttcgctctc tcagatgggg tgtggccccc
 300
 cncncncnc c
 311

<210> 1544

<211> 96

<212> PRT

<213> Homo sapiens

<400> 1544

Met Arg Ser Trp Met Leu Thr Leu Pro Pro Ile Gly Trp Ser Gln Thr
 1 5 10 15
 Asp Glu Gln Ala Phe Glu Val Ala Leu Asn Ala Gly Asp Ala Arg Lys
 20 25 30
 Leu Pro Lys Ser Val Pro Arg Leu Met Phe Leu Glu Trp Leu Thr Arg
 35 40 45
 Arg Gly Tyr Leu Leu His Gly Ser Ser Arg Ala Asp Leu Val Cys Phe
 50 55 60
 Glu Pro Arg Ala Pro Lys Asp Phe Ser Pro Asp Glu Phe Ser Lys Arg
 65 70 75 80
 Thr Ala Val Phe Ala Ser Ser Asp Gly Val Trp Pro Pro Xaa Xaa Xaa
 85 90 95

<210> 1545

<211> 362

<212> DNA

<213> Homo sapiens

<400> 1545
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 60
 caacagtagt tggcgaatcc ttcgatggtc aagtcctgtg agcttgctca tctgacggat
 120
 cgtctctgtc tcaagcacct cgctgtttc caggttcaag gcctggatag tgcgagtgct
 180
 gtactgggtc atcacttcca ccgagtggtc tgggtagccc ctggccattc gctttatgat
 240
 ctcaaccata gatgcatttg gcatgttcca gagcttgtag tccttaacga tctctctggc
 300
 gtcgtagaaa accttcacgc tatcgtcagg atgggtcact gtgggtgatgt accgtccaga
 360
 ac
 362

<210> 1546

<211> 92

<212> PRT

<213> Homo sapiens

<400> 1546

Met	Val	Lys	Ser	Cys	Glu	Leu	Ala	His	Leu	Thr	Asp	Arg	Leu	Cys	Leu
1				5					10				15		
Lys	His	Leu	Ala	Cys	Phe	Gln	Val	Gln	Gly	Leu	Asp	Ser	Ala	Ser	Val
			20					25					30		
Val	Leu	Val	Asp	His	Phe	His	Arg	Val	Val	Trp	Val	Ala	Pro	Cys	His
	35						40				45				
Ser	Leu	Tyr	Asp	Leu	Asn	His	Arg	Cys	Ile	Trp	His	Val	Pro	Glu	Leu
	50					55					60				
Val	Leu	Leu	Asn	Asp	Leu	Ser	Gly	Val	Val	Glu	Asn	Leu	His	Ala	Ile
65			70						75						80
Val	Arg	Met	Gly	His	Cys	Gly	Asp	Val	Pro	Ser	Arg				
				85					90						

<210> 1547

<211> 429

<212> DNA

<213> Homo sapiens

<400> 1547

cgcggttgcca caccgaaga cccggccagc tcacgcctgg gtgaaagttt ctgggcgttc
 60
 ctgcgcgcgtt cggtgtgggt cagcgccgtg tcggcgtgga acctggagcg cgagcgccgtg
 120
 cgcaaacctg gcctgccggc ctggcactgg aagaacgccg tgctcagtgc ctggatgtac
 180
 agcgttggtg tgtggggggg gatgattgtc tggttggggc cggcggtgat tccgttcctg
 240
 atcattcagg gtgtctacgg gttctcgttg ctggaagtgg tcaactacgt cgagcactac
 300
 gggcttaaac gccagaagt gcccaacggg cggttatgaac ggtgttcgcc tcggcactcg
 360

tggaacagca accggattgt caccaatatc tttctgttcc aacttcagcg gcattccgac
420

caccatgcc

429

<210> 1548

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1548

Arg Val Ala Thr Pro Glu Asp Pro Ala Ser Ser Arg Leu Gly Glu Ser
1 5 10 15

Phe Trp Ala Phe Leu Pro Arg Ser Val Trp Phe Ser Ala Val Ser Ala
20 25 30

Trp Asn Leu Glu Arg Glu Arg Leu Arg Lys Leu Gly Leu Pro Ala Trp
35 40 45

His Trp Lys Asn Ala Val Leu Ser Ala Trp Met Tyr Ser Val Val Leu
50 55 60

Trp Gly Val Met Ile Val Trp Leu Gly Ala Ala Val Ile Pro Phe Leu
65 70 75 80

Ile Ile Gln Gly Val Tyr Gly Phe Ser Leu Leu Glu Val Val Asn Tyr
85 90 95

Val Glu His Tyr Gly Leu Lys Arg Gln Lys Leu Pro Asn Gly Arg Tyr
100 105 110

Glu Arg Cys Ser Pro Arg His Ser Trp Asn Ser Asn Arg Ile Val Thr
115 120 125

Asn Ile Phe Leu Phe Gln Leu Gln Arg His Ser Asp His His Ala
130 135 140

<210> 1549

<211> 443

<212> DNA

<213> Homo sapiens

<400> 1549

gtcgacaggc tccagggttc tgttttgtag tgcaccgcgt gtggtgcaac atgcgtctgg
60

gcacaccaggc gtcgcccgtt tctctgttga gtctttcttc tctgactcca ggggtattgg
120

gtctttctgc cagcgcccat gcaactttgg cagcctggcc tgtctgtctgg taagtggggc
180

agaatccctg cactccacca ttcttgggca acaactccctc taggattttg gtctcccttt
240

tctctctggt ctttgaccac cgctaccagc caaactccctc catctagacc agccagcatt
300

ggttttcttc actccccag ctgcgcgctg ggaggcgcca ctgcaaaact ccctgggggc
360

tcccagctgc tcagagatcc ccatgccctt cctgatcag ctccctgccc gggtctcatc
420

ccgacgcggc tgcattgata ttc
443

<210> 1550

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1550

```

Met Arg Thr Gly Gln Gly Ala Asp Gln Gly Arg Ala Trp Gly Ser Leu
 1           5           10
Ser Ser Trp Glu Thr Pro Gly Lys Phe Ala Val Ala Pro Pro Thr Arg
          20           25           30
Gln Leu Gly Glu Trp Lys Lys Pro Met Leu Ala Gly Leu Asp Gly Gly
          35           40           45
Val Cys Trp Val Ala Val Val Lys Asp Gln Arg Glu Lys Gly Asp Gln
          50           55           60
Asn Pro Arg Gly Ser Val Ala Gln Glu Trp Trp Ser Ala Gly Ile Leu
65           70           75           80
Pro His Leu Pro Ala Asp Arg Pro Gly Cys Gln Ser Cys Met Gly Ala
          85           90           95
Gly Arg Lys Thr Gln Tyr Pro Trp Ser Gln Arg Gly Lys Thr Thr Thr
          100          105          110
Gly Asn Gly Arg Arg Trp Cys Ala Gln Thr His Val Ala Pro Gln Arg
          115          120          125
Val His Tyr Lys Thr Glu Pro Trp Ser Leu Ser
          130          135

```

<210> 1551

<211> 306

<212> DNA

<213> Homo sapiens

<400> 1551

```

ccatgggatac cccacctctg gcaactcaaca tgacttggct gccacacacc aggaaacctc
60
agaggagcag ccagctggcc aagcaccctt gcccttgccc tgcgggctcc acaaaagctg
120
gaggagcaaa cgcagctcac ctctttttct gtccactgct tcagggccta ccctgtgct
180
ttggagatgg aacaaaagtg agagagctcc ctgacacacc ctcccagggc gaggatggca
240
gtcctctcct ccatttggtc ctaacacagc ctccccagga gaccaggggc atccnnnnn
300
cccnnc
306

```

<210> 1552

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1552

```

Met Asp Thr Pro Pro Leu Ala Leu Asn Met Thr Trp Leu Pro His Thr
 1           5           10           15
Arg Lys Pro Gln Arg Ser Ser Gln Leu Ala Lys His Pro Cys Pro Cys
          20           25           30
Pro Ala Gly Ser Thr Lys Ala Gly Gly Ala Asn Ala Ala His Leu Phe

```

```

          35              40              45
Phe Cys Pro Leu Leu Gln Gly Leu Pro Leu Cys Phe Gly Asp Gly Thr
  50              55              60
Lys Val Arg Glu Leu Pro Asp Thr Pro Ser Gln Gly Glu Asp Gly Ser
  65              70              75              80
Ser Phe Leu His Leu Val Leu Thr Gln Pro Pro Gln Glu Thr Arg Gly
          85              90              95
Ile Pro Xaa Pro Xaa
          100

```

<210> 1553

<211> 657

<212> DNA

<213> Homo sapiens

<400> 1553

```

atcctgcaga atgatggcgt ggtcaccagc ccctattccc gccacgcaa ggcgggccac
60
acgctactca tcctgggggg ccagaccttc atgtgtgaca agatctacca ggtggaccac
120
aaggccaagg agatcatccc caaggccgac ctgcccagcc cccggaagga gttcagcgcc
180
tcagcgatcg gctgcaaggt ctatgtgacg gggggcaggg gctccgagaa cgggggtctcc
240
aaggatgtct ggggtgtacga caccgtacat gaggaatggt ccaaggcggc gccctgctg
300
attgcccgcg ttggccatgg ctacgctgag ctggagaact gcctctatgt ggtgggggga
360
cacacatccc tggcaggggt cttcccggcc tcgccttctg tctccctgaa acaagtggag
420
aaatacgacc ctggggccaa caagtggatg atggtggccc ctttgcgga tggcgtcagc
480
aatgccgacg tgggtgagtgc caagctgaag ctctttgttt ttggaggaac cagcatccac
540
cgggacatgg tgtccaaggt ccagtgtat gaccctcgg agaacagggt gacgatcaag
600
gccgagtgcc ccagccttg gcggtacaca gccgctgccg tcctgggcag ccagatc
657

```

<210> 1554

<211> 219

<212> PRT

<213> Homo sapiens

<400> 1554

```

Ile Leu Gln Asn Asp Gly Val Val Thr Ser Pro Tyr Ser Arg Pro Arg
  1              5              10              15
Lys Ala Gly His Thr Leu Leu Ile Leu Gly Gly Gln Thr Phe Met Cys
          20              25              30
Asp Lys Ile Tyr Gln Val Asp His Lys Ala Lys Glu Ile Ile Pro Lys
          35              40              45
Ala Asp Leu Pro Ser Pro Arg Lys Glu Phe Ser Ala Ser Ala Ile Gly
          50              55              60
Cys Lys Val Tyr Val Thr Gly Gly Arg Gly Ser Glu Asn Gly Val Ser

```

```

65          70          75          80
Lys Asp Val Trp Val Tyr Asp Thr Val His Glu Glu Trp Ser Lys Ala
      85          90          95
Ala Pro Met Leu Ile Ala Arg Phe Gly His Gly Ser Ala Glu Leu Glu
      100          105          110
Asn Cys Leu Tyr Val Val Gly Gly His Thr Ser Leu Ala Gly Val Phe
      115          120          125
Pro Ala Ser Pro Ser Val Ser Leu Lys Gln Val Glu Lys Tyr Asp Pro
      130          135          140
Gly Ala Asn Lys Trp Met Met Val Ala Pro Leu Arg Asp Gly Val Ser
145          150          155          160
Asn Ala Ala Val Val Ser Ala Lys Leu Lys Leu Phe Val Phe Gly Gly
      165          170          175
Thr Ser Ile His Arg Asp Met Val Ser Lys Val Gln Cys Tyr Asp Pro
      180          185          190
Ser Glu Asn Arg Trp Thr Ile Lys Ala Glu Cys Pro Gln Pro Trp Arg
      195          200          205
Tyr Thr Ala Ala Ala Val Leu Gly Ser Gln Ile
      210          215

```

<210> 1555

<211> 328

<212> DNA

<213> Homo sapiens

<400> 1555

```

acgcgtggga gctcgggaga gaggactctg cttctggggg ttgaagggtga gcgtgattct
60
ggaggagcct gccttcgggc gagcgtgtgt tgtggagagg atgcaggaca tgagtgatcc
120
tgtaagggtg atcagagtgtg cctcgtgaag tctggaagtc agcagagtgtg ggccgtggag
180
gtgagccacc ggtttgtgat ttgaaactga gtgagagtgc tgtggagcgc gaaatatgtg
240
tgtgtgtaga gtggagggtga gcgaatttgt gtgcatgtga gacggacgca atggcagagt
300
gtagcatcct gtgttgggat tgggattn
328

```

<210> 1556

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1556

```

Met Leu His Ser Ala Ile Ala Ser Val Ser His Ala His Lys Phe Ala
1          5          10          15
His Leu His Ser Thr His Thr His Ile Ser Arg Ser Thr Ala Leu Ser
      20          25          30
Leu Ser Phe Lys Ser Gln Thr Gly Gly Ser Pro Pro Arg Pro Thr Leu
      35          40          45
Ala Asp Phe Gln Thr Ser Arg Gly Thr Leu Asp His Pro Tyr Arg Ile
      50          55          60
Thr His Val Leu His Pro Leu His Asn Thr Arg Ser Pro Gln Gly Arg

```

```

65              70              75              80
Leu Leu Gln Asn His Ala His Leu Gln Thr Pro Glu Ala Glu Ser Ser
      85              90              95
Leu Pro Ser Ser Ser His Ala
      100

```

```

<210> 1557
<211> 390
<212> DNA
<213> Homo sapiens

```

```

<400> 1557
gtgcacagac ttttcgagcg ggccattaag tggtttacgt ctgggatcgg ctccgctttc
60
tcgcattttt cggatcaggt caaattctgt gctcggcatt gacaggaaat tgacgtgtat
120
cagtcgattc tttgcagtgt ctggacggca ggctgaatag gctgaaagca ggacaactac
180
gaccatgccg caccatgtgg atcgtctacc gttttggcct tgccgccatt gccttgatcg
240
ccctgattgc gctgttcgtg tgccagtacc ggctatcggc caggctggcg cgccggaagc
300
gaagctcgat gggcagcagg cgcattgagga acccggcgcc attgaatcgt gaggcgctgg
360
cggagcgcgg cccgttcaaa tgcgacgcgt
390

```

```

<210> 1558
<211> 114
<212> PRT
<213> Homo sapiens

```

```

<400> 1558
Met Ala Pro Gly Ser Ser Cys Ala Cys Cys Pro Ser Ser Phe Ala Ser
1      5      10      15
Gly Ala Pro Ala Trp Pro Ile Ala Gly Thr Gly Thr Arg Thr Ala Gln
20      25      30
Ser Gly Arg Ser Arg Gln Trp Arg Gln Gly Gln Asn Gly Arg Arg Ser
35      40      45
Thr Trp Cys Gly Met Val Val Val Val Leu Leu Ser Ala Tyr Ser Ala
50      55      60
Cys Arg Pro Asp Thr Ala Lys Asn Arg Leu Ile His Val Asn Phe Leu
65      70      75      80
Ser Met Pro Ser Thr Glu Phe Asp Leu Ile Arg Lys Met Arg Glu Ser
85      90      95
Gly Ala Asp Pro Arg Arg Lys Pro Leu Asn Gly Pro Leu Glu Lys Ser
100      105      110
Val His

```

```

<210> 1559
<211> 556
<212> DNA
<213> Homo sapiens

```

<400> 1559

accggtggcg acggtatcgg tggcgcgctcg atccttgctt cggaatcctt cgctgcagag
 60
 ggtgagtcga agcgacccag cgctccaggtg ggcgacccgt tcatggagaa gctgctcatc
 120
 gagtgcaccc ttgacctctt caacgcgggg gtagttgagg ccttgacagga ttccggtgcc
 180
 gccggaatct cctgtgccac ctccgagctg gccagtgctg gcgacggtgg catgcacgtc
 240
 gagctcgacc gcgttccgct gcgcgacccg aacctcgccc ctgaagagat cctcatgagc
 300
 gagtccccagg agcggatggc cgcggtggtg cgcgccgata agcttgaccg cttcatggag
 360
 atctgcgccc attgggggtgt cgctgccact gtcattggcg aggtcaccga caccggtcga
 420
 cttcacattg attggcaggg cgagcggatt gtcgacgtcg atccgcggac ggttgctcac
 480
 gacggaccgg ttctcgacat gccggccgcc cgtccgtggt ggattgatga gctcaacgag
 540
 aacgacgcta acgctg
 556

<210> 1560

<211> 185

<212> PRT

<213> Homo sapiens

<400> 1560

Thr	Gly	Gly	Asp	Gly	Ile	Gly	Gly	Ala	Ser	Ile	Leu	Ala	Ser	Glu	Ser
1			5					10						15	
Phe	Ala	Ala	Glu	Gly	Glu	Ser	Lys	Arg	Pro	Ser	Val	Gln	Val	Gly	Asp
		20					25						30		
Pro	Phe	Met	Glu	Lys	Leu	Leu	Ile	Glu	Cys	Thr	Leu	Asp	Leu	Phe	Asn
		35				40					45				
Ala	Gly	Val	Val	Glu	Ala	Leu	Gln	Asp	Phe	Gly	Ala	Ala	Gly	Ile	Ser
	50				55						60				
Cys	Ala	Thr	Ser	Glu	Leu	Ala	Ser	Ala	Gly	Asp	Gly	Gly	Met	His	Val
	65				70					75				80	
Glu	Leu	Asp	Arg	Val	Pro	Leu	Arg	Asp	Pro	Asn	Leu	Ala	Pro	Glu	Glu
			85					90						95	
Ile	Leu	Met	Ser	Glu	Ser	Gln	Glu	Arg	Met	Ala	Ala	Val	Val	Arg	Pro
			100					105						110	
Asp	Gln	Leu	Asp	Arg	Phe	Met	Glu	Ile	Cys	Ala	His	Trp	Gly	Val	Ala
		115					120						125		
Ala	Thr	Val	Ile	Gly	Glu	Val	Thr	Asp	Thr	Gly	Arg	Leu	His	Ile	Asp
		130				135					140				
Trp	Gln	Gly	Glu	Arg	Ile	Val	Asp	Val	Asp	Pro	Arg	Thr	Val	Ala	His
				150						155					160
Asp	Gly	Pro	Val	Leu	Asp	Met	Pro	Ala	Ala	Arg	Pro	Trp	Trp	Ile	Asp
				165				170						175	
Glu	Leu	Asn	Glu	Asn	Asp	Ala	Asn	Ala							
				180				185							

<210> 1561
 <211> 466
 <212> DNA
 <213> Homo sapiens

<400> 1561
 acgcgtgaaa ggtttgagag aagagagatg ccgctattga atctgctgga gttttacatc
 60
 ccaagatgaa gacagcattc agaattgatg tgatttcctt gaatgtggct taggaaatgt
 120
 ggacacttaa aactctcact tgaaattggg cacagggttg atgtagagat aaggacgggg
 180
 tgcggaatgg agaccattt tgtcattgat tcattctgacc gataaggcca tagtgcagtt
 240
 aggtgatatt cgaagcttc tttgatgctc tttatgtata tgttgggaagg aactaccagg
 300
 cgttgcttta aattcccaat gtgttggttc gttactacta atttaataacc gtaagctcta
 360
 ggtaaagttc catgttggtg aactctgact gttctctttg gaattgaacg ttttgcattc
 420
 tctcctctgtg gcttttaggtc tgacattgta tttgaccttt actagt
 466

<210> 1562
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 1562
 Met Ser Asp Leu Lys Pro Gln Glu Glu Asp Ala Lys Arg Ser Ile Pro
 1 5 10 15
 Lys Arg Thr Val Arg Val Gln Gln His Gly Thr Leu Pro Arg Ala Tyr
 20 25 30
 Gly Ile Lys Leu Val Val Thr Lys Gln His Ile Gly Asn Leu Lys Gln
 35 40 45
 Arg Leu Val Val Pro Ser Asn Ile Tyr Ile Lys Ser Ile Lys Glu Ala
 50 55 60
 Phe Glu Tyr His Leu Thr Ala Leu Trp Pro Tyr Arg Ser Asp Glu Ser
 65 70 75 80
 Met Thr Lys Trp Val Ser Ile Pro His Pro Val Leu Ile Ser Thr Ser
 85 90 95
 Asn Leu Cys Pro Ile Ser Ser Glu Ser Phe Lys Cys Pro His Phe Leu
 100 105 110
 Ser His Ile Gln Gly Asn His Ile Asn Ser Glu Cys Cys Leu His Leu
 115 120 125
 Gly Met
 130

<210> 1563
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 1563

ctgggggggtg tgttcggcct gctgtcgggtg tacttgccgc gttggctgca tgaacaccg
 60
 atcttcgctg agatgcagca gcgcaaaacc ctggctgccg agttgccatt gcgcgcggta
 120
 ttgcgtgacc accgtggcgc catcgtgctg tcgatgctgt tgacgtggtt gctgtcggcg
 180
 ggtgtggttg tggatcatcct gatgaccccg accgtgtgtc aaaccgtcta ccacttcagc
 240
 ccgagcggtg cgctgcaagc caacagcctg gcgatcgta cgctgagcct gggctgcatt
 300
 gcgtccggcg cgctgggtga ccgttttggg gccggtcgcg ttttggtcac cgggtggcgt
 360
 tgctgctggc cacttcctgg acgctgtatc acagcctgat ggcccgagcg gaatgggtga
 420
 ataagtgtac gcgt
 434

<210> 1564

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1564

Leu	Gly	Gly	Val	Phe	Gly	Leu	Leu	Ser	Val	Tyr	Leu	Pro	Arg	Trp	Leu
1				5					10					15	
His	Glu	Thr	Pro	Ile	Phe	Ala	Glu	Met	Gln	Gln	Arg	Lys	Thr	Leu	Ala
			20					25					30		
Ala	Glu	Leu	Pro	Leu	Arg	Ala	Val	Leu	Arg	Asp	His	Arg	Gly	Ala	Ile
		35					40					45			
Val	Leu	Ser	Met	Leu	Leu	Thr	Trp	Leu	Leu	Ser	Ala	Gly	Val	Val	Val
		50				55				60					
Val	Ile	Leu	Met	Thr	Pro	Thr	Val	Leu	Gln	Thr	Val	Tyr	His	Phe	Ser
65				70					75					80	
Pro	Thr	Val	Ala	Leu	Gln	Ala	Asn	Ser	Leu	Ala	Ile	Val	Thr	Leu	Ser
			85				90							95	
Leu	Gly	Cys	Ile	Ala	Ser	Gly	Ala	Leu	Ala	Asp	Arg	Phe	Gly	Ala	Gly
		100					105						110		
Arg	Val	Leu	Val	Thr	Gly	Trp	Arg	Cys	Cys	Trp	Pro	Leu	Pro	Gly	Arg
		115				120					125				
Cys	Ile	Thr	Ala												
		130													

<210> 1565

<211> 373

<212> DNA

<213> Homo sapiens

<400> 1565

ccatggctgt agcccttggt tcaacaagag ccgtctactg acgctaacc accatgagcc
 60
 agagggtgag cggttctggc acctactgga ccataaaagc aataaagagg acaaggaggc
 120
 ctgcattcgg ccatttcttc ccaagaatca ccataaaggt tgtcaaaatc aaggaccctg
 180

atccggtgat tctcgaagtc atcgatgagc agaacaagtt tacccccgag ggagaaaaagc
 240
 gggtggtgct cttgatgctc gacaacctct accgtcccag taccacacct gcattggcga
 300
 acggggggcgt cccttatctg cggtcgaaga gtgtcactgt tgacctcgta gacagccggg
 360
 acaacacggg tac
 373

<210> 1566

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1566

Met	Ser	Gln	Arg	Val	Ser	Gly	Ser	Gly	Thr	Tyr	Trp	Thr	Met	Lys	Ala
1				5					10					15	
Ile	Lys	Arg	Thr	Arg	Glu	Pro	Ala	Phe	Gly	His	Phe	Phe	Pro	Arg	Ile
			20					25					30		
Thr	Ile	Lys	Val	Val	Lys	Ile	Lys	Asp	Pro	Asp	Pro	Val	Ile	Leu	Glu
		35					40					45			
Val	Ile	Asp	Glu	Gln	Asn	Lys	Phe	Thr	Pro	Glu	Gly	Glu	Lys	Arg	Val
	50				55					60					
Val	Leu	Leu	Met	Leu	Asp	Asn	Leu	Tyr	Arg	Pro	Ser	Thr	His	Arg	Ala
65				70					75					80	
Leu	Ala	Asn	Gly	Gly	Val	Pro	Tyr	Leu	Arg	Ser	Lys	Ser	Val	Thr	Val
			85					90					95		
Asp	Leu	Val	Asp	Ser	Arg	Asp	Asn	Thr	Gly						
			100					105							

<210> 1567

<211> 917

<212> DNA

<213> Homo sapiens

<400> 1567

agcttttttcg accgctgaag gagtgggata cccgctcccc agacactccc tttctagggg
 60
 aagccgctgc actcctgggg gaccagttt gatgcctcca ggaggataag tctgaagccg
 120
 ggttggaag ggagcggaga ggcccaaaca gacgagcagg cagcgccctc tgetggcacc
 180
 ctggagacag cttcggtctg ggggccctcg cttctagtc ctcgccagct ttcaggacac
 240
 cttgacaacc tggggctcct gcagaagtgg cccggctgtc cccaagtct cctgaagcta
 300
 tctgggttagg gtgggaggca gtgctgtgag ccacaaatgc aaagcagagg ggacagatgt
 360
 tgggactcaa agacatgagg tagagctggc cccatgggta ggtgccacca ccagagccca
 420
 tgaggcttcg tgttctagaa ggtggtgggt tagtgccgca ctgagggcgt gtccggggag
 480
 gagcatgtgt caccagggtc caggaaacag catgagtcac gacgcggggg tgtttaaggc
 540

attcgtgccca cagcgggggac ctccggagcta tgccttgata aggcaagtga ggttacatgt
 600
 acgatgatgc ggtttgtgct gcagactgga aaaaagcagg ggctttgtcc tctcctgacc
 660
 ccctcacact ctgccttcac ggtaggctcc tgagaggggg gtctccaagg aggggtgtcag
 720
 tactgcagct tcagctggcg tggatgggggt gcttacagga gcagcagggc tgaggagat
 780
 gacagcagta cgaatctggt ctctcctgag gcctgggttt cctcatatgt aaaatggggg
 840
 ttgcattaga ccataccctt ggctgtgtt taggcaaata gggatgaaag tggggccaag
 900
 ggctgaagag ctgggtc
 917

<210> 1568

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1568

Met	Gly	Pro	Ala	Leu	Pro	His	Val	Phe	Glu	Ser	Gln	His	Leu	Ser	Pro
1			5						10				15		
Leu	Leu	Cys	Ile	Cys	Gly	Ser	Gln	His	Cys	Leu	Pro	Pro	Tyr	Pro	Asp
			20				25						30		
Ser	Phe	Arg	Arg	Leu	Gly	Gly	Gln	Pro	Gly	His	Phe	Cys	Arg	Asp	Pro
		35					40				45				
Arg	Leu	Ser	Arg	Cys	Pro	Glu	Ser	Trp	Gly	Gly	Leu	Glu	Gly	Arg	Gly
	50					55					60				
Pro	Ala	Ala	Glu	Ala	Val	Ser	Arg	Val	Pro	Ala	Glu	Gly	Ala	Ala	Cys
	65				70					75				80	
Cys	Ser	Val	Trp	Ala	Ser	Pro	Leu	Pro	Ser	Gln	Pro	Gly	Phe	Arg	Leu
			85						90					95	
Ile	Leu	Leu	Glu	Ala	Ser	Asn	Trp	Val	Pro	Gln	Glu	Cys	Ser	Gly	Phe
			100					105						110	

Pro

<210> 1569

<211> 379

<212> DNA

<213> Homo sapiens

<400> 1569

ggagggcctg tgattctact gcaggcagcg acccccaca acctcacatg ccgggccttc
 60
 aatgcgaagc ctgctgccac catcatctgg ttccgggacg ggacgcagca ggaggcgct
 120
 gtggccagca cggaattgct gaaggatggg aagagggaga ccacctgag ccaactgctt
 180
 attaacccca cggacctgga catagggcgt gtcttcactt gccgaagcat gaacgaagcc
 240
 atccctagtg gcaaggagac ttccatcgag ctggatgtgc accaccctcc tacagtgacc
 300

ctgtccattg agccacagac ggtgcaggag ggtgagcgtg ttgtctttac ctgccaggcc
 360
 acagccaacc cggagatctt
 379

<210> 1570

<211> 126

<212> PRT

<213> Homo sapiens

<400> 1570

Gly	Gly	Pro	Val	Ile	Leu	Leu	Gln	Ala	Gly	Thr	Pro	His	Asn	Leu	Thr
1			5						10				15		
Cys	Arg	Ala	Phe	Asn	Ala	Lys	Pro	Ala	Ala	Thr	Ile	Ile	Trp	Phe	Arg
		20						25					30		
Asp	Gly	Thr	Gln	Gln	Glu	Gly	Ala	Val	Ala	Ser	Thr	Glu	Leu	Leu	Lys
		35				40						45			
Asp	Gly	Lys	Arg	Glu	Thr	Thr	Val	Ser	Gln	Leu	Leu	Ile	Asn	Pro	Thr
	50				55					60					
Asp	Leu	Asp	Ile	Gly	Arg	Val	Phe	Thr	Cys	Arg	Ser	Met	Asn	Glu	Ala
	65				70				75				80		
Ile	Pro	Ser	Gly	Lys	Glu	Thr	Ser	Ile	Glu	Leu	Asp	Val	His	His	Pro
			85						90				95		
Pro	Thr	Val	Thr	Leu	Ser	Ile	Glu	Pro	Gln	Thr	Val	Gln	Glu	Gly	Glu
			100				105						110		
Arg	Val	Val	Phe	Thr	Cys	Gln	Ala	Thr	Ala	Asn	Pro	Glu	Ile		
		115					120					125			

<210> 1571

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1571

tgcgcacttt tccgctcccg atgggtccccc tggncgttga tcatgcccca gatgttcattc
 60
 atcggcatct tcttcttctt gccaaagcggc caagccgtgc tccagctctt ccagatggaa
 120
 gatcggttcg gcattgtcgac cgaatgggtc ggattggaca acttcgcgaa cctgctggat
 180
 gaccccaact acctgaattc cttccagcgc accgcccgtgt tctcgtgtgt ggtggcaggg
 240
 gtcgggatcg ccgtgtcact ggggtctggcg atctttgccc accccatcac tccgtgcgca
 300
 tgtgtacaag acacactgct gatcgtgccc taecgcccgtgg caccatgat cgccggc
 357

<210> 1572

<211> 119

<212> PRT

<213> Homo sapiens

<400> 1572

Cys Ala Leu Phe Arg Ser Arg Trp Val Pro Trp Xaa Leu Ile Met Pro

```

      1             5             10             15
Gln Met Phe Ile Ile Gly Ile Phe Phe Phe Leu Pro Ser Gly Gln Ala
      20             25             30
Val Leu Gln Ser Phe Gln Met Glu Asp Ala Phe Gly Met Ser Thr Glu
      35             40             45
Trp Val Gly Leu Asp Asn Phe Arg Asn Leu Leu Asp Asp Pro Thr Tyr
      50             55             60
Leu Asn Ser Phe Gln Arg Thr Ala Val Phe Ser Val Leu Val Ala Gly
      65             70             75             80
Val Gly Ile Ala Val Ser Leu Gly Leu Ala Ile Phe Ala Asp Pro Ile
      85             90             95
Thr Pro Ser Pro Cys Val Gln Asp Thr Leu Leu Ile Val Pro Tyr Ala
      100             105             110
Val Ala Pro Met Ile Ala Gly
      115

```

<210> 1573

<211> 337

<212> DNA

<213> Homo sapiens

<400> 1573

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gaattcccat tgctatctga ttccatgtct ggaaagaggg aagagagaca tcattgcagaa
60
tattgtacag attttggaaat cgggtacagtt gaaatgggaa ctttttcaga gctggacaga
120
cttttcaagg ctccatcttt ctaataaaact ggccattttt ggaattggtt ataacaccgg
180
ttggaaaagag gatatccgtt accattatgc tgagatcagc tcccaggtgc cccttggtcaa
240
gcgacttcgg gagtacttca actctgagaa gcctgaagga cggatcatta tgaccgcaggt
300
gcagaaaatg aactggaaaa atgtttacta caaatatt
337

```

<210> 1574

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1574

```

Met Gln Asn Ile Val Gln Ile Leu Glu Ser Val Gln Leu Lys Trp Glu
      1             5             10             15
Leu Phe Gln Ser Trp Thr Asp Phe Ser Arg Leu His Leu Ser Asn Lys
      20             25             30
Leu Ala Ile Phe Gly Ile Gly Tyr Asn Thr Arg Trp Lys Glu Asp Ile
      35             40             45
Arg Tyr His Tyr Ala Glu Ile Ser Ser Gln Val Pro Leu Gly Lys Arg
      50             55             60
Leu Arg Glu Tyr Phe Asn Ser Glu Lys Pro Glu Gly Arg Ile Ile Met
      65             70             75             80
Thr Arg Val Gln Lys Met Asn Trp Lys Asn Val Tyr Tyr Lys Phe
      85             90             95

```

<210> 1575
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 1575
 nnacgcgtca gagagatctg tgtgtcggga ggggtgcccc tcatcattga tgaccgcgta
 60
 catctcgttg ccgaaattgg ggccgatggt gtccatgttg ggcagctga catgccggtc
 120
 gaccaggccc gtgcgattct gggcgacgat ctactcatcg gcttgtccgc tcagactccc
 180
 gcccatgttg aggccgccct gtcccagggg cgtgacatcg tcgactatct gggagttggg
 240
 gccctgcatg gtactggaac caaacctgag gctggggagc tcggcctggc tgagattcgt
 300
 gatgtcgtca acgccagccc gtggccggtg tgcgtcatcg gtggggtgag cgcattccgat
 360
 gctcaagacg tagcccggtt gggatgtgac ggcctgagcg tcgtctcggc gatttgccgg
 420
 agtaccgacc ccaagtccag tgcacgggaa cttgcggagg cgtggcgctac g
 471

<210> 1576
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 1576
 Xaa Arg Val Arg Glu Ile Cys Val Ser Gly Gly Val Pro Leu Ile Ile
 1 5 10 15
 Asp Asp Arg Val His Leu Val Ala Glu Ile Gly Ala Asp Gly Val His
 20 25 30
 Val Gly Gln Ser Asp Met Pro Val Asp Gln Ala Arg Ala Ile Leu Gly
 35 40 45
 Asp Asp Leu Leu Ile Gly Leu Ser Ala Gln Thr Pro Ala His Val Glu
 50 55 60
 Ala Ala Leu Ser Gln Gly Arg Asp Ile Val Asp Tyr Leu Gly Val Gly
 65 70 75 80
 Ala Leu His Gly Thr Gly Thr Lys Pro Glu Ala Gly Glu Leu Gly Leu
 85 90 95
 Ala Glu Ile Arg Asp Val Val Asn Ala Ser Pro Trp Pro Val Cys Val
 100 105 110
 Ile Gly Gly Val Ser Ala Ser Asp Ala Gln Asp Val Ala Arg Val Gly
 115 120 125
 Cys Asp Gly Leu Ser Val Val Ser Ala Ile Cys Arg Ser Thr Asp Pro
 130 135 140
 Lys Ser Ser Ala Arg Glu Leu Ala Glu Ala Trp Arg Thr
 145 150 155

<210> 1577
 <211> 287
 <212> DNA
 <213> Homo sapiens

<400> 1577

ctcgtctccc agcgtccgat cagtgcgctc aggatgctga tcggcgggccc cttgcgcatc
 60
 ccccatcctg cgggcttgcg cacggttgcg ctggaacccg gcgtcgcgca cgcgcgcacc
 120
 ttgcgcgttg ccggggcagg cttccccgct cgcggccagc gcgcgcgcgg cgatctgggtg
 180
 atcgagctgg agccgatgct gccgcaggcg cccgacaagc aactgcacgc gctgatcgag
 240
 cagctcgacg tggcgctcgg gaagagcgcg acacgccatt ttccgga
 287

<210> 1578

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1578

Leu Val Leu Gln Arg Pro Ile Ser Ala Leu Arg Met Leu Ile Gly Gly
 1 5 10 15
 Pro Leu Arg Ile Pro His Pro Ala Gly Leu Arg Thr Val Ala Leu Glu
 20 25 30
 Pro Gly Val Ala His Ala Arg Thr Leu Arg Val Ala Gly Ala Gly Phe
 35 40 45
 Pro Ala Arg Gly Gln Arg Ala Ala Gly Asp Leu Val Ile Glu Leu Glu
 50 55 60
 Pro Met Leu Pro Gln Ala Pro Asp Lys Gln Leu His Ala Leu Ile Glu
 65 70 75 80
 Gln Leu Asp Val Ala Leu Gly Lys Ser Ala Thr Arg His Phe Pro
 85 90 95

<210> 1579

<211> 2829

<212> DNA

<213> Homo sapiens

<400> 1579

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 120
 ggggcggggg ggagccccgg cagtccgggg tcgcccgcga gggccatgtc gctgttgggg
 180
 gacccgctac aggccttgcc gccctcgggc gccccacgg ggccgctgct cgcccttcgg
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 gccggcgcca cctcaaccg cctcggggag cogetgctgc ggaggtctag cgagctcctg
 300
 gatcaggcgc ccgagggcgg gggctggagg agactggcgg agctggcggg gagtcgggg
 360
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540
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720
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1140
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1380
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1980
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2040
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2100

gcaataaag gcacacctga agaaactggc agctacttgg tatcaaagga tcttccaag
 2160
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 2220
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 2280
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 2340
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 2520
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 2580
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 2640
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 2700
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 2820
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 2829

<210> 1580

<211> 824

<212> PRT

<213> Homo sapiens

<400> 1580

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala
 1 5 10 15
 Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
 20 25 30
 Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
 35 40 45
 Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg
 50 55 60
 Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
 65 70 75 80
 Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
 85 90 95
 Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
 100 105 110
 Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
 115 120 125
 Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
 130 135 140
 Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
 145 150 155 160
 Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile

```

165      170      175
Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
180      185      190
Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
195      200      205
Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
210      215      220
Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225      230      235      240
Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
245      250      255
His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
260      265      270
Lys Leu Tyr Met Val Pro Tyr Ala Asp Leu Glu His Gln Thr Tyr
275      280      285
Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
290      295      300
Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305      310      315      320
Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
325      330      335
Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
340      345      350
Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
355      360      365
Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
370      375      380
Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385      390      395      400
Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
405      410      415
Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
420      425      430
Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
435      440      445
Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
450      455      460
Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465      470      475      480
Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
485      490      495
Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
500      505      510
Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
515      520      525
Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
530      535      540
Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545      550      555
Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565      570      575
Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580      585      590
Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Glu Phe

```

```

          595                600                605
Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
  610                615                620
Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
  625                630                635
Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
          645                650                655
Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
          660                665                670
Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
          675                680                685
Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
          690                695                700
Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Thr Met His Arg Gly
  705                710                715                720
Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
          725                730                735
Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
          740                745                750
Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
          755                760                765
Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
          770                775                780
Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
  785                790                795                800
Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
          805                810                815
Asp Arg Leu Arg Ile Ser Glu Lys
          820

```

<210> 1581

<211> 426

<212> DNA

<213> Homo sapiens

<400> 1581

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gatccgcac gcccgcttat tgacgagggtg accttcaccc gagagggcca tacctatcac
  60
cggggtgccc aggtggctga cgcttggtc gattcgggct cgatgccctt cgccagtggtg
  120
ggataccgcg atgtgcccgg ttcgaaggag aagttcagat ccactaccc gggtgacttc
  180
atctgtgagg ccatcgacca gaccgcggg tggttttaca ccatgatggc cgtcggaacc
  240
ctgggtgttt acgagtcctc gtaccgcaat gtgctgtgtc tgggccacat cttggccgag
  300
gacgggtcgca agatgagcaa gcaccttggc aacatcctgt tgccatcccc gctcatggat
  360
tcccacgggt cgcacgcgct gcgttggttc atggcgccgc acggctcccc atggagtgcg
  420
cgacgc
  426

```

<210> 1582

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1582

```

Asp Pro His Arg Pro Phe Ile Asp Glu Val Thr Phe Thr Arg Glu Gly
 1             5             10             15
His Thr Tyr His Arg Val Pro Glu Val Ala Asp Ala Trp Leu Asp Ser
      20             25             30
Gly Ser Met Pro Phe Ala Gln Trp Gly Tyr Pro His Val Pro Gly Ser
      35             40             45
Lys Glu Lys Phe Glu Ser His Tyr Pro Gly Asp Phe Ile Cys Glu Ala
      50             55             60
Ile Asp Gln Thr Arg Gly Trp Phe Tyr Thr Met Ala Val Gly Thr
      65             70             75             80
Leu Val Phe Asp Glu Ser Ser Tyr Arg Asn Val Leu Cys Leu Gly His
      85             90             95
Ile Leu Ala Glu Asp Gly Arg Lys Met Ser Lys His Leu Gly Asn Ile
      100            105            110
Leu Leu Pro Ile Pro Leu Met Asp Ser His Gly Ala Asp Ala Leu Arg
      115            120            125
Trp Phe Met Ala Ala Asp Gly Ser Pro Trp Ser Ala Arg Arg
      130            135            140

```

<210> 1583

<211> 450

<212> DNA

<213> Homo sapiens

<400> 1583

```

nnacgcgtga agggttatgg agatggttca gggagtaagg aaggtttcag ggaatgggtta
60
ggggggttctg aggaatatgg gtcaatggat gaggcagggt ataggaagga tttgggggct
120
cctaaggga taggttcagg gagtaaggca ggtttcaggg atggtttagg gagttctggg
180
gaaatgggggt caatggatga ggcagattat aggaaggatt tgggagctcc tgaggaaatg
240
ggttcaggca gttacacaga ttacaggaat ggtttaggca gttctggaaa aatcagttca
300
gggggatgagg caggttataa gaatgtttta ggggggtctg ggaggaatcc attaggggag
360
gaggcagggt ctaggggtag ttggaggat tctgggtaca tcttgtcatg gaatgaggca
420
ggtttcaggc aaggctttgg gggaactagt
450

```

<210> 1584

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1584

```

Xaa Arg Val Lys Gly Tyr Gly Asp Gly Ser Gly Ser Lys Glu Gly Phe

```

```

      1             5             10             15
Arg Asp Gly Leu Gly Gly Ser Glu Glu Met Gly Ser Met Asp Glu Ala
      20             25             30
Gly Tyr Arg Lys Asp Leu Gly Ala Pro Lys Gly Ile Gly Ser Gly Ser
      35             40             45
Lys Ala Gly Phe Arg Asp Gly Leu Gly Ser Ser Gly Glu Met Gly Ser
      50             55             60
Met Asp Glu Ala Asp Tyr Arg Lys Asp Leu Gly Ala Pro Glu Glu Met
      65             70             75             80
Gly Ser Gly Ser Tyr Thr Asp Tyr Arg Asn Gly Leu Gly Ser Ser Gly
      85             90             95
Lys Ile Ser Ser Gly Asp Glu Ala Gly Tyr Lys Asn Val Leu Gly Gly
      100            105            110
Ser Gly Arg Asn Pro Leu Gly Ser Glu Ala Gly Ser Arg Gly Ser Leu
      115            120            125
Glu Asp Ser Gly Tyr Ile Leu Ser Trp Asn Glu Ala Gly Ser Arg Gln
      130            135            140
Gly Phe Gly Gly Thr Ser
145             150

```

<210> 1585

<211> 596

<212> DNA

<213> Homo sapiens

<400> 1585

```

tgatcatctg taattcttgt ccgtgggcgt ttgaactgag aatgtcttaa gaagtggga
60
tctaataccga gctgctgctg gcaaagttagg gtgaggtctg cacagagtgc gtccatctgt
120
ggcagctgca gggcaagctg gggaggaagc gcagggtggt gcacagggtg catcataatg
180
gaaggaaaga gcggcaggtc cagagaaacc ggcctctccc aaaaagtatt caaacactgg
240
tttagaaata cgcttttttaa ggaacgacag agaaataaag attcaccata caacttcagt
300
aaccttctta taacggtttt agaagatata agaattgata cacagccac ctcttagaa
360
cattacaaat ctgatgcata attcagtaaa aggtcttcta gaacgagatt tactgactac
420
cagcttaggg ttctgcaaga cttttttgac acaaacgctt acccaaaaga tgatgaaata
480
gaacaactct ccactgttct caatctgcct acccggggta ttgtgtatg gttccagaat
540
gctcgtcaga aagcacgaaa gagttatgag aatcaagcag aaaccccttc acgcgt
596

```

<210> 1586

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1586

Met Glu Gly Lys Ser Gly Arg Ser Arg Glu Thr Gly Leu Ser Gln Lys

```

      1           5           10           15
Val Ile Lys His Trp Phe Arg Asn Thr Leu Phe Lys Glu Arg Gln Arg
      20           25           30
Asn Lys Asp Ser Pro Tyr Asn Phe Ser Asn Pro Pro Ile Thr Val Leu
      35           40           45
Glu Asp Ile Arg Ile Asp Pro Gln Pro Thr Ser Leu Glu His Tyr Lys
      50           55           60
Ser Asp Ala Ser Phe Ser Lys Arg Ser Ser Arg Thr Arg Phe Thr Asp
      65           70           75           80
Tyr Gln Leu Arg Val Leu Gln Asp Phe Phe Asp Thr Asn Ala Tyr Pro
      85           90           95
Lys Asp Asp Glu Ile Glu Gln Leu Ser Thr Val Leu Asn Leu Pro Thr
      100          105          110
Arg Val Ile Val Val Trp Phe Gln Asn Ala Arg Gln Lys Ala Arg Lys
      115          120          125
Ser Tyr Glu Asn Gln Ala Glu Thr Pro Ser Arg
      130          135

```

<210> 1587

<211> 501

<212> DNA

<213> Homo sapiens

<400> 1587

```

tgtacacaca gtgatttggg gtcctttttc ctaaaacagc ttctttatca ggactttgga
60
attctgggtg agatagaaac actgaaaaca gggcggaagt tttttcttct ggcttcttag
120
tccacggagg gctcagcgtg gagaggatat gccgtggcat tctccctggg agaccacaca
180
tgttcccgac agctcagacc ccagaccgca tgtgtcctctg acagctcaga cccagaccg
240
cgcgtgtctc tgacagctca gaccccgagc cgcaggtgct cccgacagct cagaccccg
300
accgcgggtg ctctcgacag ctccagacccc agaccgcgcg tgcctccgac agctcagacc
360
ccagaccgcg ggtgtcctctg acagctcaga cccagaccg cgcgtgtctc cgacagctca
420
gaccccgagc cgcgggtgct cctgacagct cagaccccg accgcgggtg ctctcgacag
480
ctcagacccc agaccgcg t
501

```

<210> 1588

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1588

```

Ser Thr Glu Gly Ser Ala Trp Arg Gly Tyr Ala Val Ala Phe Ser Leu
1           5           10           15
Gly Asp His Thr Cys Ser Arg Gln Leu Arg Pro Gln Thr Ala Cys Ala
20           25           30
Pro Asp Ser Ser Asp Pro Arg Pro Arg Val Leu Leu Thr Ala Gln Thr

```

```

      35              40              45
Pro Asp Arg Arg Cys Ser Arg Gln Leu Arg Pro Gln Thr Ala Gly Ala
  50              55              60
Pro Asp Ser Ser Asp Pro Arg Pro Arg Val Leu Pro Thr Ala Gln Thr
  65              70              75              80
Pro Asp Arg Gly Cys Ser
      85

```

<210> 1589

<211> 407

<212> DNA

<213> Homo sapiens

<400> 1589

```

aagcttgctg gggacaccct ttttacgggg cctcgtgggg gagaggttac ctgcattgac
  60
tccaccgggtt ccactaacgc cgacatggct gctttcgtgc gagcaggggg aacgtctttc
  120
tgcctactcg ttgctgacca ccaagagggc gggcgtggac gggtcacgcg cagttggcag
  180
gatgtccccc gtacgagttt ggcgatctca gcgttggtgc ccaatgatcg tccgtcgcac
  240
gactggggct ggctgctgat gggtgcgggg ctcgctgttg tcaaggtcat caaggaggtc
  300
ggtggggctg accgttcccg agtgacgctg aagtggccca atgatgtgct cgtggatctg
  360
gacactgacc agggcgggcaa agtgtgcgga attctctcag aacgcgt
  407

```

<210> 1590

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1590

```

Lys Leu Ala Gly Asp Thr Leu Phe Thr Gly Pro Arg Gly Gly Val
  1              5              10              15
Thr Cys Ile Asp Ser Thr Gly Ser Thr Asn Ala Asp Met Ala Ala Phe
      20              25              30
Val Arg Ala Gly Gly Thr Ser Phe Cys Leu Leu Val Ala Asp His Gln
      35              40              45
Glu Gly Gly Arg Gly Arg Phe Thr Arg Ser Trp Gln Asp Val Pro Gly
      50              55              60
Thr Ser Leu Ala Ile Ser Ala Leu Val Pro Asn Asp Arg Pro Ser Gln
      65              70              75              80
Asp Trp Gly Trp Leu Ser Met Val Ala Gly Leu Ala Val Val Lys Val
      85              90              95
Ile Lys Glu Val Gly Gly Ala Asp Arg Ser Arg Val Thr Leu Lys Trp
      100             105             110
Pro Asn Asp Val Leu Val Asp Leu Asp Thr Asp Gln Gly Lys Val
      115             120             125
Cys Gly Ile Leu Ser Glu Arg
      130             135

```

<210> 1591

<211> 424

<212> DNA

<213> Homo sapiens

<400> 1591

```

agatctctct ccttgagata acccaggctt tagaaccaaa gagctgagag accctgtccc
60
ttcagagagg cacttgacc tagaggagtc tctgggaagc agatggggat atgggacaga
120
cgcatcttga aaaagcccc agatgctctc ctatggagga cctcaccac ccacatcacc
180
agtagggagc ttgggactta cctaaccac aggggggtga ctgtgtcgt ccctgcacag
240
aacgtccagc gagtcctgac ttccagccg ctgcgcttca tccaggagca cgtcctgatc
300
cctgtctttg acctcagcgg cccagcagc ctggcccagc ctgtccagta ctcccttgac
360
tgtgggatcc ctggctgctc acgcccctga ggaccctcg gatctgctcc agcacgtgaa
420
atctt
424

```

<210> 1592

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1592

```

Met Gly Ile Trp Asp Arg Arg Ile Leu Lys Lys Pro Pro Asp Ala Ser
1 5 10 15
Leu Trp Arg Thr Ser Pro Thr His Ile Thr Ser Arg Glu Leu Gly Thr
20 25 30
Tyr Pro Asn His Arg Gly Val Thr Val Val Val Pro Ala Gln Asn Val
35 40 45
Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln Glu His Val
50 55 60
Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro
65 70 75 80
Val Gln Tyr Ser Leu Asp Cys Gly Ile Pro Gly Cys Ser Arg Pro
85 90 95

```

<210> 1593

<211> 1678

<212> DNA

<213> Homo sapiens

<400> 1593

```

cttgaatcta aaataaatga aataaacaca gaaattaacc agttgattga aaagaaaatg
60
atgagaaatg agcccattga aggcacaaactc tcaactgtata ggcaacaggc atctatcatt
120
tcccgtaaaa aagaagccaa agctgaggaa cttcaggagg ccaaggagaa gttagccagg
180

```


ctagagagag aagcatcagt aaagagaaat cagaccctgt aatttgatgg tactgaagtt
240
ttaaaggagg atgagttcaa acgatatgtc aataaacttc gaagcaagag tacagttttc
300
aaaaagaagc atcacataat agctgaactt aaagctgaat tcggtctttt gcagaggact
360
gaagaacttc ttaagcaacg tcatgaaat attcaacaac aactgcaaac tatggaggag
420
aaaaagggta tatctggata tagttacacc caagaagagc tagaaagagt atctgcactg
480
aagagtgaag ttgatgaaat gaaaggacga acattggatg atatgtctga aatggtgaaa
540
aaactgtatt catttggtatc tgaaaagaag tcagctcttg cctcagttat aaaagagcta
600
cgacagtgc gtcaaaaaa tcaagaactg acccaggagt gtgatgaaaa gaaatcccag
660
tatgatagct gtgcagcagg cctcgaaagc aatcggtcca aattagaaca ggaagttaga
720
agactccgtg aagaatgtct tcaagaagaa agtagatacc attatacaaa ttgtatgatt
780
aagaacctag aagttcaact tcgtcgtgct actgatgaga tgaaggcata tatctcttct
840
gatcaacaag aaaaaagaaa ggcaattagg gaacagtata ccaaaaatac tgctgaacaa
900
gaaaaccttg gaaagaaact tcgggaaaaa caaaaagtta tacgagaaa gtcattgtcca
960
aatatgaac aagcaaaaat gtggcgtgat ttggaacaat taatggaatg taagaacag
1020
tgctttctga aacaacaaag ccaaacttcc attggtcagg taattcagga ggggtgggag
1080
gaccggctaa tactgtgaat tcttgtgtca tcgtttgggg ttttacttga taccactagc
1140
tataagccta atctcataat gtatttcttt tttgaaactg atttgtttag cattttgttt
1200
tcagaagagc cattctttat taagttttca tagaaaataa tgttaaggta gatttagttt
1260
gaatgttttt tcatatgaaa aagaggcttt tattcttttc catagtttag acatcactgg
1320
cgtcttctga gttttatgag acaggaaact aagtttacta tctgtaaatg taacatcatg
1380
tccattaaga aacatgtagt ttttttttag aatgtaataa cccagtggtc tactgttttt
1440
cttaactctt tttaaaaaaa ctttagaaga atcttttagg aactaatatc tctgttctg
1500
aagaaacatt tatctgacgt tcagcagttc ctacagtttt acttcagttt atttttcttc
1560
tgtaaaatgc aagaaaattt aatattttga ctaacatgct ttttctgttt gtatcattta
1620
aaggcaaata aacttggtac gtatttcata tctatttaaa aaatgaaaa aaaaaaaa
1678

<210> 1594

<211> 365

<212> PRT

<213> Homo sapiens

<400> 1594

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Leu Glu Ser Lys Ile Asn Glu Ile Asn Thr Glu Ile Asn Gln Leu Ile
 1          5          10          15
Glu Lys Lys Met Met Arg Asn Glu Pro Ile Glu Gly Lys Leu Ser Leu
 20          25          30
Tyr Arg Gln Gln Ala Ser Ile Ile Ser Arg Lys Lys Glu Ala Lys Ala
 35          40          45
Glu Glu Leu Gln Glu Ala Lys Glu Lys Leu Ala Ser Leu Glu Arg Glu
 50          55          60
Ala Ser Val Lys Arg Asn Gln Thr Arg Glu Phe Asp Gly Thr Glu Val
 65          70          75          80
Leu Lys Gly Asp Glu Phe Lys Arg Tyr Val Asn Lys Leu Arg Ser Lys
 85          90          95
Ser Thr Val Phe Lys Lys Lys His His Ile Ile Ala Glu Leu Lys Ala
100         105         110
Glu Phe Gly Leu Leu Gln Arg Thr Glu Glu Leu Leu Lys Gln Arg His
115         120         125
Glu Asn Ile Gln Gln Gln Leu Gln Thr Met Glu Glu Lys Lys Gly Ile
130         135         140
Ser Gly Tyr Ser Tyr Thr Gln Glu Glu Leu Glu Arg Val Ser Ala Leu
145         150         155         160
Lys Ser Glu Val Asp Glu Met Lys Gly Arg Thr Leu Asp Asp Met Ser
165         170         175
Glu Met Val Lys Lys Leu Tyr Ser Leu Val Ser Glu Lys Lys Ser Ala
180         185         190
Leu Ala Ser Val Ile Lys Glu Leu Arg Gln Leu Arg Gln Lys Tyr Gln
195         200         205
Glu Leu Thr Gln Glu Cys Asp Glu Lys Lys Ser Gln Tyr Asp Ser Cys
210         215         220
Ala Ala Gly Leu Glu Ser Asn Arg Ser Lys Leu Glu Gln Glu Val Arg
225         230         235         240
Arg Leu Arg Glu Glu Cys Leu Gln Glu Glu Ser Arg Tyr His Tyr Thr
245         250         255
Asn Cys Met Ile Lys Asn Leu Glu Val Gln Leu Arg Arg Ala Thr Asp
260         265         270
Glu Met Lys Ala Tyr Ile Ser Ser Asp Gln Gln Glu Lys Arg Lys Ala
275         280         285
Ile Arg Glu Gln Tyr Thr Lys Asn Thr Ala Glu Gln Glu Asn Leu Gly
290         295         300
Lys Lys Leu Arg Glu Lys Gln Lys Val Ile Arg Glu Ser His Gly Pro
305         310         315
Asn Met Lys Gln Ala Lys Met Trp Arg Asp Leu Glu Gln Leu Met Glu
325         330         335
Cys Lys Lys Gln Cys Phe Leu Lys Gln Gln Ser Gln Thr Ser Ile Gly
340         345         350
Gln Val Ile Gln Glu Gly Gly Glu Asp Arg Leu Ile Leu
355         360         365

```

<210> 1595

<211> 559

<212> DNA

<213> Homo sapiens

<400> 1595
 accggtcccg ctcacaggcc cacacctgct tctcctcctg gggcagggca gcctgggtggg
 60
 gcatggccgg ggagccgccc acttggcgag gaacaggctc catagcgacc tcagaacact
 120
 ggtgctgggg cccagccagg gagagcatct tcccgctggg accttccccg gggcggtcca
 180
 tcccttgtag atgtaggggtg cagctgagat ggtggcgccc ccattctctg tgttcgccag
 240
 cctgggctgg ggggtactagg atcacccctg ggctgatgag gagccccgggt cttgggcagt
 300
 taccaagtgg ggggtcacag tctggaagt ggtggaacca agggagcggc ctgcccagg
 360
 ccacactctc aaatactggc cctcgacaaa aggcagctgg gctctcaaga cagggccacc
 420
 tcctctctgc tgggcccgcg cccgtggaga gcaagtggga actgacccta tcttctgtcc
 480
 cagcttgtag agccagcatc aaggtcaggc ctcaacttgc caagaaagag gagtgaggag
 540
 gcccaactgga ggaacgcgt
 559

<210> 1596
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 1596
 Met Leu Ala Leu Gln Ala Gly Thr Glu Asp Arg Val Ser Ser His Leu
 1 5 10 15
 Leu Ser Thr Gly Ala Gly Pro Ala Glu Arg Arg Trp Pro Cys Leu Glu
 20 25 30
 Ser Pro Ala Ala Phe Cys Arg Gly Pro Val Phe Glu Ser Val Ala Trp
 35 40 45
 Ala Arg Pro Leu Pro Trp Phe His His Phe Pro Asp Cys Asp Pro Pro
 50 55 60
 Leu Gly Asn Cys Pro Arg Pro Gly Leu Leu Ile Ser Pro Arg Val Ile
 65 70 75 80
 Leu Val Pro Pro Ala Gln Ala Gly Glu Gln Gln Glu Trp Gly Arg His
 85 90 95
 His Leu Ser Cys Thr Leu His Leu Gln Gly Met Ser Arg Pro Gly Glu
 100 105 110
 Gly Pro Ser Gly Lys Met Leu Ser Leu Ala Gly Pro Gln His Gln Cys
 115 120 125
 Ser Glu Val Ala Met Glu Pro Val Pro Arg Gln Val Gly Gly Ser Pro
 130 135 140
 Ala Met Pro His Gln Ala Ala Leu Pro Gln Glu Glu Lys Gln Val Trp
 145 150 155 160
 Ala Cys Glu Arg Asp Arg
 165

<210> 1597
 <211> 609

<212> DNA

<213> Homo sapiens

<400> 1597

tcgtcaacgg aaacttcggc cttcgggcct acccataatc cttgggacct tgaacgggta
 60
 ccgggtgggtt ccgggtggtg ttcagcagct agcttggtt cctttcaggc cccgttggtg
 120
 ttggggcactg ataccggggg ctcgatccgc caacctggag cggtagccgg caccgtcggg
 180
 atcaagccga cctacggttc gacctccga tacggcggtta tcgctatggc ttcattcttg
 240
 gatactcctg ggcctcgcgc ccgtaccgtc cttgacgccg cgttgctcca tcaggccatt
 300
 gccgggtcacg acgctatgga ccagaccacg attaatcagc ccaccccgcc ggctcgttag
 360
 gctgcgcggc aggcagacgt ttccgggggt cgcattggcg ttgtcacgga gttgagcggg
 420
 cagggttacg accctcaggt cgaggcccg ttcacagagg ctgtcgagat gctaatagag
 480
 gcgggggctg aggtcgttga ggtctcttgc ccgaactttg acctgcctt acctgcttat
 540
 taccttattc agcctgcga ggtgtctagc aacctggctc gttacgacgc catgcgttac
 600
 ggcttacgc
 609

<210> 1598

<211> 203

<212> PRT

<213> Homo sapiens

<400> 1598

Ser Ser Thr Glu Thr Ser Ala Phe Gly Pro Thr His Asn Pro Trp Asp
 1 5 10 15
 Leu Glu Arg Val Pro Gly Gly Ser Gly Gly Gly Ser Ala Ala Ser Leu
 20 25 30
 Ala Ser Phe Gln Ala Pro Leu Ala Leu Gly Thr Asp Thr Gly Gly Ser
 35 40 45
 Ile Arg Gln Pro Gly Ala Val Thr Gly Thr Val Gly Ile Lys Pro Thr
 50 55 60
 Tyr Gly Ser Thr Ser Arg Tyr Gly Val Ile Ala Met Ala Ser Ser Leu
 65 70 75 80
 Asp Thr Pro Gly Pro Cys Ala Arg Thr Val Leu Asp Ala Ala Leu Leu
 85 90 95
 His Gln Ala Ile Ala Gly His Asp Ala Met Asp Gln Thr Thr Ile Asn
 100 105 110
 Gln Pro Thr Pro Ala Val Val Glu Ala Ala Arg Gln Ala Asp Val Ser
 115 120 125
 Gly Val Arg Ile Gly Val Val Thr Glu Leu Ser Gly Gln Gly Tyr Asp
 130 135 140
 Pro Gln Val Glu Ala Arg Phe His Glu Ala Val Glu Met Leu Ile Glu
 145 150 155 160
 Ala Gly Ala Glu Val Val Glu Val Ser Cys Pro Asn Phe Asp Leu Ala

```

                165                170                175
Leu Pro Ala Tyr Tyr Leu Ile Gln Pro Ala Glu Val Ser Ser Asn Leu
                180                185                190
Ala Arg Tyr Asp Ala Met Arg Tyr Gly Leu Arg
                195                200

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<210> 1599
 <211> 526
 <212> DNA
 <213> Homo sapiens

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<400> 1599
gcgtggccga cggctgctgt gtggtcagcg atctttattt ttcttgatcg attcagaacc
60
cggcacctgc acgtgtgggt tctctgcttt tggtggggag cgtgcgtcgc gacctggatt
120
agcatgcacg tgaacacgtg gatggccggg atgctctcgg tgacaggtgg ggttgatcca
180
gcatcgggag ccgggtccggc agtgatttcg gctccctttg ttgaggaatc atgcaaggcg
240
cttggtcttt tcgcgctggc catcggcatg gggcgacgga tgacctcggt agttcagacg
300
gtgagcatgg ccgggctctc ggcaattggt ttgccttttg ttgagaacat tatgtactac
360
gcccgtgcag ataactacgc ccgtgtgacg gcttcgggtg gggaccccaa acaaggcggt
420
gatgaagtgt gtgctgttgc ggggagtgtg tgcctcgttt gggcatccgc tggtcaccag
480
catgacgggt atcgggtctg cccttgggct gaggtcacga agttga
526

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<210> 1600
 <211> 134
 <212> PRT
 <213> Homo sapiens

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<400> 1600
Met His Val Asn Thr Trp Met Ala Gly Met Leu Ser Val Thr Gly Gly
1          5          10          15
Val Asp Pro Ala Ser Gly Ala Gly Pro Ala Val Tyr Ser Ala Pro Phe
20         25         30
Val Glu Glu Ser Cys Lys Ala Leu Val Leu Phe Ala Leu Ala Ile Gly
35         40         45
Met Gly Arg Arg Met Thr Ser Val Val Gln Thr Val Ser Met Ala Gly
50         55         60
Leu Ser Ala Ile Gly Phe Ala Phe Val Glu Asn Ile Met Tyr Tyr Ala
65         70         75         80
Arg Ala Asp Asn Tyr Ala Arg Val Thr Ala Ser Gly Gly Asp Pro Lys
85         90         95
Gln Gly Val Asp Glu Val Gly Ala Val Ala Gly Ser Val Cys Leu Val
100        105        110
Trp Ala Ser Ala Val His Gln His Asp Gly Tyr Arg Ser Gly Pro Trp
115        120        125
Ala Glu Val Thr Lys Leu

```

130

<210> 1601

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1601

gcccggccgcc ccgtttccgc agattctgga ggagtgccga tggccgagtt catctacacc
 60
 atgcacaaacg tccgaaaggc ggtgggtgac aaagttatcc ttgacaatgt cacgctgtcg
 120
 ttcttcccg gcgccaagat tggtgttgtc ggaccgaatg gcgctggcaa atcgacgatg
 180
 ctcaagctca tggctgggtct cgataagccc aataacggcg atgccaaactt ggctaaaggc
 240
 gccaccgtcg gaattctgct tcaggagccc ccgctcacgc aggacaaaac tgttcgcgag
 300
 aacgtcgaag agggcgtcgg cgacatcaaa gccaaagctgg cacgggttcca ggaagtctcc
 360
 gccgagatgg ccaaccctga cgccgacttt gacgccctga tggcggagat gggtagagctg
 420
 cagaccgagc tcgataacgc caacgcg
 447

<210> 1602

<211> 136

<212> PRT

<213> Homo sapiens

<400> 1602

Met	Ala	Glu	Phe	Ile	Tyr	Thr	Met	His	Asn	Val	Arg	Lys	Ala	Val	Gly
1				5						10				15	
Asp	Lys	Val	Ile	Leu	Asp	Asn	Val	Thr	Leu	Ser	Phe	Phe	Pro	Gly	Ala
			20				25						30		
Lys	Ile	Gly	Val	Val	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Met	Leu
	35					40					45				
Lys	Leu	Met	Ala	Gly	Leu	Asp	Lys	Pro	Asn	Asn	Gly	Asp	Ala	Asn	Leu
	50				55						60				
Ala	Lys	Gly	Ala	Thr	Val	Gly	Ile	Leu	Leu	Gln	Glu	Pro	Pro	Leu	Thr
65					70					75				80	
Glu	Asp	Lys	Thr	Val	Arg	Glu	Asn	Val	Glu	Glu	Ala	Val	Gly	Asp	Ile
			85						90				95		
Lys	Ala	Lys	Leu	Ala	Arg	Phe	Glu	Glu	Val	Ser	Ala	Glu	Met	Ala	Asn
			100				105						110		
Pro	Asp	Ala	Asp	Phe	Asp	Ala	Leu	Met	Ala	Glu	Met	Gly	Glu	Leu	Gln
			115				120					125			
Thr	Glu	Leu	Asp	Asn	Ala	Asn	Ala								
	130					135									

<210> 1603

<211> 540

<212> DNA

<213> Homo sapiens

<400> 1603

acgcgtaagc tcaccgaagc catgatggca atgctgctgg aactgcatta cagcaagcag
 60
 gaaatccttg aggcgtacct caacgagggtc ttcgtcgggtc aggatggcca ggcgcgctg
 120
 cacgggtttg gcttggtccag tcagtctctc tttggccagc ctttgtccga gctgaagttg
 180
 catcaagtcg cggtgttggt cgggatgggtc aagggcccggt cctattacaa cccgcggcgc
 240
 aatccggaac gtgcgctcga gcgtcgtaac ctggtgctgg atgtgctgga acagcagggt
 300
 gtagccactg ccgaacaagt cgctgccgca aagaaaatgc cgctgggtgt aaccactcgc
 360
 ggcaagctgg cggacagctc cttcccaggc tttatcgacc tggtaaagc ccagttgctg
 420
 gaagattacc gcgacgaaga cttgaccgaa gaaggcctgc ggattttcac cagtttcgac
 480
 ccgattctgc agatgaaagc cgaagcatcg gtgaacgaca cattcaagcg cctgaccggc
 540

<210> 1604

<211> 180

<212> PRT

<213> Homo sapiens

<400> 1604

Thr	Arg	Lys	Leu	Thr	Glu	Ala	Met	Met	Ala	Met	Leu	Leu	Glu	Leu	His
1			5						10					15	
Tyr	Ser	Lys	Gln	Glu	Ile	Leu	Glu	Ala	Tyr	Leu	Asn	Glu	Val	Phe	Val
			20					25					30		
Gly	Gln	Asp	Gly	Gln	Arg	Ala	Val	His	Gly	Phe	Gly	Leu	Ala	Ser	Gln
			35				40					45			
Phe	Phe	Phe	Gly	Gln	Pro	Leu	Ser	Glu	Leu	Lys	Leu	His	Gln	Val	Ala
	50				55					60					
Leu	Leu	Val	Gly	Met	Val	Lys	Gly	Pro	Ser	Tyr	Tyr	Asn	Pro	Arg	Arg
65					70					75				80	
Asn	Pro	Glu	Arg	Ala	Leu	Glu	Arg	Arg	Asn	Leu	Val	Leu	Asp	Val	Leu
				85					90					95	
Glu	Gln	Gln	Gly	Val	Ala	Thr	Ala	Glu	Gln	Val	Ala	Ala	Ala	Lys	Lys
			100					105					110		
Met	Pro	Leu	Gly	Val	Thr	Thr	Arg	Gly	Lys	Leu	Ala	Asp	Ser	Ser	Phe
			115					120				125			
Pro	Gly	Phe	Ile	Asp	Leu	Val	Lys	Arg	Gln	Leu	Arg	Glu	Asp	Tyr	Arg
	130					135					140				
Asp	Glu	Asp	Leu	Thr	Glu	Glu	Gly	Leu	Arg	Ile	Phe	Thr	Ser	Phe	Asp
145					150				155					160	
Pro	Ile	Leu	Gln	Met	Lys	Ala	Glu	Ala	Ser	Val	Asn	Asp	Thr	Phe	Lys
				165					170					175	
Arg	Leu	Thr	Gly												
			180												

<210> 1605

<211> 427

<212> DNA

<213> Homo sapiens

<400> 1605

acgcgttggt gcggtcggtc gcacgcagtc cgtccaagag gtacaggcca gcgttgccgc
 60
 cattctttgc gggcggtgac tgcactggga tattcgggcc catcgccgtg gaccacacat
 120
 cgcagcgctg gaccaccag cccacctggt cccactcgca cgtgccagta ctgtccgcac
 180
 gcaagaaatc gcggtgagct gcgtgcccct gctgggtgcc gcctgccact acggcaagac
 240
 ccagcgctac ggcgactgcc atgatgaccg aaaggacgcg acccctaata gatgcagtca
 300
 tctttctcct tcacaaagta ttggttaatt gtcacttagc tttatcgctc ggaatctgtg
 360
 aaccgttaac atcccgcgc ggaagctaac tagcaagcag tctaattgcac tcccgggcca
 420
 aatgttg
 427

<210> 1606

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1606

Met	Thr	Ala	Ser	Ile	Arg	Gly	Arg	Val	Leu	Ser	Val	Ile	Met	Ala	Val
1			5						10				15		
Ala	Val	Ala	Leu	Gly	Leu	Ala	Val	Val	Ala	Gly	Gly	Thr	Gln	Gln	Ala
		20					25					30			
His	Ala	Ala	His	Arg	Asp	Phe	Leu	Arg	Ala	Asp	Ser	Thr	Gly	Thr	Cys
		35				40					45				
Glu	Trp	Asp	Gln	Val	Gly	Trp	Trp	Val	Gln	Arg	Cys	Asp	Val	Trp	Ser
	50				55						60				
Gln	Ala	Met	Gly	Arg	Asn	Ile	Pro	Val	Gln	Ile	Pro	Pro	Ala	Lys	Asn
65				70			75							80	
Gly	Gly	Asn	Ala	Gly	Leu	Tyr	Leu	Leu	Asp	Gly	Leu	Arg	Ala	Thr	Asp
		85					90						95		
Arg	Thr	Asn	Ala												
		100													

<210> 1607

<211> 396

<212> DNA

<213> Homo sapiens

<400> 1607

gcacggctcc gctcgcggtc gccgtgatgg tacataccgg cgcgaccgtg atcgattctt
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 tgccgcaagg caatttactt ccacgtcacg gccgatgcga tgaagatgac gattcgtaac
 120
 cggatgggac tgatcccgtc cgaggcgatc gtggcgggga cgatgatgat cgtggcgagc
 180

ttgctgtacg gattcatttt gtagcataaa taaggagggg ttcatgaac aggaaaaccc ,
 240
 tttctgttgg caccgattc gttcaaggaa agcatgacgg caaaagaagt ctgtatcgcg
 300
 atggaaaaag gactgagccg cgtctacccc gacgccgggt ttatccatgt gccgatggcg
 360
 gacggaggcg aaggcacggg gcagtcgctg gtcgac
 396

<210> 1608
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1608
 Thr Gly Lys Pro Phe Leu Leu Ala Pro Asp Ser Phe Lys Glu Ser Met
 1 5 10 15
 Thr Ala Lys Glu Val Cys Ile Ala Met Glu Lys Gly Leu Ser Arg Val
 20 25 30
 Tyr Pro Asp Ala Arg Phe Ile His Val Pro Met Ala Asp Gly Gly Glu
 35 40 45
 Gly Thr Val Gln Ser Leu Val Asp
 50 55

<210> 1609
 <211> 505
 <212> DNA
 <213> Homo sapiens

<400> 1609
 acgcgtagat gccacagcgc caggacacac gccaccgcgg agccgaggat gatccacatg
 60
 ggctcgactc acatggacgc catggattcg gcagtggaga gcaggccgcg agcttcgcac
 120
 gcggcccgac tgcgtagtcg cgtcatctca gtgcacatct gttcttcccc gtcgatgagg
 180
 ttccggcggt aggacatcgt tacgtccagc atggtggcga tctcagcaat gtcacagccg
 240
 gccctgtgga gggcgaggag ccgagcgcg gtgcttcctg ctggcacgat gcgttcacgt
 300
 gctgcgttga tgctgctgat actgatatgc aggatgcgcc cgggggtcgaa gacggggaat
 360
 ggggtgaatt ggacggtccc ccctggccag cgagtcggtg gacgattcga ctggggacat
 420
 gcgcgagcag ggcgacgaca cgccacggaa cgcggcattc atggacgagg gaacggacat
 480
 ggagcgagaa aaagcgggcg tcgac
 505

<210> 1610
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1610

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Met Pro Arg Ser Val Ala Cys Arg Arg Pro Ala Arg Ala Cys Pro Gln
 1             5             10             15
Ser Asn Arg Pro Thr Thr Arg Trp Pro Gly Gly Thr Val Gln Phe Thr
      20             25             30
Pro Phe Pro Val Phe Asp Pro Gly Arg Ile Leu His Ile Ser Ile Asp
      35             40             45
Asp Ile Asn Ala Ala Arg Glu Arg Ile Val Pro Ala Gly Ser Thr Arg
      50             55             60
Ala Arg Leu Leu Ala Leu His Lys Ala Gly Cys Asp Ile Ala Glu Ile
65             70             75             80
Ala Thr Met Leu Asp Val Thr Met Ser Tyr Ala Ala Asn Leu Met Ser
      85             90             95
Gly Glu Glu Gln Met Cys Thr Glu Met Thr Arg Leu Arg Ser Arg Ala
      100            105            110
Ala Cys Glu Ala Arg Gly Leu Leu Ser Thr Ala Glu Ser Met Ala Ser
      115            120            125
Met

```

<210> 1611

<211> 532

<212> DNA

<213> Homo sapiens

<400> 1611

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acgcgtgctg cggttacagt tgcgtctatt gatttaggtg cgcattccaga atttttagga
60
aaaaaatgata ttcaattagg caaaaaagaa tctgtagagg atactgcgaa agtattagggt
120
agaatgttgc atggtattga attccgtggt ttttcacaac aagctggtga agatttagcg
180
aagttctctg gtgtaccggg gtggaatgga ttaacagacg attggcatcc tacacaaatg
240
ttagctgatt ttatgacaat aaaagagaat tttggatatc tagaaggaat aaacttaact
300
tacgttgagg atggacgtaa taatattgcg cattcattaa tggtagcagg tgctatgtta
360
gggtgttaatg taagaatttg tacacctaaa tcattaaatc caaaagaggg atatgttgat
420
attgcaaaag aaaagcgag tcaatatggt gggttcagtca tgattacgga taatattgca
480
gaagcagttg aaaatacaga tgctatatat acagatgttt ggggtatcgac gg
532

```

<210> 1612

<211> 177

<212> PRT

<213> Homo sapiens

<400> 1612

```

Thr Arg Ala Ala Phe Thr Val Ala Ser Ile Asp Leu Gly Ala His Pro
 1             5             10             15
Glu Phe Leu Gly Lys Asn Asp Ile Gln Leu Gly Lys Lys Glu Ser Val

```

```

                20                25                30
Glu Asp Thr Ala Lys Val Leu Gly Arg Met Phe Asp Gly Ile Glu Phe
      35      40      45
Arg Gly Phe Ser Gln Gln Ala Gly Glu Asp Leu Ala Lys Phe Ser Gly
      50      55      60
Val Pro Gly Trp Asn Gly Leu Thr Asp Asp Trp His Pro Thr Gln Met
      65      70      75      80
Leu Ala Asp Phe Met Thr Ile Lys Glu Asn Phe Gly Tyr Leu Glu Gly
      85      90      95
Ile Asn Leu Thr Tyr Val Gly Asp Gly Arg Asn Asn Ile Ala His Ser
      100      105      110
Leu Met Val Ala Gly Ala Met Leu Gly Val Asn Val Arg Ile Cys Thr
      115      120      125
Pro Lys Ser Leu Asn Pro Lys Glu Ala Tyr Val Asp Ile Ala Lys Glu
      130      135      140
Lys Ala Ser Gln Tyr Gly Gly Ser Val Met Ile Thr Asp Asn Ile Ala
      145      150      155      160
Glu Ala Val Glu Asn Thr Asp Ala Ile Tyr Thr Asp Val Trp Val Ser
      165      170      175
Thr

```

```

<210> 1613
<211> 584
<212> DNA
<213> Homo sapiens

```

```

<400> 1613
nnacgcgcttc agccgagaaa tatgctgctt tttgcctgcc acctcacaaa tgctacggca
60
caggggctcc aggttttgcg cctcctggta cggtgctaca cacttgctca cctcccagcg
120
gtatcaatac aacttgcgaa atgcagacaa ggcccaggcc taagacatgg tagacataca
180
tatatacaag gaattcacta tatattgggt gaaaggagat cttcccgttc ctgttcttcc
240
ctgctcgcat cctgtgaagc gttcaggggag gtcgacatgg ataagtgcg tatgcctggc
300
acgggtaaagt gtcgcgggct tgtagatgcg tgtgaacgtt ttcgtgactt gaagaggctg
360
aagctgatgt gttcgcgtga gtcgatgca gcgcgctgcy ttgcgtgcct tgtggctgat
420
cgctgccccg atccgataga atgcggagtt gtattttcgt agtactgctc gacaatgcca
480
gtgggagagg cgatgagttc ctcatttgcg tctttctoga ggtcttggtc catgtccata
540
aacataccaa agctggatgg gtcatacgac ggccgagcat gcat
584

```

```

<210> 1614
<211> 153
<212> PRT
<213> Homo sapiens

```

<400> 1614

```

Xaa Arg Val Gln Pro Arg Asn Met Leu Leu Phe Ala Cys His Leu Thr
 1           5           10           15
Asn Ala Thr Ala Gln Gly Val Gln Val Leu Arg Leu Leu Val Arg Cys
 20           25           30
Tyr Thr Leu Ala His Leu Pro Ala Val Ser Ile Gln Leu Ala Lys Cys
 35           40           45
Arg Gln Gly Pro Gly Leu Arg His Gly Arg His Thr Tyr Ile Gln Gly
 50           55           60
Ile His Tyr Ile Leu Gly Glu Arg Arg Ser Ser Arg Ser Cys Ser Ser
 65           70           75           80
Ser Ala Ala Ser Cys Glu Ala Phe Arg Glu Val Asp Met Asp Asn Val
 85           90           95
Arg Met Pro Gly Thr Val Lys Cys Arg Gly Leu Val Asp Ala Cys Glu
100           105           110
Arg Phe Arg Asp Leu Lys Arg Ser Lys Leu Met Cys Ser Arg Glu Leu
115           120           125
Asp Ala Ala Arg Cys Val Ala Cys Leu Val Val Asp Arg Arg Pro Asp
130           135           140
Pro Ile Glu Cys Gly Val Val Phe Ser
145           150

```

<210> 1615

<211> 363

<212> DNA

<213> Homo sapiens

<400> 1615

```

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120
ctactgtgctg gtgagacgat gcaggtgccg ggtgaggacg gcaccatgcc gaaactgttc
180
ggacgggatca acaaacatga ggctccagct cccgctttgt ggatcaccaa catcgtctcc
240
cagatatgcc ttgtcatgac ggtgttgggtg gacgggtgctt acctggcgat ggcgacccctg
300
gctgccgcgcc tcactctggt gccgtacctg ctgtcagccg cattcgccct gaagatgggtg
360
atc
363

```

<210> 1616

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1616

```

Ala Gly Leu Pro Asp Ala Ser Met Gly Asp Val Leu Ser Ser Val Val
 1           5           10           15
Gly Pro Trp Gly Ser Val Leu Val Ser Ala Gly Val Ile Ile Ser Leu
 20           25           30
Leu Gly Ala Leu Leu Ala Trp Ile Leu Leu Cys Gly Glu Thr Met Gln

```

```

      35              40              45
Val Pro Gly Glu Asp Gly Thr Met Pro Lys Leu Phe Gly Arg Ile Asn
 50              55              60
Lys His Glu Ala Pro Ala Pro Ala Leu Trp Ile Thr Asn Ile Val Ser
 65              70              75              80
Gln Ile Cys Leu Val Met Thr Val Leu Trp Asp Gly Ala Tyr Leu Ala
      85              90              95
Met Ala Thr Leu Ala Ala Ala Leu Ile Leu Val Pro Tyr Leu Leu Ser
      100              105              110
Ala Ala Phe Ala Leu Lys Met Val Ile
      115              120

```

<210> 1617

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1617

```

accggtgact acctgtggga gaagaagggc atcggtccca tcctcaagat tgataagggc
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 120
gtgcaccgcg ccgtcgagga gaagcacatc ttcggtacca aggagcgcgc tgtcatcctg
 180
gatgacgaca aagctggcat cgaaaagatt gtgcaccagc agttogaact ggccgaacag
 240
gtgcgcgctg cgggtcttgt gccgacccct gaaccogagg tcgacatcca cgctccacat
 300
aaggagaagg ctgaggaaaag gctgcacaac ctcacccgag agcacatcga ctctctgcgc
 360
ctcgacgcca agatcatggt gaagctgacg atcccgagtt ccgaagacct gtatgccgac
 420
ctcattgcgg atccgaaggt cctacgc
 447

```

<210> 1618

<211> 149

<212> PRT

<213> Homo sapiens

<400> 1618

```

Thr Gly Asp Tyr Leu Trp Glu Lys Lys Gly Ile Val Pro Ile Leu Lys
 1              5              10              15
Ile Asp Lys Gly Leu Ala Asp Glu Gly Cys His Val Arg Leu Met Lys
 20              25              30
Pro Ile Pro Gly Leu Asp Glu Leu Val His Arg Ala Val Glu Glu Lys
 35              40              45
His Ile Phe Gly Thr Lys Glu Arg Ser Val Ile Leu Asp Asp Lys
 50              55              60
Ala Gly Ile Glu Lys Ile Val Asp Gln Gln Phe Glu Leu Ala Glu Gln
 65              70              75              80
Val Arg Ala Ala Gly Leu Val Pro Ile Leu Glu Pro Glu Val Asp Ile
      85              90              95
His Ala Pro His Lys Glu Lys Ala Glu Glu Arg Leu His Asn Leu Ile

```

```

          100              105              110
Arg Glu His Ile Asp Ser Leu Pro Leu Asp Ala Lys Ile Met Leu Lys
          115              120              125
Leu Thr Ile Pro Ser Ser Glu Asp Leu Tyr Ala Asp Leu Ile Ala Asp
          130              135              140
Pro Lys Val Leu Arg
145

```

```

<210> 1619
<211> 355
<212> DNA
<213> Homo sapiens

```

```

<400> 1619
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60
acaacaaatg gtgcctccat tcccgccctt ggccttgga ctttccgtat gcccgcgaa
120
gatgtgcttc gcctcgtccc ttacgcgctc aaggctggtt ttgccatgt cgataccgcy
180
cagatttatg gcaatgaagt cgaggtcggg gaagcaattg cgacttccgg cgttcagcgt
240
ggcgacatct ttctgaccac aaaagtctgg gtagataatt ataagcatga tgccttcac
300
gcctctgtcg atgaaagcct taccaagctt aagaccgact atgtcgatct gctgc
355

```

```

<210> 1620
<211> 118
<212> PRT
<213> Homo sapiens

```

```

<400> 1620
Xaa Val Pro Lys Pro Val Ser Leu Pro His Lys Ile Lys Gly Thr Ser
1      5      10
Met His Asn Val Thr Thr Asn Gly Ala Ser Ile Pro Ala Leu Gly Leu
20     25     30
Gly Thr Phe Arg Met Pro Gly Glu Asp Val Leu Arg Ile Val Pro Tyr
35     40     45
Ala Leu Lys Ala Gly Phe Arg His Val Asp Thr Ala Gln Ile Tyr Gly
50     55     60
Asn Glu Val Glu Val Gly Glu Ala Ile Ala Thr Ser Gly Val Gln Arg
65     70     75     80
Gly Asp Ile Phe Leu Thr Thr Lys Val Trp Val Asp Asn Tyr Lys His
85     90     95
Asp Ala Phe Ile Ala Ser Val Asp Glu Ser Leu Thr Lys Leu Lys Thr
100    105    110
Asp Tyr Val Asp Leu Leu
115

```

```

<210> 1621
<211> 386
<212> DNA
<213> Homo sapiens

```

<400> 1621
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 60
 gctggggctg gcgggacccg cgggccatgt acggcgacat attcaacgcc acggggcggg
 120
 cccccgaggc ggcggtaggc agcgcgctgg cccagggagc cacgggtcaag gcagaaggcg
 180
 ctttgccgct ggagctggcc actgcgcgcy gtatgagga cggcgcgccg acaaaagccg
 240
 acctgcccac ctacctgctg ctcttcttcc tgctgctgct ctcgggggcg ctcgggggcc
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 360
 ctgcgcacgc ccgcgcgccc ggaagg
 386

<210> 1622
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 1622
 Met Glu Ala Pro Arg Val Ala Pro Gly Cys Ser Arg Pro Ser Glu Ala
 1 5 10 15
 Val Arg Leu Gly Ser Ala Gly Pro Ala Gly His Val Arg Arg His Ile
 20 25 30
 Gln Arg His Gly Ala Gly Pro Arg Gly Gly Gly Arg Gln Arg Ala Gly
 35 40 45
 Pro Arg Ser His Gly Gln Gly Arg Arg Arg Phe Ala Ala Gly Ala Gly
 50 55 60
 His Cys Ala Arg Tyr Glu Gly Arg Arg Gly His Lys Ala Arg Pro Ala
 65 70 75 80
 His Leu Pro Ala Ala Leu Leu Pro Ala Ala Leu Gly Gly Ala Arg
 85 90 95
 Arg Pro Leu His Arg Leu Pro Ala Ala Pro Phe Gly Leu Arg Arg Ala
 100 105 110
 Ala Pro Arg Pro Leu Arg Ser Arg Arg Pro Arg Ala Arg Lys
 115 120 125

<210> 1623
 <211> 314
 <212> DNA
 <213> Homo sapiens

<400> 1623
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 60
 ggcccttgct tgtggttttt ctgggagctt tgggcccagg gttccccgga cccttcctctg
 120
 aacttttccg cagtttcaga ggagagtctg caagtgcagc ctgcagtgac tgtgccttgt
 180
 gcttgccacc caagcagggc atgggagtct taagtgaac cagggcctca aggacaacag
 240

agagccgcat ggcagggttag acacctggat aaaagtgggt gggggaagcc cactgctgca
 300
 ccccgggcat tgct
 314

<210> 1624

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1624

Met	Pro	Gly	Val	Gln	Gln	Trp	Ala	Ser	Pro	Thr	His	Phe	Tyr	Pro	Gly
1				5					10					15	
Val	Tyr	Pro	Ala	Met	Arg	Leu	Ser	Val	Val	Leu	Glu	Ala	Leu	Val	Pro
			20					25					30		
Leu	Lys	Thr	Pro	Met	Pro	Cys	Leu	Gly	Ala	Lys	His	Lys	Ala	Gln	Ser
			35				40					45			
Leu	Gln	Leu	Ser	Leu	Ala	Asp	Ser	Pro	Leu	Lys	Leu	Arg	Lys	Ser	Ser
			50			55					60				
Gly	Lys	Gly	Pro	Gly	Asn	Pro	Arg	Pro	Lys	Ala	Pro	Arg	Lys	Thr	Thr
			65		70				75					80	
Ser	Lys	Gly	Pro	Lys	Cys	Leu	Thr	Arg	Lys	Gly	Pro	Gly	Ala	Gly	Pro
				85					90					95	
Arg	Arg	Gly	Ser	Gly	His	Gln									
															100

<210> 1625

<211> 619

<212> DNA

<213> Homo sapiens

<400> 1625

acgcgtactc agcagcaagt tctgctgagc cccaaatcca cacagactga gcctggacca
 60
 gggctgggcc ctccttatcc aagccaatcc agggaaacac tgtgctgact tcaaggcaga
 120
 agggacaaga aagcatgact gtgcacaaat tggtcttgca gccatctcca ccaggtagcc
 180
 ctgggagcac ctgggaagaa gccgggcat gcaggagacc caacctcacc ctgcattcag
 240
 aaccgggcct tggaatggcc tgatctgagc cctagcacc ctgggaagcc gccacacctt
 300
 cttctggcct ctgggaagaa gatgggaatt ttaaggccat gggagaagac actcctggat
 360
 tctttcagct tctccacca cccctgctc cagatgtaat ctgggaagac tggggagtca
 420
 ggggcacagt gagttggagc aggggattgg agggtttggg ggacagcctt ccagggcacc
 480
 tcaggagctg aattatttaa gccagctgcc cgtgggcccc gctcccagcc cttcctgttt
 540
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 600
 gttttctgca atcttatag
 619

<210> 1626
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 1626
 Met Asp Gly Val Cys Val Asn Arg Lys Gly Trp Glu Arg Gly Pro Arg
 1 5 10 15
 Ala Ala Gly Leu Asn Asn Ser Ala Pro Glu Val Pro Trp Lys Ala Val
 20 25 30
 Pro Gln Thr Leu Gln Ser Pro Ala Pro Thr His Cys Ala Pro Asp Ser
 35 40 45
 Pro Val Phe Pro Asp Tyr Ile Trp Ser Arg Gly Trp Val Glu Lys Leu
 50 55 60
 Lys Glu Ser Arg Ser Val Phe Ser His Gly Leu Lys Ile Pro Ile Phe
 65 70 75 80
 Phe Pro Glu Ala Arg Arg Lys Val Gly Gly Phe Pro Gly Val Leu Gly
 85 90 95
 Leu Arg Ser Gly His Ser Lys Ala Arg Phe
 100 105

<210> 1627
 <211> 481
 <212> DNA
 <213> Homo sapiens

<400> 1627
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 60
 gatcaccagt gggcgagggg gcaacgcgcg tgccgcgcgg atgcaaatca gtcattgatga
 120
 caccgaagtct atcgggatcc gctgacagac tccggtaaag ttcccgcctt ggcagaacct
 180
 actggaaacc cggtgagtc cagctcggac ttcattcatt aggtgtgttc gcgcggacatc
 240
 caacaggaca cctacggcgg gcgcgtccag acccggttcc cacttgagcc taacggctac
 300
 cttccacattg gccacgcgaa ggccatcgct accgatttcg gcgtttccga ggatttcggc
 360
 ggcacctgca acctgagact tgatgatact aatccaggca ccgaggaaac cgagtattgtc
 420
 gagtcgatcg ttgcagacat tgagtgggta gggtactccc cggeccacgt tgtccacgcg
 480
 t
 481

<210> 1628
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1628
 Met Ala Glu Pro Thr Gly Asn Pro Ala Glu Ser Ser Ser Asp Phe Ile

```

      1             5             10             15
His Gln Val Val Arg Ala Asp Ile Gln Gln Asp Thr Tyr Gly Gly Arg
      20             25             30
Val Gln Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly
      35             40             45
His Ala Lys Ala Ile Val Thr Asp Phe Gly Val Ala Glu Asp Phe Gly
      50             55             60
Gly Thr Cys Asn Leu Arg Leu Asp Asp Thr Asn Pro Gly Thr Glu Glu
      65             70             75             80
Thr Glu Tyr Val Glu Ser Ile Val Ala Asp Ile Glu Trp Leu Gly Tyr
      85             90             95
Ser Pro Ala His Val Val His Ala
      100

```

<210> 1629

<211> 4519

<212> DNA

<213> Homo sapiens

<400> 1629

```

ccaaattgct gggaaatgtcc aaagtgtctac caggaggaca gctcggagaa agcccagaag
60
cggaataatgg aagagagtga cgaagaagct gtgcaagcca aagtcctctgcg gccctctgagg
120
agctgcgatg agcctctctac gcccccgctt cattcaacca ctccatgtct gcagctctac
180
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240
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360
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420
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480
gccaaccttc gccattcccc ccgtgtgcta gtgcagcact gccagcccg aacccccag
540
cgtgggggatg aggaggggct ggggggagag gaggaggagg agggaggagg ggaggaggaa
600
gatgacagtg cagaggaggg ggggtgcagc aggctgaatg gccggggcag ttgggctcag
660
gatggagagc aaagctggat gcagcgggag gtctggatgt ctgtctctcc ctacctcagc
720
cgacagagaac tttgtgaatg tatgcgagtg tgcaagacgt ggtataaatg gtgctgcgac
780
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840
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900
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960
tgctcctggt ctgcagcttc tgccctcagc acctccagct gcccccttct caggaccctt
1020

```

gatcttcgggt gggcagtagg aatcaaggac cctcaaatc gggacttgct tactccaccg
1080
gctgataaac caggtcagga caatcgcagc aagctccgga acatgaccga ctccggctg
1140
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3300
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3720
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4260

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 4380
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 4500
 aggcctttaa aacaaaaaa
 4519

<210> 1630

<211> 496

<212> PRT

<213> Homo sapiens

<400> 1630

Pro	Asn	Cys	Trp	Glu	Cys	Pro	Lys	Cys	Tyr	Gln	Glu	Asp	Ser	Ser	Glu
1			5						10					15	
Lys	Ala	Gln	Lys	Arg	Lys	Met	Glu	Glu	Ser	Asp	Glu	Glu	Ala	Val	Gln
		20						25					30		
Ala	Lys	Val	Leu	Arg	Pro	Leu	Arg	Ser	Cys	Asp	Glu	Pro	Leu	Thr	Pro
		35					40					45			
Pro	Pro	His	Ser	Pro	Thr	Ser	Met	Leu	Gln	Leu	Ile	His	Asp	Pro	Val
		50				55					60				
Ser	Pro	Arg	Gly	Met	Val	Thr	Arg	Ser	Ser	Pro	Gly	Ala	Gly	Pro	Ser
65				70					75					80	
Asp	His	His	Ser	Ala	Ser	Arg	Asp	Glu	Arg	Phe	Lys	Arg	Arg	Gln	Leu
			85					90						95	
Leu	Arg	Leu	Gln	Ala	Thr	Glu	Arg	Thr	Met	Val	Arg	Glu	Lys	Glu	Asn
			100				105						110		
Asn	Pro	Ser	Gly	Lys	Lys	Glu	Leu	Ser	Glu	Val	Glu	Lys	Ala	Lys	Ile
			115				120					125			
Arg	Gly	Ser	Tyr	Leu	Thr	Val	Thr	Leu	Gln	Arg	Pro	Thr	Lys	Glu	Leu
			130			135					140				
His	Gly	Thr	Ser	Ile	Val	Pro	Lys	Leu	Gln	Ala	Ile	Thr	Ala	Ser	Ser
145				150						155				160	
Ala	Asn	Leu	Arg	His	Ser	Pro	Arg	Val	Leu	Val	Gln	His	Cys	Pro	Ala
			165					170						175	
Arg	Thr	Pro	Gln	Arg	Gly	Asp	Glu	Glu	Gly	Leu	Gly	Gly	Glu	Glu	Glu
			180				185						190		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asp	Ser	Ala	Glu	Glu	Gly	Gly
		195					200					205			
Ala	Ala	Arg	Leu	Asn	Gly	Arg	Gly	Ser	Trp	Ala	Gln	Asp	Gly	Asp	Glu
		210				215						220			
Ser	Trp	Met	Gln	Arg	Glu	Val	Trp	Met	Ser	Val	Phe	Arg	Tyr	Leu	Ser
225				230					235					240	
Arg	Arg	Glu	Leu	Cys	Glu	Cys	Met	Arg	Val	Cys	Lys	Thr	Trp	Tyr	Lys
			245						250					255	
Trp	Cys	Cys	Asp	Lys	Arg	Leu	Trp	Thr	Lys	Ile	Asp	Leu	Ser	Arg	Cys
		260					265					270			
Lys	Ala	Ile	Val	Pro	Gln	Ala	Leu	Ser	Gly	Ile	Ile	Lys	Arg	Gln	Pro
		275					280					285			
Val	Ser	Leu	Asp	Leu	Ser	Trp	Thr	Asn	Ile	Ser	Lys	Lys	Gln	Leu	Thr

290		295		300											
Trp	Leu	Val	Asn	Arg	Leu	Pro	Gly	Leu	Lys	Asp	Leu	Leu	Leu	Ala	Gly
305			310						315						320
Cys	Ser	Trp	Ser	Ala	Val	Ser	Ala	Leu	Ser	Thr	Ser	Ser	Cys	Pro	Leu
			325						330					335	
Leu	Arg	Thr	Leu	Asp	Leu	Arg	Trp	Ala	Val	Gly	Ile	Lys	Asp	Pro	Gln
			340					345					350		
Ile	Arg	Asp	Leu	Leu	Thr	Pro	Pro	Ala	Asp	Lys	Pro	Gly	Gln	Asp	Asn
		355				360						365			
Arg	Ser	Lys	Leu	Arg	Asn	Met	Thr	Asp	Phe	Arg	Leu	Ala	Gly	Leu	Asp
		370				375					380				
Ile	Thr	Asp	Ala	Thr	Leu	Arg	Leu	Ile	Ile	Arg	His	Met	Pro	Leu	Leu
385			390						395					400	
Ser	Arg	Leu	Asp	Leu	Ser	His	Cys	Ser	His	Leu	Thr	Asp	Gln	Ser	Ser
			405						410				415		
Asn	Leu	Leu	Thr	Ala	Val	Gly	Ser	Ser	Thr	Arg	Tyr	Ser	Leu	Thr	Glu
		420						425					430		
Leu	Asn	Met	Ala	Gly	Cys	Asn	Lys	Leu	Thr	Asp	Gln	Thr	Leu	Ile	Tyr
		435				440					445				
Leu	Arg	Arg	Ile	Ala	Asn	Val	Thr	Leu	Ile	Asp	Leu	Arg	Gly	Cys	Lys
		450			455						460				
Gln	Ile	Thr	Arg	Lys	Ala	Cys	Glu	His	Phe	Ile	Ser	Asp	Leu	Ser	Ile
465			470						475					480	
Asn	Ser	Leu	Tyr	Cys	Leu	Ser	Asp	Glu	Lys	Leu	Ile	Gln	Lys	Ile	Ser
			485					490						495	

<210> 1631

<211> 330

<212> DNA

<213> Homo sapiens

<400> 1631

acgcgtgctc agccaagcct tagatgaaaa tgcgcttgct gacttttgtg cgatgcaatg
60
tcagaaccgg aacacacgtg cttcagacat ggcgggatgg aagacattc agactctttt
120
ccatgttgac tctcgcgacg agcttgttga gttgcttggc ttttcgaaag acgacattac
180
caaccaagtt cagcaagctg tgggcgcctt ggggtttaccg ccaactagaag atgaaaacgc
240
acaaggtgaa gatccggcgt cgcaggtccc gccagtcacc gacgaggacc ccaactgcttt
300
cttcgatcaa gttccagatg tgcctctaga
330

<210> 1632

<211> 92

<212> PRT

<213> Homo sapiens

<400> 1632

Met Gln Cys Gln Asn Pro Asn Thr Arg Ala Ser Asp Met Ala Gly Trp
1 5 10 15
Lys Thr Leu Gln Thr Leu Phe His Val Asp Ser Arg Asp Glu Leu Val

```

          20          25          30
Glu Leu Leu Gly Phe Ser Lys Asp Asp Ile Thr Asn Gln Val Gln Gln
   35          40          45
Ala Val Gly Ala Leu Gly Leu Pro Pro Leu Glu Asp Glu Asn Ala Gln
   50          55          60
Gly Glu Asp Pro Ala Ser Gln Val Pro Pro Val Thr Asp Glu Asp Pro
   65          70          75          80
Thr Ala Phe Phe Asp Gln Val Pro Asp Val Pro Leu
          85          90

```

<210> 1633
 <211> 259
 <212> DNA
 <213> Homo sapiens

```

<400> 1633
nggggggacgt tggctatcaa tcttgtcgga gctttcgtac tggcgacttt gctcgagctg
60
ctcgccacg ctggccctgg ccagggggtt cgtcgagcgg tgccgctatg catcggtacc
120
ggattgttag gtggatttac gacttattcc gccctcacgg tggaaacgg ccaacgtgtg
180
atgtcagggc agtggttatg ggggtattgcc tatcttttga cgagtgtcgt ggcaggtgca
240
ttgttggcat gggtcatga
259

```

<210> 1634
 <211> 86
 <212> PRT
 <213> Homo sapiens

```

<400> 1634
Xaa Gly Thr Leu Ala Ile Asn Leu Val Gly Ala Phe Val Leu Ala Thr
1   5          10          15
Leu Leu Glu Leu Leu Val His Ala Gly Pro Gly Pro Gly Val Arg Arg
   20          25          30
Ala Val Arg Leu Cys Ile Gly Thr Gly Leu Leu Gly Gly Phe Thr Thr
   35          40          45
Tyr Ser Ala Leu Thr Val Glu Thr Gly Gln Arg Val Met Ser Gly Gln
   50          55          60
Trp Leu Trp Gly Ile Ala Tyr Leu Leu Thr Ser Val Val Ala Gly Ala
   65          70          75          80
Leu Leu Ala Trp Val Met
          85

```

<210> 1635
 <211> 792
 <212> DNA
 <213> Homo sapiens

```

<400> 1635
nngtcctttt ttatgaaccg gcggactcgg ttggcgttgt ggggcagggg gtggtggagc
60

```

aagatggcgg ctcattctgtc ctacggccga gtgaacctaa acgtgttgcg cgaggcgggtg
 120
 cgtcgcgagc tgcgcgagtt cctggacaag tgcgcaggaa gcaaggcaat agtttgggat
 180
 gaatacctaa ctggaccctt tggcctgatt gcacagtatt cactattgaa ggaacatgaa
 240
 gtggaaaaaa tgttcacact taaaggaaat cgtttgccgg cagctgatgt gaagaatata
 300
 attttttttg tcagaccctg gctagagttg atggatataa tcgctgaaaa cgtgctcagt
 360
 gaagatagac gaggcccaac gagagatatt catattctgt ttgtgccacg ccgtagcctg
 420
 ttgtgcgaac agcgggtgaa ggatctgggt gtcttgggat cctttattca cagggaggag
 480
 tacagcttag atctcattcc attcgatggg gatctcttat ccatggaatc agaggggtgca
 540
 ttcaaagagt gctacctgga gggtagaccg acgagcctgt accacgcagc caaggggctg
 600
 atgaccctgc aagctctgta tggaaacgat ccccgatctc ttgggaaagg agaatgcgct
 660
 cgggtgagaa ccggctgctt tgtgtgtgga aaggagggcc cttcacaccc caaaagggag
 720
 gaggaacggg aagctcctta caaacaatt cagttgatct taattattta tgaatactgt
 780
 actcatgaat tc
 792

<210> 1636

<211> 243

<212> PRT

<213> Homo sapiens

<400> 1636

Met Ala Ala His Leu Ser Tyr Gly Arg Val Asn Leu Asn Val Leu Arg
 1 5 10 15
 Glu Ala Val Arg Arg Glu Leu Arg Glu Phe Leu Asp Lys Cys Ala Gly
 20 25 30
 Ser Lys Ala Ile Val Trp Asp Glu Tyr Leu Thr Gly Pro Phe Gly Leu
 35 40 45
 Ile Ala Gln Tyr Ser Leu Leu Lys Glu His Glu Val Glu Lys Met Phe
 50 55 60
 Thr Leu Lys Gly Asn Arg Leu Pro Ala Ala Asp Val Lys Asn Ile Ile
 65 70 75 80
 Phe Phe Val Arg Pro Arg Leu Glu Leu Met Asp Ile Ile Ala Glu Asn
 85 90 95
 Val Leu Ser Glu Asp Arg Arg Gly Pro Thr Arg Asp Phe His Ile Leu
 100 105 110
 Phe Val Pro Arg Arg Ser Leu Leu Cys Glu Gln Arg Leu Lys Asp Leu
 115 120 125
 Gly Val Leu Gly Ser Phe Ile His Arg Glu Glu Tyr Ser Leu Asp Leu
 130 135 140
 Ile Pro Phe Asp Gly Asp Leu Leu Ser Met Glu Ser Glu Gly Ala Phe
 145 150 155 160
 Lys Glu Cys Tyr Leu Glu Gly Asp Gln Thr Ser Leu Tyr His Ala Ala


```

                165                170                175
Lys Gly Leu Met Thr Leu Gln Ala Leu Tyr Gly Thr Ile Pro Gln Ile
                180                185                190
Phe Gly Lys Gly Glu Cys Ala Arg Val Arg Thr Gly Cys Phe Val Val
                195                200                205
Val Lys Glu Gly Pro Ser His Pro Lys Arg Glu Glu Glu Arg Glu Ala
                210                215                220
Pro Tyr Lys Gln Ile Gln Leu Ile Leu Ile Tyr Glu Tyr Cys Thr
225                230                235                240
His Glu Phe

```

<210> 1637

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1637

```

ntcatgatga cacagacccc cgcgacccca ggcttgatct ccttgcaagg catcggaaca
60
cgttatcagt tggcggggca aaagctgtcc attctcaatg acgtgtgcct gtccatctcc
120
cgcggtgaca gctcgggcat cctcgggcgc tccgggtccg gcaagagcac cctgctcaat
180
atccttggcc tgctggacct gcccaacagc ggccagtacc actttgccgg ccacgatatt
240
ttggcgctca ccccgacga actgtcggcg atccgcaact cagntnnaat ggttgtgttc
300
cagagcttca acctgctgcc gcgcctcagc gccctggaga acgtcgcctt gccctgt
357

```

<210> 1638

<211> 119

<212> PRT

<213> Homo sapiens

<400> 1638

```

Xaa Met Met Thr Gln Thr Pro Ala His Pro Gly Leu Ile Ser Leu Gln
1          5          10          15
Gly Ile Gly Lys Arg Tyr Gln Leu Ala Gly Gln Lys Leu Ser Ile Leu
20          25          30
Asn Asp Val Cys Leu Ser Ile Ser Arg Gly Asp Ser Cys Gly Ile Leu
35          40          45
Gly Ala Ser Gly Ser Gly Lys Ser Thr Leu Leu Asn Ile Leu Gly Leu
50          55          60
Leu Asp Leu Pro Asn Ser Gly Gln Tyr His Phe Ala Gly His Asp Ile
65          70          75          80
Leu Ala Leu Thr Pro Asp Glu Leu Ser Ala Ile Arg Asn Ser Xaa Xaa
85          90          95
Met Val Val Phe Gln Ser Phe Asn Leu Leu Pro Arg Leu Ser Ala Leu
100          105          110
Asp Asn Val Ala Leu Pro Leu
115

```

<210> 1639
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 1639
 acgcgtgtac gtgcgcgtgt gatttcacat gccctcaaag atattcttac tgaaggcgat
 60
 aaagttatcg ttatgggaca taagcgacca gatttagatg ctatagggtgc agctatcgga
 120
 gtttcgcgct ttgcatcaat gaataattta gaggcattta tcgttcttaa tgattctgat
 180
 attgatccga cattacgtcg tgttatggat gagattgata agaaaccgga actaaaagaa
 240
 cgctttgtaa catcggatga ggcttgggat atgatgactt ctaagacgac tgcgttgggt
 300
 gtatagatcac ataaacctga aatgggtctta gatgaaaatg tcttaataaa agcaaaccgc
 360
 aaagtagtca ttgatcatca tagacgtggc gaaact
 396

<210> 1640
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 1640
 Thr Arg Val Arg Ala Arg Val Ile Ser His Ala Leu Lys Asp Ile Leu
 1 5 10 15
 Thr Glu Gly Asp Lys Val Ile Val Met Gly His Lys Arg Pro Asp Leu
 20 25 30
 Asp Ala Ile Gly Ala Ala Ile Gly Val Ser Arg Phe Ala Ser Met Asn
 35 40 45
 Asn Leu Glu Ala Phe Ile Val Leu Asn Asp Ser Asp Ile Asp Pro Thr
 50 55 60
 Leu Arg Arg Val Met Asp Glu Ile Asp Lys Lys Pro Glu Leu Lys Glu
 65 70 75 80
 Arg Phe Val Thr Ser Asp Glu Ala Trp Asp Met Met Thr Ser Lys Thr
 85 90 95
 Thr Val Val Val Val Asp Thr His Lys Pro Glu Met Val Leu Asp Glu
 100 105 110
 Asn Val Leu Asn Lys Ala Asn Arg Lys Val Val Ile Asp His His Arg
 115 120 125
 Arg Gly Glu Thr
 130

<210> 1641
 <211> 376
 <212> DNA
 <213> Homo sapiens

<400> 1641
 ttatcagcaa acgacagcag acaagagctc ctggggctct ggggaaatgc tgcgtcctgc
 60

tggccaaacg aactgatgga tgggctcttg gagtgggaga gactgggcag aagctgtgtg
 120
 ggggtgggtga ctcccaacct aaagaaccca ctgagacata tgtggcttcc ctcttccacc
 180
 ttcatgtcct ctttccgtct agatgctggc aaggggggac ttggtggaca aagagagcta
 240
 ctattcattc aggagctatg ttacaccagt cactttacat gtgccacttg ctctgggtta
 300
 aactgtgcct cccctcactc atatgttgaa gtcctaacc taactacctc agaatgggag
 360
 gttatttggg aaaaag
 376

<210> 1642

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1642

Met Asp Gly Leu Leu Glu Trp Glu Arg Leu Gly Arg Ser Cys Val Gly
 1 5 10 15
 Trp Val Thr Pro Asn Leu Lys Asn Pro Leu Arg His Met Trp Leu Pro
 20 25 30
 Ser Ser Thr Phe Ile Ala Ser Phe Arg Leu Asp Ala Gly Lys Gly Gly
 35 40 45
 Leu Gly Gly Gln Arg Glu Leu Leu Phe Ile Gln Glu Leu Cys Tyr Thr
 50 55 60
 Ser His Phe Thr Cys Ala Thr Cys Ser Gly Leu Asn Cys Ala Ser Pro
 65 70 75 80
 His Ser Tyr Val Glu Val Leu Thr Leu Thr Ser Glu Trp Asp Val
 85 90 95
 Ile Trp Lys Lys
 100

<210> 1643

<211> 494

<212> DNA

<213> Homo sapiens

<400> 1643

aagcttccag aattccatag gaaccagct gcccttctgg tacctcagtg aggtggagcc
 60
 gagggtctga gagcaggtgc aggagaaggt gtgggctcca cctgggcctc tgaagccagg
 120
 ggccagaate cccagatcta ggtccaagag ggggctccat gacctcccca tgctgtcctc
 180
 ctgcttggat ccaggatata agaaaggagg ggcacacact gtgggggaac tctgggggtc
 240
 cctgtgtgca tcagcagatc ccgggtctgc cccaccagga tgcaaagggc ctggctgtct
 300
 cagccccatg ctcacagccc tataagtgca cgaatggcacc ctatatcacc taagcggggc
 360
 tgtgctcctc gaggctttag ggacaccaga atgagcccc ctcggcgagg tctggtctct
 420

gggtgtgtgga gatgccacct gggacgggaa cccaggtgc atggagcccc actgcagaca
 480
 ccattccccg tgtg
 494

<210> 1644
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1644
 Met Gly Leu Glu Gln Pro Gly Pro Leu His Pro Gly Gly Ala Asp Pro
 1 5 10 15
 Gly Leu Ala Asp Ala His Arg Gly Pro Gln Ser Ser Pro Thr Val Cys
 20 25 30
 Ala Pro Pro Phe Leu Tyr Pro Gly Ser Lys Gln Arg Ser Ser Met Gly
 35 40 45
 Arg Ser Trp Ser Pro Leu Leu Asp Leu Asp Leu Gly Ile Leu Ala Pro
 50 55 60
 Gly Phe Arg Gly Pro Gly Gly Ala His Thr Phe Ser Cys Thr Cys Ser
 65 70 75 80
 Gln Thr Leu Gly Ser Thr Ser Leu Arg Tyr Gln Lys Gly Ser Trp Val
 85 90 95
 Pro Met Glu Phe Trp Lys Leu
 100

<210> 1645
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1645
 nnagatctgt cggataatgg ctttggtccc gacatggtga cactggtgct tgccatcggg
 60
 aggagccggt ctctgaaaca cgtggccctt ggaaggaact tcaacgttcg gtgcaaggag
 120
 accctggacg atgtcctgca tcggatagcc cagctaatagc aggatgacga ctgtcctttg
 180
 cagtcactat ccgtggctga gtcgcggttg aagcagggtg ccagcatcct gatccgggct
 240
 ttgggcacca atcctaaact gacagcgctg gatatcagtg gcaatgccat aggggatgct
 300
 ggggccaaga tgctagccaa ggctctacgc
 330

<210> 1646
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1646
 Xaa Asp Leu Ser Asp Asn Gly Phe Gly Ser Asp Met Val Thr Leu Val
 1 5 10 15
 Leu Ala Ile Gly Arg Ser Arg Ser Leu Lys His Val Ala Leu Gly Arg

```

                20                25                30
Asn Phe Asn Val Arg Cys Lys Glu Thr Leu Asp Asp Val Leu His Arg
      35                40                45
Ile Ala Gln Leu Met Gln Asp Asp Asp Cys Pro Leu Gln Ser Leu Ser
      50                55                60
Val Ala Glu Ser Arg Leu Lys Gln Gly Ala Ser Ile Leu Ile Arg Ala
      65                70                75                80
Leu Gly Thr Asn Pro Lys Leu Thr Ala Leu Asp Ile Ser Gly Asn Ala
      85                90                95
Ile Gly Asp Ala Gly Ala Lys Met Leu Ala Lys Ala Leu Arg
      100                105                110

```

<210> 1647

<211> 501

<212> DNA

<213> Homo sapiens

<400> 1647

```

aggccgctcg gtgatccgcg gcggcgccag cggcgcttcc tgctaggacc ggccggggcc
60
gtaccggagg ctcgggctcc accgaccctc ctccacccc ctccactca cctctcgggc
120
cgcgactcgc cagggcgggg ccggccgaac catgggccgc ggtgtgggct aagctgggtg
180
ccccggcttt agactggacc ccacaatggt tgcagagatg ttcaggcacg cgggagctga
240
ttacacacaa tgaatggggg caatgagagc agtggagcag acagagctgg gggccctgtg
300
gccacatctg tccccatcgg ctggcagcgc tgtgtgcgag aggggtgctgt gctctacatc
360
agtccaagtg gcacagagct gtcttccttg gagcaaaccc ggagctacct cctcagcgat
420
gggacctgca agtcgggtct ggagtgtcca cttaatgtcc ccaagggttt caactttgac
480
cctttggccc cggtgacccc g
501

```

<210> 1648

<211> 84

<212> PRT

<213> Homo sapiens

<400> 1648

```

Met Asn Gly Gly Asn Glu Ser Ser Gly Ala Asp Arg Ala Gly Gly Pro
  1                5                10                15
Val Ala Thr Ser Val Pro Ile Gly Trp Gln Arg Cys Val Arg Glu Gly
      20                25                30
Ala Val Leu Tyr Ile Ser Pro Ser Gly Thr Glu Leu Ser Ser Leu Glu
      35                40                45
Gln Thr Arg Ser Tyr Leu Leu Ser Asp Gly Thr Cys Lys Cys Gly Leu
      50                55                60
Glu Cys Pro Leu Asn Val Pro Lys Val Phe Asn Phe Asp Pro Leu Ala
      65                70                75                80
Pro Val Thr Pro

```

<210> 1649
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 1649
 gcgtcggcag ctgaacgggt gctactggca atcgcgcaac ccgaactgct ggatacgtcc
 60
 accaactcac ggttgtcgcg catcttctcc aacaagggtga tccggcgcta tccggccttt
 120
 gaagacttcc acgggatgga agaatgcacg gatcagatcg ttctgtatatt ccgccacgcc
 180
 gcccaaggcc tggaagagaa gaaacagatc ctttacctgc tcggccccgt cggcgggcgg
 240
 aaatcgtccc tggccgaaaa gctgaaacag ctgatcgaga aggtcccttt ctacgccatc
 300
 aaggcgctcgc cggctcttca gtcgcccctg gggttgttca acgccactga agacggcgcg
 360
 atcctcgagg aagacttcgg gattccacgg cgttacctga acaccatcat gtcgcccctg
 420
 gcgaccaagc gcctggccga a
 441

<210> 1650
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 1650
 Ala Ser Ala Ala Glu Arg Val Leu Leu Ala Ile Gly Glu Pro Glu Leu
 1 5 10 15
 Leu Asp Thr Ser Thr Asn Ser Arg Leu Ser Arg Ile Phe Ser Asn Lys
 20 25 30
 Val Ile Arg Arg Tyr Pro Ala Phe Glu Asp Phe His Gly Met Glu Glu
 35 40 45
 Cys Ile Asp Gln Ile Val Ser Tyr Phe Arg His Ala Ala Gln Gly Leu
 50 55 60
 Glu Glu Lys Lys Gln Ile Leu Tyr Leu Leu Gly Pro Val Gly Gly Gly
 65 70 75 80
 Lys Ser Ser Leu Ala Glu Lys Leu Lys Gln Leu Ile Glu Lys Val Pro
 85 90 95
 Phe Tyr Ala Ile Lys Gly Ser Pro Val Phe Glu Ser Pro Leu Gly Leu
 100 105 110
 Phe Asn Ala Thr Glu Asp Gly Ala Ile Leu Glu Glu Asp Phe Gly Ile
 115 120 125
 Pro Arg Arg Tyr Leu Asn Thr Ile Met Ser Pro Trp Ala Thr Lys Arg
 130 135 140
 Leu Ala Glu
 145

<210> 1651
 <211> 408

<212> DNA

<213> Homo sapiens

<400> 1651

nccgcgatc cctcggcat cctgggtatc gctccctcga aggaatccgg agccccgactg
 60
 cgccgcgagc ttctcgaacg cctcgaggat tacgccgcac aaacttccat ggtgcgttcc
 120
 gtacactccc tcgcattcgc gttgctgcgc acagcgcccg aggaggagct gcgccttatt
 180
 accggtgcgg acnaagacgc cgttatccgc gagctgctca cgggccaagc agaagacgga
 240
 catggctcgt ggcccccgga gatgcgcccc gcgtggaatn natgtgggct ttccgggcag
 300
 ctgcgcgatt tccttttgcg ttccattgaa cgcggcctgg gaccgggtga cctagagagc
 360
 ctccgtgccg agcacggccg ccccatgtgg tctgcggcgg gtgaattc
 408

<210> 1652

<211> 136

<212> PRT

<213> Homo sapiens

<400> 1652

Xaa	Ala	Asp	Pro	Ser	Gly	Ile	Leu	Val	Ile	Ala	Pro	Ser	Lys	Glu	Ser
1				5				10					15		
Gly	Ala	Arg	Leu	Arg	Arg	Glu	Leu	Ser	Glu	Arg	Leu	Glu	Asp	Tyr	Ala
			20					25				30			
Ala	Gln	Thr	Ser	Met	Val	Arg	Ser	Val	His	Ser	Leu	Ala	Phe	Ala	Leu
			35					40				45			
Leu	Arg	Thr	Ala	Ala	Glu	Glu	Glu	Leu	Arg	Leu	Ile	Thr	Gly	Ala	Asp
			50			55					60				
Xaa	Asp	Ala	Val	Ile	Arg	Glu	Leu	Leu	Thr	Gly	Gln	Ala	Glu	Asp	Gly
65				70					75					80	
His	Gly	Ser	Trp	Pro	Ala	Glu	Met	Arg	Pro	Ala	Trp	Asn	Xaa	Cys	Gly
				85				90						95	
Leu	Ser	Arg	Gln	Leu	Arg	Asp	Phe	Leu	Leu	Arg	Ser	Ile	Glu	Arg	Gly
			100					105				110			
Leu	Gly	Pro	Gly	Asp	Leu	Glu	Ser	Leu	Gly	Ala	Glu	His	Gly	Arg	Pro
			115				120					125			
Met	Trp	Ser	Ala	Ala	Gly	Glu	Phe								
			130				135								

<210> 1653

<211> 398

<212> DNA

<213> Homo sapiens

<400> 1653

ccagcctctc tccgaccgcg tcctttcttcc ggccatacgg caccctaatgt cgcgtcacca
 60
 tcaccgcgcg acatggccat cgctccaccg gacgagttga gtgacaagat ccggtgcatt
 120

ctgcgcaccc ttgaacctgg tgacagtgtg aaggagattc tcaacacgtc gcgtgtcgtc
 180
 ggcattgacg tccagagcag cctgcttatt gctggtgctc agcatctgta cttgttggag
 240
 gattacttcc agcgtccgaa cggtgaaatc gtcaatgtct gggaagctcc gccacacgag
 300
 cgcatgcctc tgatcgtggc ggccggtgtc gcacaggtgg cacaagcag cacacccgtg
 360
 cagatatggc gctgggaaca gctccgactt tgtctaga
 398

<210> 1654
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 1654
 Pro Ala Ser Leu Arg Pro Arg Pro Ser Ser Gly His Thr Ala Pro Asn
 1 5 10 15
 Val Ala Ser Pro Ser Pro Ala His Met Ala Ile Ala Pro Pro Asp Glu
 20 25 30
 Leu Ser Asp Lys Ile Arg Cys Ile Leu Arg Thr Leu Glu Pro Gly Asp
 35 40 45
 Ser Val Lys Glu Ile Leu Asn Thr Ser Arg Val Val Gly Ile Asp Val
 50 55 60
 Gln Ser Ser Leu Leu Ile Ala Gly Ala Gln His Leu Tyr Leu Leu Asp
 65 70 75 80
 Asp Tyr Phe Gln Arg Pro Asn Gly Glu Ile Val Asn Val Trp Glu Ala
 85 90 95
 Pro Pro His Glu Arg Asp Ala Leu Ile Val Ala Ala Gly Val Ala Gln
 100 105 110
 Val Ala Gln Ser Ser Thr Pro Val Gln Ile Trp Arg Trp Glu Gln Leu
 115 120 125
 Arg Leu Cys Leu
 130

<210> 1655
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<400> 1655
 nccctgacct gacctgtcct cgccatggcc gaggccgcct ccggcgccgg gggcacgtcc
 60
 ctggagggcg agcgtggcaa gaggcccccg ccggaggcg agcctgcagc ccggcgctcc
 120
 ggagttctcg ataagctttt cggaagcgg ctccctgcagg ctggctcgcta cctggtgtcc
 180
 cacaaggcgt ggaatgaagc ggtgcctaca gagaactgcg acgtgctgat gaccttccca
 240
 gacacgaccg atgaccacac gctgctatgg ctgctgaacc acatccgcgt gggcattccc
 300
 gagctcatcg tgcaagtcgg ccaccaccgc cacacgcgtg cctacgcctt ctttgtcacc
 360


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gccagctatg agagcctact ccgagggggc gacgagctgg gtctgcgcaa agcagtgaag
420
gccgagtttg gcggggggcac ccgcggttc tcctgcgagg aggaatttat ctatgagaat
480
gtggagagcg agctacgctt cttcacctcc caggaacgcc agagcatcat ccgcttctgg
540
ctgcagaatt tgcgtgccaa gcagggagaa gcaactccaca acgtgcgctt cctggaggagc
600
cagccaatca tcccgagctt ggcagcacgt gggatcatcc agcaggtgtt cctgtgccac
660
gagcagcgta ttctgaaccg cctcatgaag tcatgggtgc aggccgtgtg tgaaccagg
720
cctctagatg acatctgtga ttactttggt gtgaaaattg ccatgtactt cgcttggtg
780
ggcttctaca cgctggctat ggtataccca gctgtcttcg ggtctgtcct gtacacattc
840
acagaggctg atcagacaag ccgggatgtt tcctgcgtgg tctttgccct cttcaacgtg
900
atctgggtga cgctgttctt ataggaatgg aagcgatatg gggctgagct gggatataat
960
tgggggagcg tggactcacc ctgggaagcc gtggaggagc cagccccca gttcaggtgc
1020
gtgcgacgta tcacccccat cactcggggc gaggagtctt actaccgcc ctggaagcgg
1080
ctgctcttcc agctgcttgt tagcctccgc ctgtg
1115

```

<210> 1656

<211> 299

<212> PRT

<213> Homo sapiens

<400> 1656

```

Met Ala Glu Ala Ala Ser Gly Ala Gly Gly Thr Ser Leu Glu Gly Glu
1      5      10      15
Arg Gly Lys Arg Pro Pro Pro Glu Gly Glu Pro Ala Ala Pro Ala Ser
20     25     30
Gly Val Leu Asp Lys Leu Phe Gly Lys Arg Leu Leu Gln Ala Gly Arg
35     40     45
Tyr Leu Val Ser His Lys Ala Trp Met Lys Thr Val Pro Thr Glu Asn
50     55     60
Cys Asp Val Leu Met Thr Phe Pro Asp Thr Thr Asp Asp His Thr Leu
65     70     75     80
Leu Trp Leu Leu Asn His Ile Arg Val Gly Ile Pro Glu Leu Ile Val
85     90     95
Gln Val Arg His His Arg His Thr Arg Ala Tyr Ala Phe Phe Val Thr
100    105    110
Ala Thr Tyr Glu Ser Leu Leu Arg Gly Ala Asp Glu Leu Gly Leu Arg
115    120    125
Lys Ala Val Lys Ala Glu Phe Gly Gly Gly Thr Arg Gly Phe Ser Cys
130    135    140
Glu Glu Asp Phe Ile Tyr Glu Asn Val Glu Ser Glu Leu Arg Phe Phe
145    150    155    160
Thr Ser Gln Glu Arg Gln Ser Ile Ile Arg Phe Trp Leu Gln Asn Leu

```

```

          165              170              175
Arg Ala Lys Gln Gly Glu Ala Leu His Asn Val Arg Phe Leu Glu Asp
          180              185              190
Gln Pro Ile Ile Pro Glu Leu Ala Ala Arg Gly Ile Ile Gln Gln Val
          195              200              205
Phe Pro Val His Glu Gln Arg Ile Leu Asn Arg Leu Met Lys Ser Trp
          210              215              220
Val Gln Ala Val Cys Glu Asn Gln Pro Leu Asp Asp Ile Cys Asp Tyr
          225              230              235
Phe Gly Val Lys Ile Ala Met Tyr Phe Ala Trp Leu Gly Phe Tyr Thr
          240              245              250
Ser Ala Met Val Tyr Pro Ala Val Phe Gly Ser Val Leu Tyr Thr Phe
          255              260              265
Thr Glu Ala Asp Gln Thr Ser Arg Asp Val Ser Cys Val Val Phe Ala
          270              275              280
Leu Phe Asn Val Ile Trp Ser Thr Leu Phe Leu
          285              290              295

```

<210> 1657

<211> 333

<212> DNA

<213> Homo sapiens

<400> 1657

```

tgtagaggct cggagtcac cggaccatgt ggtccaggac gcccccgtcc tccgggcccc
60
gcacggagac gcggcgctcag caccgacagc acgcagctctg tgagccctctg caggcagttc
120
ttggagcccc cgggcttccc gcgccgcttc agggggcggg cggcagctcg ggccggctact
180
tctcccaaaa ctgctccggg caggggcgct ccagcagcct ctgcatgaga cggacggcat
240
ccacgcggcc cgtgtaagt gccactcct gcggcgacat tccacggcgg gggtaccctc
300
gcgtgggacat ccgccctgc tagcatcagg gct
333

```

<210> 1658

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1658

```

Met Leu Ala Gly Ala Asp Val His Ala Arg Val Pro Pro Pro Trp Asn
1      5      10      15
Val Ala Ala Gly Val Gly His Leu His Gly Pro Arg Gly Cys Arg Pro
20     25     30
Ser His Ala Glu Ala Ala Gly Ala Pro Leu Pro Gly Ala Val Leu Gly
35     40     45
Glu Val Pro Ala Arg Ala Ala Arg Pro Leu Lys Arg Arg Gly Lys
50     55     60
Pro Ala Gly Ser Lys Asn Cys Leu Gln Arg Leu Thr Asp Cys Val Leu
65     70     75     80
Ser Val Leu Thr Pro Arg Leu Arg Ala Gly Pro Gly Gly Arg Gly Arg

```

```

      85              90              95
Pro Gly Pro His Gly Pro Asp Asp Leu Glu Pro Leu
      100              105

<210> 1659
<211> 382
<212> DNA
<213> Homo sapiens

<400> 1659
nnaagcttat ttgttattac taatattttc cgtgaccaga tgggccccta tggtgagatt
60
tacacaactt acaagatgat tttggatgct attcgtaagg tgcctactgc cactgttttc
120
cttaatggag acagtccact tttctacaag ccagctattc caaatcctgt acagtatttt
180
ggttttgact tggagaaaagg cccagcccaa ctggctcact ataataccga aggaattctc
240
tgtcccgcact gccaaggcat cctcaaatat gagcataata cctatgcaaa cttgggcgcc
300
tatatctgtg aagactgtgg atgtaaacgt cctgatctcg actatcgctt gacagaactg
360
gttgagttaa ccaacaatcg cn
382

<210> 1660
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1660
Xaa Ser Leu Phe Val Ile Thr Asn Ile Phe Arg Asp Gln Met Gly Arg
1              5              10              15
Tyr Gly Glu Ile Tyr Thr Thr Tyr Lys Met Ile Leu Asp Ala Ile Arg
20              25              30
Lys Val Pro Thr Ala Thr Val Leu Leu Asn Gly Asp Ser Pro Leu Phe
35              40              45
Tyr Lys Pro Ala Ile Pro Asn Pro Val Gln Tyr Phe Gly Phe Asp Leu
50              55              60
Glu Lys Gly Pro Ala Gln Leu Ala His Tyr Asn Thr Glu Gly Ile Leu
65              70              75              80
Cys Pro Asp Cys Gln Gly Ile Leu Lys Tyr Glu His Asn Thr Tyr Ala
85              90              95
Asn Leu Gly Ala Tyr Ile Cys Glu Asp Cys Gly Cys Lys Arg Pro Asp
100              105              110
Leu Asp Tyr Arg Leu Thr Glu Leu Val Glu Leu Thr Asn Asn Arg
115              120              125

<210> 1661
<211> 524
<212> DNA
<213> Homo sapiens

<400> 1661

```

acgcgtcgcg gatcatggag aagacgcggg ccggctcctt gcctgtgacc ttcttgtaga
 60
 gctgcgggta gtagagctcc aggcctctga ggaaggccac gtagcccttg tggccgggtcc
 120
 gctgcaggat gtccaggagc acaccactt tccgtttgcg gatgaccagg ttgggggtcgc
 180
 tgagcacctg ctccctcatca tcagggttca ggaccttgca ctgccgcagg taagggtgtga
 240
 tgcgtagagg gtcgatgacc gaggtgagcg tcacccggaa gccctccagg acgttccagg
 300
 actcgtcatc gttctcgtag tccgacatgg cctcagcagg caggctgggg agtggtggggc
 360
 agtgctgaga gcgatgccgg ctccctgcccc caccggggcc cagctccac tccttctcag
 420
 acgctggggc agggctctcg tcagggcac gagggggatc agcccaggcg catccaggag
 480
 aggtgcccag ctccgtgtcc catccacgc ttgatcgtg catg
 524

<210> 1662

<211> 174

<212> PRT

<213> Homo sapiens

<400> 1662

Met	Gln	Arg	Ser	Ser	Val	Gly	Trp	Asp	Thr	Glu	Leu	Gly	Thr	Ser	Pro
1				5					10					15	
Gly	Cys	Ala	Trp	Ala	Asp	Pro	Pro	Arg	Cys	Pro	Asp	Glu	Ser	Pro	Gly
		20						25					30		
Pro	Ala	Ser	Glu	Lys	Glu	Trp	Glu	Leu	Gly	Pro	Gly	Gly	Gly	Arg	Ser
		35					40					45			
Arg	His	Arg	Ser	Gln	His	Cys	Pro	Thr	Leu	Pro	Ser	Leu	Pro	Ala	Glu
		50				55					60				
Ala	Met	Ser	Asp	Tyr	Glu	Asn	Asp	Asp	Glu	Cys	Trp	Asn	Val	Leu	Glu
65				70					75					80	
Gly	Phe	Arg	Val	Thr	Leu	Thr	Ser	Val	Ile	Asp	Pro	Ser	Arg	Ile	Thr
		85						90					95		
Pro	Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Gly	Gln
		100						105					110		
Val	Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val
		115					120					125			
Leu	Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe
		130				135				140					
Leu	Glu	Ser	Leu	Glu	Leu	Tyr	Tyr	Pro	Gln	Leu	Tyr	Lys	Lys	Val	Thr
145				150						155				160	
Gly	Lys	Glu	Pro	Ala	Arg	Val	Phe	Ser	Met	Ile	Ile	Asp	Ala		
		165							170						

<210> 1663

<211> 321

<212> DNA

<213> Homo sapiens

<400> 1663

```

nnagtacttg tcatgattac gcctagtttg ggtatctatt tctctcagcg ttctcagatc
60
tcccgaaccc aagacgacga ggctcggaca cgcgcttcta tctcgacctt tcaagacgag
120
gtcaagaggt ggcacgatcc cgactacgtc cgtgctcagg cgcgctccca gctcggctgg
180
gtgatgccgg gcgaactcgg gtatcaggtc attggagaaa acggttaagg cattggatcg
240
acgactttct tggacgaaaa agatccggcg agtgaagcca gcgctgacgc tcggtggtgg
300
caagaggctt gcggatcagt c
321

```

<210> 1664

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1664

```

Xaa Val Leu Val Met Ile Thr Pro Ser Leu Gly Ile Tyr Phe Ser Gln
1      5      10
Arg Ser Gln Ile Ser Arg Thr Gln Asp Asp Glu Ala Arg Thr Arg Ala
20     25     30
Ser Ile Ser Thr Leu Gln Asp Glu Val Lys Arg Trp His Asp Pro Asp
35     40     45
Tyr Val Arg Ala Gln Ala Arg Ser Gln Leu Gly Trp Val Met Pro Gly
50     55     60
Glu Thr Gly Tyr Gln Val Ile Gly Glu Asn Gly Lys Val Ile Gly Ser
65     70     75     80
Thr Thr Ser Leu Asp Glu Lys Asp Pro Ala Ser Glu Ala Ser Ala Asp
85     90     95
Ala Arg Trp Trp Gln Glu Ala Cys Gly Ser Val
100    105

```

<210> 1665

<211> 431

<212> DNA

<213> Homo sapiens

<400> 1665

```

gcttccgaac tcatcaagaa gctcaagagg tataaaatgg ttttgcgctc taccggcggc
60
ggcccgacta tctccggtgg tgaagtactc atgcaacgcg ctttttcgctg gaacttgctc
120
atgagtgccta agtcgatggg cattcatacc tgtatcgata cctccggttt ttggggggct
180
ggcgcaacag atgacttttt agagtctgtt gatttggtgt tgctcgacgt caaatcggga
240
gatgaagaaa tctaccgtgc cctcaccggc agagcggttg aacctaccat cgattttggt
300
gatcgtctca ccgcgctcgg taaagaaatc tggattcggg tcggttggtg ccccgatac
360
accgactcgg tagagaacgt ggaaaagggt gccgatatcg tccgcagatg gcgcaccgct
420

```

gtttcacgcg t
431

<210> 1666

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1666

Ala	Ser	Glu	Leu	Ile	Lys	Lys	Leu	Lys	Arg	Tyr	Lys	Met	Val	Leu	Arg
1				5					10					15	
Ser	Thr	Gly	Gly	Gly	Pro	Thr	Ile	Ser	Gly	Gly	Glu	Val	Leu	Met	Gln
		20						25					30		
Arg	Ala	Phe	Ala	Trp	Asn	Leu	Leu	Met	Ser	Ala	Lys	Ser	Met	Gly	Ile
		35				40					45				
His	Thr	Cys	Ile	Asp	Thr	Ser	Gly	Phe	Leu	Gly	Ala	Ala	Ala	Thr	Asp
	50				55					60					
Asp	Phe	Leu	Glu	Ser	Val	Asp	Leu	Val	Leu	Leu	Asp	Val	Lys	Ser	Gly
65				70					75					80	
Asp	Glu	Glu	Ile	Tyr	Arg	Ala	Leu	Thr	Gly	Arg	Ala	Leu	Gln	Pro	Thr
			85					90					95		
Ile	Asp	Phe	Gly	Asp	Arg	Leu	Thr	Ala	Leu	Gly	Lys	Glu	Ile	Trp	Ile
		100				105						110			
Arg	Phe	Val	Val	Val	Pro	Gly	Tyr	Thr	Asp	Ser	Val	Glu	Asn	Val	Glu
	115					120						125			
Lys	Val	Ala	Asp	Ile	Val	Arg	Arg	Trp	Arg	Thr	Ala	Val	Ser	Arg	
	130					135					140				

<210> 1667

<211> 370

<212> DNA

<213> Homo sapiens

<400> 1667

tccgctgaga ccagcgttg tgacttccca ggtgagactg tccgcaccat ggccaagatc
60
gttgagtcta ctgaggcccg tggcttggac aagatcgcca agatcgactg ggatccgcac
120
accaccagtg gcatcatgtc gaaggcagct gctgagatcg ctgagcgcgc cgaggccaag
180
ttcatcgtgg cctttaccaa gtccggtgac accgccgctc gtatcgctcg tctgctccg
240
agcaccgccg tcatcgtttt cacctctgat gagaccacga ccaagacctc cgctggggtc
300
tggggcgctc acgccgtcgt taccgccgtg tttaagaatg cggaggagct gtaccgctgg
360
gttaacgcgt
370

<210> 1668

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1668

```

Ser Ala Glu Thr Ser Val Gly Asp Phe Pro Gly Glu Thr Val Arg Thr
 1           5           10           15
Met Ala Lys Ile Val Glu Ser Thr Glu Ala Arg Gly Leu Asp Lys Ile
           20           25           30
Ala Lys Ile Asp Trp Asp Pro His Thr Thr Ser Gly Ile Met Ser Lys
           35           40           45
Ala Ala Ala Glu Ile Ala Glu Arg Ala Glu Ala Lys Phe Ile Val Ala
           50           55           60
Phe Thr Lys Ser Gly Asp Thr Ala Arg Arg Ile Ala Arg Leu Arg Pro
65           70           75           80
Ser Thr Pro Leu Ile Val Phe Thr Ser Asp Glu Thr Thr Thr Lys Thr
           85           90           95
Leu Ala Trp Val Trp Gly Ala His Ala Val Val Thr Pro Val Phe Lys
           100          105          110
Asn Ala Glu Glu Leu Tyr Arg Trp Val Asn Ala
           115          120

```

<210> 1669

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 1669

```

ggatcctgca gtggtgatct gtcacgtgca cgtcacagaa ctgaacatgg aaatgaacaa
60
cgaaaactcc acccccttct caaacgagtt attcctagct ccgccccag tccttgcttc
120
tcccagcctt ggtgtaatt agcttgaaag tgggaacgag agtgcgggtcc gcaaagaaa
180
gacttctggt tagacactga aatacaaaac gactgccaac gagctctggg caaagctgcc
240
ccgtcttctt ttttcgaaag accctcaaaa actgcctttc cttctgctac caaaacttgg
300
gccttagaaa gtggctgcgg agtggagcag atggacatca ctgagaatgg tagaggagg
360
gctgtgtttt ctgaggggga gtcattggcag cttgtgctgg gggccaggaa gggaaaaaac
420
caatctggca ttcaggttgt ggaaggcaaa gtgaaacaag aagtcatttg ggaatatatt
480
atattataaa cacatagaat aatatgtaca cgctcatata catcccaag agaagcctca
540
aggagttccg tttcttctca aaagaaactt cactatgata aagcattcct atagtgggaa
600
ttaactacaa tgaataaatt taacaatttc atttatgcta tatctgtgtc cactacagag
660
tctacgggtg aggctgtgtg gagcgagtggt gtctagtgga ctgcaacacc aacgcgttct
720
tcaaaaatag gcaatgacct gtttttttct attcacattt acaatagcta cacagtgtat
780
aaacgcagac tgaataatca aatggcagga cgtatggaact gtgcgaagg ttctcagact
840
tgtggtctct gcacctgtta tactttttgga tacgagtgag ctccacttag cttcggttaa
900

```

attagaaatt tccatgaaac acttaccac atataaattc tgtgtaaagc tttatttttt
 960
 tcccacaccta ctttaatttt ttttaaaaag tgaaataaga ggaaaaaactc ttataaaaaa
 1020
 taagggttaa catacgagag agcgaggaaac accccggagg ctgccgtgac gtgtggcttc
 1080
 atgtttctgt gctacatgag tctagtgttc tcattctcca ttgtgacaac ccttctcccc
 1140
 ccatcacact gtcaatgagc tctaggcaaa gctgccccgt ttgcttttaa cctaagggat
 1200
 gctgtgggtt gggtgactac atttgactac caccactgaa ggccggcgac gtctgaagcg
 1260
 gctggatacc gcaacgatgg aaaatcaggc gaggtactag cgtggagggc cggtgctcca
 1320
 ggtcaaggtc gtctgggttc tcaggagcca gtctgtgcca cagaaccatc ggcagctgcc
 1380
 ttcgtaaggc acctcggtct ggcattcgga aaaccacccc atcttgccag agtcccttgg
 1440
 tccttgggta gcaaaagccg tatgcgatct aaatcaagct ttcaatcatg a
 1491

<210> 1670

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1670

Met	Pro	Asp	Trp	Phe	Phe	Pro	Phe	Leu	Ala	Pro	Ser	Thr	Ser	Cys	His
1				5					10					15	
Asp	Ser	Pro	Ser	Glu	Asn	Thr	Ala	Pro	Pro	Leu	Pro	Phe	Ser	Val	Met
			20				25					30			
Ser	Ile	Cys	Ser	Thr	Pro	Gln	Pro	Leu	Ser	Arg	Ala	Gln	Val	Leu	Val
		35				40					45				
Ala	Glu	Gly	Lys	Ala	Val	Phe	Glu	Gly	Leu	Ser	Lys	Lys	Glu	Asp	Gly
	50					55				60					
Ala	Ala	Leu	Pro	Arg	Ala	Arg	Trp	Gln	Ser	Val	Cys	Ile	Ser	Val	Ser
65				70					75						
Asn	Gln	Lys	Ser	Phe	Leu	Cys	Gly	Pro	His	Ser	Arg	Ser	His	Phe	Gln
				85				90					95		
Ala	Asn	Tyr	His	Gln	Gly	Trp	Glu	Arg	Gln	Gly	Leu	Gly	Ala	Glu	Leu
		100					105						110		
Gly	Ile	Thr	Arg	Leu	Arg	Arg	Gly	Trp	Ser	Phe	Arg	Cys	Ser	Phe	Pro
		115				120						125			
Cys	Ser	Val	Leu												
		130													

<210> 1671

<211> 432

<212> DNA

<213> Homo sapiens

<400> 1671

gcgcgccggg gcgggaggac gccagtcgtc ttcccgcccc tcaccacgac acgaccatta
 60

tcgcgacgaa ggaagcccat ggctgaaacc acatcgccgg cacagcgaa acccagggc
 120
 gcatcccgca tgaagccggt gtcgcggtc ggggacacga ttttcgctgg cgccctgctg
 180
 gttattgcca tagccctggc cgtcatcgtc atcctgatgt tcgtcttctt catgaagacg
 240
 gcagccccga cgttggtggc taacaccgat aactttttca cgtcccgggc ttggacaacg
 300
 gatcagaacc cgccggcctt tggatccag gccctgctat ggaagacagt catctcatcc
 360
 ctgcttgccc tgctcatcg agtgccgctc tcggtgggca tcgctctgtt tatcaccgag
 420
 ctgcaccta gg
 432

<210> 1672

<211> 144

<212> PRT

<213> Homo sapiens

<400> 1672

Ala	Arg	Arg	Gly	Gly	Arg	Thr	Pro	Val	Val	Phe	Pro	Pro	Leu	Thr	Thr
1			5					10					15		
Thr	Arg	Pro	Leu	Ser	Arg	Arg	Arg	Lys	Pro	Met	Ala	Glu	Thr	Thr	Ser
			20					25				30			
Pro	Ala	Gln	Arg	Lys	Pro	Thr	Ala	Ala	Ser	Arg	Met	Lys	Pro	Val	Ser
		35				40						45			
Arg	Val	Gly	Asp	Thr	Ile	Phe	Ala	Gly	Ala	Ser	Ser	Val	Ile	Ala	Ile
50					55					60					
Ala	Leu	Ala	Val	Ile	Val	Ile	Leu	Met	Phe	Val	Phe	Leu	Met	Lys	Thr
65				70					75					80	
Ala	Ala	Pro	Thr	Leu	Leu	Ala	Asn	Thr	Asp	Asn	Phe	Phe	Thr	Ser	Arg
			85					90						95	
Ala	Trp	Thr	Thr	Asp	Gln	Asn	Pro	Pro	Ala	Phe	Gly	Ile	Gln	Ala	Leu
		100					105					110			
Leu	Trp	Thr	Thr	Val	Ile	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Ile	Ala	Val
	115				120						125				
Pro	Leu	Ser	Val	Gly	Ile	Ala	Leu	Phe	Ile	Thr	Gln	Leu	Ala	Pro	Arg
130					135						140				

<210> 1673

<211> 401

<212> DNA

<213> Homo sapiens

<400> 1673

tcgcgagcac actccagcct ctggggcgctc tgccagggcc tctgtgtttt gatatactct
 60
 gacctggcag tgaagctgct gatgaatgca cgacaaagac cagtttgctc cgtaaccccc
 120
 ggctcccgag gtctttttcca tgagccaaag gcctggctct ggaggggggt gccctgcagc
 180
 tctgtggccc ttcttcagg ggagttcatt gctgggggtg gccctgcagg gacctccact
 240

gtgctggggga ggggaagaag aaggatgcaa cagggggagg ggagaatttg agaaaatagg
 300
 atgcaaattc tccacttggtg aataaagaaa tagagagcca ttgctaagaa ctatgtttac
 360
 gcagggttag tgctgggacc cagaaccagt caactgggtt t
 401

<210> 1674
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1674
 Met Ala Leu Tyr Phe Phe Ile His Lys Trp Arg Ile Cys Ile Leu Phe
 1 5 10 15
 Ser Gln Ile Leu Pro Ser Pro Cys Cys Ile Leu Leu Pro Leu Pro
 20 25 30
 Ser Thr Val Glu Val Pro Ala Gly Pro Pro Pro Ala Met Asn Ser Pro
 35 40 45
 Gly Arg Arg Pro Ala Glu Leu Gln Gly Thr Pro Leu Gln Asp Gln Ala
 50 55 60
 Phe Gly Ser Trp Lys Arg Arg Trp Glu Pro Gly Val Thr Glu Gln Thr
 65 70 75 80
 Gly Leu Cys Arg Ala Phe Ile Ser Ser Phe Thr Ala Arg Ser Glu Tyr
 85 90 95
 Ile Lys Thr Gln Arg Pro Trp Gln Thr Pro Gln Arg Leu Glu Cys Ala
 100 105 110
 Arg

<210> 1675
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 1675
 gccggcgac ccacctggga cgtggtgaaa tcggcaaac tcacctctt agctacctgc
 60
 gcgccaaccg cacgggcagc ctcccacacg ccctctagag cgctgctgga cagaatgggt
 120
 tgattgtttg gcatgctctc aggatacccg tttagccagg aaacaccggg aggcttgcta
 180
 ctatgcgagc agccgacgca cgggtagagg gaattccac cacagtccct cgcactccac
 240
 ccgcacacgc cctgggaacc gtcaccgcg gtaccaccgg gtcaatcggc tccgcaaatg
 300
 cgaccgctgg atgtgccacc accccgcnc a tccgcagtgc gctccgtaac gccgtctgca
 360
 acaccgtccc ctccgtatct gccgacacct gtgccaacac ttgtaccgat gcattgcaccg
 420
 atgcagcaac aggcgctccg ctccgtatcg atctgggata cggcgccgccc ccctggacca
 480
 ctggttgagat ggctacgcgt
 500

<210> 1676
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 1676
 Arg Glu Phe Pro Pro Gln Ser Leu Ala Leu His Pro His Thr Pro Trp
 1 5 10 15
 Glu Pro Ser Pro Ala Val Pro Pro Gly Gln Ser Ala Pro Gln Met Arg
 20 25 30
 Pro Leu Asp Val Pro Pro Pro Arg Xaa Ser Ala Val Arg Ser Val Thr
 35 40 45
 Pro Ser Ala Thr Pro Ser Pro Pro Tyr Leu Pro Thr Pro Val Pro Thr
 50 55 60
 Leu Val Pro Met His Ala Pro Met Gln Gln Gln Ala Leu Arg Ser Leu
 65 70 75 80
 Ser Ile Trp Asp Thr Ala Pro Pro Pro Gly Pro Leu Leu Arg Trp Leu
 85 90 95
 Arg

<210> 1677
 <211> 631
 <212> DNA
 <213> Homo sapiens

<400> 1677
 nntcatgatt tcctcaatga tgccaagggtg atggaggccg gctataacctg ggtgcagggtg
 60
 gatttgcgcg gtacgggtgc ttctactggg tgtttngac tggaatggtc cncgggggag
 120
 cagcaggatg ttgtgaccgc cgtggaatgg gcggcggtag agccgtggtc gaatggtcgg
 180
 gtggggcgttt tcggtaaatc ctacgatggg gggacggggt cttattgctg caggtaatca
 240
 gccgcggggg ttggctgctg tgggtggcga ggagccagct atggagccct acacttacct
 300
 gtataacaat gaggtccttt actacaacgc tattggtacg agcctttctt atgatgagat
 360
 tgctgcctcc cccggcgtg tccttcacga cactcccgaa tatatgaaga acagtgtcta
 420
 cgaggtggcc caccgcatt gcctgtccga caatttgcgt aattctttag accccatccg
 480
 tagccacaaa taatggggcg gatcggtctt tccctcacca agacgcataa tttccccctg
 540
 gcccttgctt atttccgctg gccttattga ggacaatacg gagcctgatg gtttgggtgga
 600
 attgttgaag gaccgtaagg ctccgacgcg t
 631

<210> 1678
 <211> 78
 <212> PRT

<213> Homo sapiens

<400> 1678

```

Xaa His Asp Phe Leu Asn Asp Ala Lys Val Met Glu Ala Gly Tyr Thr
 1             5             10             15
Trp Val Gln Val Asp Leu Arg Gly Thr Gly Ala Ser Thr Gly Cys Leu
          20             25             30
Xaa Leu Glu Trp Ser Xaa Gly Glu Gln Gln Asp Val Val Thr Ala Val
          35             40             45
Glu Trp Ala Ala Val Gln Pro Trp Ser Asn Gly Arg Val Gly Leu Phe
          50             55             60
Gly Lys Ser Tyr Asp Gly Gly Thr Gly Ser Tyr Cys Cys Arg
          65             70             75

```

<210> 1679

<211> 531

<212> DNA

<213> Homo sapiens

<400> 1679

```

nctacttaga gcaaaggtag gaaaagaagg cagctaggcg tggctctcat tccttcccc
60
agaatggatt ataagtcgag cctgatccag gatgggaatc ccatggagaa cttggagaag
120
cagctgatct gccctatctg cctggagatg tttaccaagc cagtggctcat cttgccgtgc
180
cagcacaacc tgtgccgga ggtgtccaat gacatcttcc aggtgcaaa tccctactgg
240
accagccggg gcagctcagt gtccatgtct ggaggccgtt tccgctgccc tacctgccgc
300
cacgagtgta tcatggatcg tcacggagtg tacggcctgc agaggaacct gctggtggag
360
aacatcatcg acatctacaa acaggagtg cccagtcggc cgctgcagaa gggcagtcac
420
cccatgtaca aggagcacga agatgagaaa atcaacatct actgtctcac gtgtgaggtg
480
cccacgtgct ccatgtgcaa ggtgtttggg atccacaagg cctgcgaggt g
531

```

<210> 1680

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1680

```

Met Glu Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
 1             5             10             15
Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
          20             25             30
Lys Cys Ala Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Ser
          35             40             45
Arg Gly Ser Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Thr
          50             55             60
Cys Arg His Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln

```

```

65          70          75          80
Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys
      85          90          95
Ser Ser Arg Pro Leu Gln Lys Gly Ser His Pro Met Tyr Lys Glu His
      100        105        110
Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Thr Cys Glu Val Pro Thr
      115        120        125
Cys Ser Met Cys Lys Val Phe Gly Ile His Lys Ala Cys Glu Val
      130        135        140

<210> 1681
<211> 396
<212> DNA
<213> Homo sapiens

<400> 1681
gagttccaca actgcaggac agatgacaag acgttccaat gtgagatgtg tttcagattc
60
ttttccacca acagcaacct ctccaagcac aagaagaagc acggcgacaa gaagtttgcc
120
tgtgaggtct gcagcaagat gttctaccgc aaggacgtca tgctggacca ccagcgccgg
180
cacnctggaa ggagtgcggc gagtgaagcg nnagaggacc tggaggccgg tggggagaaac
240
ctggtccggt acaagaagga gccttccggg tgcccgtgtg gtggcaaggt gttctcctgc
300
cggagcaata tgaacaagca cctgctcacc cacggcgaca agaagtacac ctgcgagatc
360
tgccggcgca agttcttccg cgtggatgtg ctcagg
396

<210> 1682
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1682
Glu Phe His Asn Cys Arg Thr Asp Asp Lys Thr Phe Gln Cys Glu Met
1          5          10          15
Cys Phe Arg Phe Phe Ser Thr Asn Ser Asn Leu Ser Lys His Lys Lys
      20          25          30
Lys His Gly Asp Lys Lys Phe Ala Cys Glu Val Cys Ser Lys Met Phe
      35          40          45
Tyr Arg Lys Asp Val Met Leu Asp His Gln Arg Arg His Xaa Gly Arg
      50          55          60
Ser Ala Ala Ser Glu Ala Xaa Glu Asp Leu Glu Ala Gly Gly Glu Asn
      65          70          75          80
Leu Val Arg Tyr Lys Lys Glu Pro Ser Gly Cys Pro Val Cys Gly Lys
      85          90          95
Val Phe Ser Cys Arg Ser Asn Met Asn Lys His Leu Leu Thr His Gly
      100        105        110
Asp Lys Lys Tyr Thr Cys Glu Ile Cys Gly Arg Lys Phe Phe Arg Val
      115        120        125
Asp Val Leu Arg

```

130

<210> 1683

<211> 676

<212> DNA

<213> Homo sapiens

<400> 1683

```

nncggccgga caggtcccg gcagccccgc ccaacatgga cccagacccc caggcgggcg
60
tgcaggtggg catgcgggtg gtgcgcggcg tggaccggaa gtggggccag caggacggcg
120
gcgagggcgg cgtgggcacg gtggtggagc ttggccgcca cggcagcccc tcgacacccc
180
accgcacagt ggtcgtgcag tgggaccagg gcacgcgcac caactaccgc gccggctacc
240
agggcgcgca cgacctgctg ctgtacgaca acgcccagat cggcgctccg caccccaaca
300
tcactctgta ctgctgcaag aagcacgggc tgcgggggat gcgctggaag tgccgtgtgt
360
gcctggacta cgacctctgc acgcagtgtc acatgcacaa caagcatgag ctcgccccag
420
ccttcgacgg ctacgagacc gctcaactgc gccctgtcac actgagtcgc cgccaggggc
480
tcccagggat cccactaagg ggcattcttc agggagcgaa ggtggtgcga gggcccagat
540
gggagtgagg ctcacaggat ggtgagtgga ggcagagggg cggggtcagg gctgggctgt
600
ggctggctca tggctcagcc ttacgcctgt gggggggcct ctttccccag gagggaaggg
660
aaaccgggccc gccgga
676

```

<210> 1684

<211> 154

<212> PRT

<213> Homo sapiens

<400> 1684

```

Xaa Gly Arg Thr Gly Pro Glu Gln Pro Arg Pro Thr Trp Thr Gln Thr
1 5 10 15
Pro Arg Arg Ala Cys Arg Trp Ala Cys Gly Trp Cys Ala Ala Trp Thr
20 25 30
Gly Ser Gly Ala Ser Arg Thr Ala Ala Arg Ala Trp Thr Ala Arg Trp
35 40 45
Trp Ser Leu Ala Ala Thr Ala Ala Pro Arg His Pro Thr Ala Gln Trp
50 55 60
Ser Cys Ser Gly Thr Arg Ala Arg Ala Pro Thr Thr Ala Pro Ala Thr
65 70 75 80
Arg Ala Arg Thr Thr Cys Cys Cys Thr Thr Pro Arg Ser Ala Ser
85 90 95
Gly Thr Pro Thr Ser Ser Val Thr Ala Ala Arg Ser Thr Gly Cys Gly
100 105 110
Gly Cys Ala Gly Ser Ala Val Cys Ala Trp Thr Thr Thr Ser Ala Arg

```

115	120	125
Ser Ala Thr Cys Thr Thr Ser Met Ser Ser Pro Thr Pro Ser Thr Ala		
130	135	140
Thr Arg Pro Leu Thr Arg Ala Leu Ser His		
145	150	

<210> 1685

<211> 2740

<212> DNA

<213> Homo sapiens

<400> 1685

```

ngaggaggag ccggcgggcg ctccggggaa agggaggggg gcgctccga gccgcccgcg
60
cccagggggt ggcgagggaa aggcgtacgc gctcagcaga gggcgggcag cggcggggag
120
ggggcctccc ctctccatc ctctctctct gcgggcaaaa cccaggaac cggcagcaga
180
aactccgaa gccggcgttg gggggcggc agcgggtgtg gagggagcta ctggaagaa
240
ggatgtctgc agtctgagct catccagttc catctcaaga aggagcgggc gccagcggcg
300
gcggcccgcg ctcatagca cgctaagaac gcggcgcgca gcagtagccg cagctccccg
360
gtgtctggcc cccctgccgt ttgcgagacc ctggcgcgtc cctccgcctc ccaatggcg
420
gcggcgcgcg agggccccc gcagagcgca gagggcagcg cgagcggcg gggcatgcag
480
gcggcagcgc ccccttcgtc gcagccgcac ccgcagcagc tccaagagca ggaagaaatg
540
caagaggaga tgagaagct gcgagaggaa aacgagactc tcaagaacga gatcgatgag
600
ctgagaaccg agatggacga gatgagggac actttcttcg aggaggatgc ctgtcaactg
660
caggaaatgc gccacgagtt ggagagagcc aacaaaaact gccggatcct gcagtaccgc
720
ctccgcaaag ccgagcgcaa aaggctccgc tacgcccaga ccgggggaaat cgacggggag
780
ctgttcgcga gcctggagca ggacctcaag gttgcaaagg atgtatctgt gagacttcac
840
catgaattag aaaatgtgga agaaaagaga acaacaacag aagatgaaaa tgagaaactg
900
aggcaacagc tcatagaagt tgaatttga aagcaagctt tacagaatga actggaaaaa
960
atgaaagagt tatccttaaa aagaagagga agcaagatt tgccaaaatc tgaaaaaag
1020
gctcaacaga cccccacaga ggaggacaat gaagatctga agtgccagct gcagtttgtt
1080
aagggaaga ccgctttgat gagaagaaa atggccaaga ttgataaaga aaaggacaga
1140
tttgaacacg agctccagaa gtacagatcc ttttatgggg atctggacag tcctttggcc
1200
aaaggagaag ccggaggccc tcccagcact agggaggcgc agctcaagct acggctaagg
1260

```

ctggtggagg aagaagccaa catcctgggc aggaaaatcg tcgaactgga ggtggagAAC
 1320
 agaggcctga aggcggaact ggacgacctt aggggagatg acnnttcaac ggctcggcca
 1380
 acccgctcat gagggagca gagcgaatcc ctgtcggagc tgccggcagca cctgcagctg
 1440
 gtggaagacg agacggagct gctgcggagg aacgtggccg acctggagga gcagaacaag
 1500
 cgcatacggc cggagctcaa caagtacaag tacaagnntc cggcggccac gacagcgcgC
 1560
 ggcaaccaga caacgccana gaccgaggcc ctgcaggagg agctgaaggc ggcgcgctg
 1620
 cagatcaacg agctcagcgg caaggtcatg cagctgcagt acgagaaccg cgtgcttatg
 1680
 tccaacatgc agcgctacga cctggcctcg cacctgggca tcccgcgag ccccgcgac
 1740
 agcgacggcg agagcgacgc gggcaagaag gagagcgacg acgactcggc gcctccgcac
 1800
 cgcaagcgcg aaggggcccat cggcggcgag agcgactcgg agggagtggn cgcaacatcc
 1860
 gctgcctcan cgcctactcg ctctttctac ccggcgcccg ggcctgggcc caagagcttc
 1920
 tccgatcggc agcagatgaa ggacatccg tcggaggccg agcgccctgg caagaccatc
 1980
 gaccggctca tcgccgacac gagcaccatc atcaccgagg cgcgcacnt acgtggccaa
 2040
 cggggagcctg ttncggact catggacgag gaggacgacg gcagccgcac ccgggagcac
 2100
 gagctgctct accgcatcaa cgctcagatg aaggccttcc gcaaggagct gcagaccttc
 2160
 atcgaccgcc tcgaggtgcc caagtctgag gacgaccgag cgcgcgagga gccattttcc
 2220
 gtgagtcaga tgttcagacc tatcatttta cttatttctca ttcttgtatt attttcatca
 2280
 ctttttaca caacaatatt taaacttgct ttctttttta cactgttttt tgtactgtaa
 2340
 atctttcatc atttaccatt cattgtagta ttttcagttt gttttatttg ttcacccttc
 2400
 aagacaagaa gtaaaagaag tataattttc gtatgaacca atgtataaa aacactgaag
 2460
 actgcttatt tttttacaaa gatacaactc atcttaccaa gaccaaatcc aataagaagc
 2520
 ccaaacacta aatatatttc ggtaagaaag tgtgacattt ttctgtatga attgttttaa
 2580
 tttttacttc ttttttcat cctgtttgtc toctcttgat aaataattgg catactgaat
 2640
 ataaaaatgg actacatgtc tcataattat ttctcagtag ttactatta ttattcaaaa
 2700
 gctggacgga cattcacaat ttggtcacat ttccaaaaag
 2740

<210> 1686

<211> 463

<212> PRT

<213> Homo sapiens

<400> 1686

Xaa Gly Gly Ala Gly Gly Gly Ser Gly Glu Arg Glu Gly Gly Ala Pro
 1 5 10 15
 Gln Pro Pro Pro Arg Gly Trp Arg Gly Lys Gly Val Arg Ala Gln
 20 25 30
 Gln Arg Gly Gly Ser Gly Gly Glu Gly Ala Ser Pro Ser Ser Ser
 35 40 45
 Ser Ser Ala Gly Lys Thr Pro Gly Thr Gly Ser Arg Asn Ser Gly Ser
 50 55 60
 Gly Val Ala Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr Trp Lys Glu
 65 70 75 80
 Gly Cys Leu Gln Ser Glu Leu Ile Gln Phe His Leu Lys Lys Glu Arg
 85 90 95
 Ala Ala Ala Ala Ala Ala Ala Gln Met His Ala Lys Asn Gly Gly
 100 105 110
 Gly Ser Ser Ser Arg Ser Ser Pro Val Ser Gly Pro Pro Ala Val Cys
 115 120 125
 Glu Thr Leu Ala Val Ala Ser Ala Ser Pro Met Ala Ala Ala Ala Glu
 130 135 140
 Gly Pro Gln Gln Ser Ala Glu Gly Ser Ala Ser Gly Gly Met Gln
 145 150 155 160
 Ala Ala Ala Pro Pro Ser Ser Gln Pro His Pro Gln Gln Leu Gln Glu
 165 170 175
 Gln Glu Glu Met Gln Glu Glu Met Glu Lys Leu Arg Glu Glu Asn Glu
 180 185 190
 Thr Leu Lys Asn Glu Ile Asp Glu Leu Arg Thr Glu Met Asp Glu Met
 195 200 205
 Arg Asp Thr Phe Phe Glu Glu Asp Ala Cys Gln Leu Gln Glu Met Arg
 210 215 220
 His Glu Leu Glu Arg Ala Asn Lys Asn Cys Arg Ile Leu Gln Tyr Arg
 225 230 235 240
 Leu Arg Lys Ala Glu Arg Lys Arg Leu Arg Tyr Ala Gln Thr Gly Glu
 245 250 255
 Ile Asp Gly Glu Leu Leu Arg Ser Leu Glu Gln Asp Leu Lys Val Ala
 260 265 270
 Lys Asp Val Ser Val Arg Leu His His Glu Leu Glu Asn Val Glu Glu
 275 280 285
 Lys Arg Thr Thr Thr Glu Asp Glu Asn Glu Lys Leu Arg Gln Gln Leu
 290 295 300
 Ile Glu Val Glu Ile Ala Lys Gln Ala Leu Gln Asn Glu Leu Glu Lys
 305 310 315 320
 Met Lys Glu Leu Ser Leu Lys Arg Arg Gly Ser Lys Asp Leu Pro Lys
 325 330 335
 Ser Glu Lys Lys Ala Gln Gln Thr Pro Thr Glu Glu Asp Asn Glu Asp
 340 345 350
 Leu Lys Cys Gln Leu Gln Phe Val Lys Glu Glu Ala Ala Leu Met Arg
 355 360 365
 Lys Lys Met Ala Lys Ile Asp Lys Glu Lys Asp Arg Phe Glu His Glu
 370 375 380
 Leu Gln Lys Tyr Arg Ser Phe Tyr Gly Asp Leu Asp Ser Pro Leu Pro
 385 390 395 400
 Lys Gly Glu Ala Gly Gly Pro Pro Ser Thr Arg Glu Ala Glu Leu Lys

```

                405                410                415
Leu Arg Leu Arg Leu Val Glu Glu Ala Asn Ile Leu Gly Arg Lys
                420                425                430
Ile Val Glu Leu Glu Val Glu Asn Arg Gly Leu Lys Ala Glu Leu Asp
                435                440                445
Asp Leu Arg Gly Asp Asp Xaa Ser Thr Ala Arg Pro Thr Arg Ser
                450                455                460

```

<210> 1687
 <211> 326
 <212> DNA
 <213> Homo sapiens

```

<400> 1687
gtgcacacag gtgagcgtcc ctacaagtgt ccacactgcg actatgcagg tacccagtcg
60
ggctcgctca agtatcacct tcagcgtcac caccgagagc agaagaacag tgcgggttcc
120
tgggcctccc ccagaacccc cgccaccttc ccagcggggc tcaactgcagc cgcagtcagg
180
agccaagcca actcaggcct cagccacctg ggtagagggc actgcaagta cccggcctcc
240
ttcgaagcagc accggaccag ggtcccgtag gaagcctgct agccctggga ggaccctgag
300
aaacggcgat gtggtgaagc cgaact
326

```

<210> 1688
 <211> 89
 <212> PRT
 <213> Homo sapiens

```

<400> 1688
Val His Thr Gly Glu Arg Pro Tyr Lys Cys Pro His Cys Asp Tyr Ala
1      5      10      15
Gly Thr Gln Ser Gly Ser Leu Lys Tyr His Leu Gln Arg His His Arg
20     25     30
Glu Gln Lys Asn Ser Ala Gly Ser Trp Ala Ser Pro Arg Thr Pro Ala
35     40     45
Thr Phe Pro Ala Gly Leu Thr Ala Ala Val Arg Ser Gln Ala Asn
50     55     60
Ser Gly Leu Ser His Leu Gly Arg Gly His Cys Lys Tyr Pro Ala Ser
65     70     75     80
Phe Glu Gln His Arg Thr Arg Val Pro
85

```

<210> 1689
 <211> 301
 <212> DNA
 <213> Homo sapiens

```

<400> 1689
nggggaagcc atggctgctt aaggacaatg cactgtcagc tcggtgatgt cttgatttgg
60

```

```

tctgggattc tgcacttagt aattgcagat aatactcatg tggcgccaag gaaaaaaaaa
120
ttggcctttt cccagtcctat taagcctaaa caaacacat cactttacat caggcagatc
180
atgtgggtacc agaattttcc agtttggcgg actatcttga tcaaataaac taaattattg
240
ccactgtggc tatctgtgaa agaacacaat gaagaaaatc tggagcctta tctcatactc
300
a
301

```

<210> 1690

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1690

```

Met His Cys Gln Leu Gly Asp Val Leu Ile Trp Ser Gly Ile Leu His
1           5           10           15
Leu Val Ile Ala Asp Asn Thr His Val Ala Pro Arg Lys Lys Lys Leu
20           25           30
Ala Phe Ser Gln Ser Ile Lys Pro Lys Gln Thr Thr Ser Leu Tyr Ile
35           40           45
Arg Gln Ile Met Trp Tyr Gln Asn Phe Pro Val Trp Arg Thr Ile Leu
50           55           60
Ile Lys Ser Thr Lys Leu Leu Pro Leu Trp Leu Ser Val Lys Glu His
65           70           75           80
Asn Glu Glu Asn Leu Glu Pro Tyr Leu Ile Leu
85           90

```

<210> 1691

<211> 483

<212> DNA

<213> Homo sapiens

<400> 1691

```

nacgcgttcc ggtatgccga tgggcccgtg ctgctgggcg tccgccggcg gcgcggtgag
60
ttgtgccttg aagtgtggga ccgcggcccc ggcattcctc aagacaaca aaagtcattc
120
ttcgaagaat tcaaaccgct ggacagtcac cagaccgcg ccgagaaagg cctgggcctg
180
ggcctggcga ttgccgacgg cttgtgccgc gtgctcgggc atcgcttgag cgtgcgttcg
240
tggccgggca agggcagcgt gttcagcgtg cgcgtgccgt tggcgcgcac ccagggtcagc
300
gcgcctgccca agccggcgca ggaaagcggc cagccgttga gtggcgcgca ggtgctgtgt
360
gtgaataaca aagaagcat cctgatcggc atgcgcagct tgctcccgcg ctggggctgc
420
gaagtcctggc ccgcgcgcga ccaggcgcaa tgtgccgcgc tgttggctga ggggtgtgcg
480
ccg
483

```

<210> 1692
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 1692
 Xaa Ala Phe Arg Tyr Ala Asp Gly Pro Val Leu Leu Gly Val Arg Arg
 1 5 10 15
 Arg Arg Gly Glu Leu Cys Leu Glu Val Trp Asp Arg Gly Pro Gly Ile
 20 25 30
 Pro Gln Asp Lys Gln Lys Ser Phe Phe Glu Glu Phe Lys Arg Leu Asp
 35 40 45
 Ser His Gln Thr Arg Ala Glu Lys Gly Leu Gly Leu Gly Leu Ala Ile
 50 55 60
 Ala Asp Gly Leu Cys Arg Val Leu Gly His Arg Leu Ser Val Arg Ser
 65 70 75 80
 Trp Pro Gly Lys Gly Ser Val Phe Ser Val Arg Val Pro Leu Ala Arg
 85 90 95
 Thr Gln Val Ser Ala Pro Ala Lys Pro Ala Gln Glu Ser Gly Gln Pro
 100 105 110
 Leu Ser Gly Ala Gln Val Leu Cys Val Asn Asn Lys Glu Ser Ile Leu
 115 120 125
 Ile Gly Met Arg Ser Leu Leu Pro Arg Trp Gly Cys Glu Val Trp Pro
 130 135 140
 Ala Arg Asp Gln Ala Gln Cys Ala Ala Leu Leu Ala Glu Gly Val Arg
 145 150 155 160
 Pro

<210> 1693
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 1693
 acgcgtgttc catctgcagc cgtgcgaaaa ctctcccacc atgtcgcaga ctggatactt
 60
 cgaggattca agctactaca agtgtgacac agatgacacc ttccgaagccc gagaggagat
 120
 actggggggg atgaggcctt cgacactgcc aactcctcca tcgtgtcttg cgagagtatc
 180
 cgtttttttg tcaatgtcaa ccttgagatg caggccacca acactgagaa tgaagcgact
 240
 tcgggtggct gtgtgtctct gcacacctcc cgaaaggcca gcactgcctt gaacgagacg
 300
 gccacctccc tggataacgt gctgcggacc atg
 333

<210> 1694
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1694

```

Met Val Arg Ser Thr Leu Ser Arg Glu Val Ala Val Ser Phe Arg Thr
 1             5             10             15
Met Leu Ala Phe Arg Glu Val Cys Arg Ser Thr Gln Pro Pro Glu Val
             20             25             30
Ala Ser Phe Ser Val Leu Val Ala Cys Ile Ser Arg Leu Thr Leu Thr
             35             40             45
Lys Lys Arg Ile Leu Ser Pro Asp Thr Met Glu Glu Leu Ala Val Ser
             50             55             60
Lys Ala Ser Ser Pro Pro Val Ser Pro Leu Gly Leu Arg Arg Cys His
65             70             75             80
Leu Cys His Thr Cys Ser Ser Leu Asn Pro Arg Ser Ile Gln Ser Ala
             85             90             95
Thr Trp Trp Glu Ser Phe Arg Thr Ala Ala Asp Gly Thr Arg
             100             105             110

```

<210> 1695

<211> 485

<212> DNA

<213> Homo sapiens

<400> 1695

```

tgatcagctt tatcaggagt ttttgcaagt accgcagatt tatgttgaat cctagtaagc
60
gccaggaatt tgaagactat cttcaccagg aaatgcaaaa tagcaaggaa aatttcacca
120
cagcacacaaa cacatcgga cgttcagctc caccctccac aaatgtccgg agtcgacagc
180
aagagaatgg agaaataacc cttgtaaagc gtcgtatatt tggccacagg attatcactg
240
tcaactttgc gatcaatgat ctatatctt tttctgaaat ggagaaatatt aatgatctgg
300
tcagttcagc ccacatgctg caggtcacac gggcatataa tgagaatgat gtgaccta
360
tgcggtccaa aatgaacatt atccaaaaac ttttctgaa tcttgacatc cctccaaagc
420
tgagggtgaa tgtccctgag ttccagaagg atgccatcct tgctgccatc acagagggct
480
accta
485

```

<210> 1696

<211> 148

<212> PRT

<213> Homo sapiens

<400> 1696

```

Met Leu Asn Pro Ser Lys Arg Gln Glu Phe Glu Asp Tyr Leu His Gln
 1             5             10             15
Glu Met Gln Asn Ser Lys Glu Asn Phe Thr Thr Ala His Asn Thr Ser
             20             25             30
Gly Arg Ser Ala Pro Pro Ser Thr Asn Val Arg Ser Ala Asp Gln Glu
             35             40             45
Asn Gly Glu Ile Thr Leu Val Lys Arg Arg Ile Phe Gly His Arg Ile

```

```

      50              55              60
Ile Thr Val Asn Phe Ala Ile Asn Asp Leu Tyr Phe Phe Ser Glu Met
65              70              75              80
Glu Lys Phe Asn Asp Leu Val Ser Ser Ala His Met Leu Gln Val Asn
      85              90              95
Arg Ala Tyr Asn Glu Asn Asp Val Ile Leu Met Arg Ser Lys Met Asn
      100             105             110
Ile Ile Gln Lys Leu Phe Leu Asn Ser Asp Ile Pro Pro Lys Leu Arg
      115             120             125
Val Asn Val Pro Glu Phe Gln Lys Asp Ala Ile Leu Ala Ala Ile Thr
      130             135             140
Glu Gly Tyr Leu
145

```

```

<210> 1697
<211> 337
<212> DNA
<213> Homo sapiens

```

```

<400> 1697
accaggttcc caccatcctc aggggaatca caggttactg gctttggaga ccgagatgtc
60
ttccccgcctc ccaggggcct gtggatggga ctccctcgga attcgactcc caggggaaaa
120
gccaaagagct gcctccttgg gacaactggg gcggcagctg tgatcgacac tggcttcagc
180
agaggcctga gcggctgcct ccgttgccca gcaggctctg agagcactcg cccggcctga
240
ctgttcaccc atcctttcac ccggaggcca gctgtggctg tctgtgctct cagaggggag
300
gcgatgggca aggcgcctgc catgcagatg ggtggtg
337

```

```

<210> 1698
<211> 107
<212> PRT
<213> Homo sapiens

```

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<400> 1698
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Gln Leu Leu Ala Phe Pro Leu Gly Val Glu Phe Ala Gly Ser Pro Ile
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<211> 442

<212> DNA

<213> Homo sapiens

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			565					570						575				
Val	Thr	Thr	Ile	Ser	Ser	Asn	Leu	Thr	Glu	Met	Ser	Arg	Gly	Val	Lys			
			580					585					590					
Leu	Leu	Ala	Ala	Leu	Leu	Glu	Asp	Glu	Gly	Gly	Ser	Gly	Arg	Pro	Leu			
		595				600						605						
Leu	Gln	Ala	Ala	Lys	Gly	Leu	Ala	Gly	Ala	Val	Ser	Glu	Leu	Leu	Arg			
		610				615				620								
Ser	Ala	Gln	Pro															

[illegible]

1170	1175	1180
Leu Ala Gln Val	Ala Lys Ala Val	Thr Gln Ala Leu Asn Arg Cys Val
1185	1190	1195
Ser Cys Leu Pro	Gly Gln Arg Asp	Val Asp Asn Ala Leu Arg Ala Val
	1205	1210
Gly Asp Ala Ser	Lys Arg Leu Leu Ser	Asp Ser Leu Pro Pro Ser Thr
	1220	1225
Gly Thr Phe Gln	Glu Ala Gln Ser Arg	Leu Asn Glu Ala Ala Ala Gly
	1235	1240
Leu Asn Gln Ala	Ala Thr Glu Leu Val	Gln Ala Ser Arg Gly Thr Pro
	1250	1255
Gln Asp Leu Ala	Arg Ala Ser Gly Arg	Phe Gly Gln Asp Phe Ser Thr
	1265	1270
Phe Leu Glu Ala	Gly Val Glu Met	Ala Gly Gln Ala Pro Ser Gln Glu
	1285	1290
Asp Arg Ala Gln	Val Val Ser Asn Leu	Lys Gly Ile Ser Met Ser Ser
	1300	1305
Ser Lys Leu Leu	Leu Ala Ala Lys Ala	Leu Ser Thr Asp Pro Ala Ala
	1315	1320
Pro Asn Leu Lys	Ser Gln Leu Ala Ala	Ala Arg Ala Val Thr Asp
	1330	1335
Ser Ile Asn Gln	Leu Ile Thr Met	Cys Thr Gln Gln Ala Pro Gly Gln
	1345	1350
Lys Glu Cys Asp	Asn Ala Leu Arg	Glu Leu Glu Thr Val Arg Glu Leu
	1365	1370
Leu Glu Asn Pro	Val Gln Pro Ile Asn	Asp Met Ser Tyr Phe Gly Cys
	1380	1385
Leu Asp Ser Val	Met Glu Asn Ser	Lys Val Leu Gly Glu Ala Met Thr
	1395	1400
Gly Ile Ser Gln	Asn Ala Lys Asn	Gly Asn Leu Pro Glu Phe Gly Asp
	1410	1415
Ala Ile Ser Thr	Ala Ser Lys Ala	Leu Cys Gly Phe Thr Glu Ala Ala
	1425	1430
Ala Gln Ala Ala	Tyr Leu Val Gly	Val Ser Asp Pro Asn Ser Gln Ala
	1445	1450
Gly Gln Gln Gly	Leu Val Glu Pro	Thr Gln Phe Ala Arg Ala Asn Gln
	1460	1465
Ala Ile Gln Met	Ala Cys Gln Ser	Leu Gly Glu Pro Gly Cys Thr Gln
	1475	1480
Ala Gln Val Leu	Ser Ala Ala Thr	Ile Val Ala Lys His Thr Ser Ala
	1490	1495
Leu Cys Asn Ser	Cys Arg Leu Ala	Ser Ala Arg Thr Thr Asn Pro Thr
	1505	1510
Ala Lys Arg Gln	Phe Val Gln Ser	Ala Lys Glu Val Ala Asn Ser Thr
	1525	1530
Ala Asn Leu Val	Lys Thr Ile Lys	Ala Leu Asp Gly Ala Phe Thr Glu
	1540	1545
Glu Asn Arg Ala	Gln Cys Arg Ala	Ala Thr Ala Pro Leu Leu Glu Ala
	1555	1560
Val Asp Asn Leu	Ser Ala Phe Ala	Ser Asn Pro Glu Phe Ser Ser Ile
	1570	1575
Pro Ala Gln Ile	Ser Pro Glu Gly	Arg Ala Ala Met Glu Pro Ile Val
	1585	1590
Ile Ser Ala Lys	Thr Met Leu Glu	Ser Ala Gly Gly Leu Ile Gln Thr

1605 1610 1615
 Ala Arg Ala Leu Ala Val Asn Pro Arg Asp Pro Pro Ser Trp Ser Val
 1620 1625 1630
 Leu Ala Gly His Ser Arg Thr Val Ser Asp Ser Ile Lys Lys Leu Ile
 1635 1640 1645
 Thr Ser Met Arg Asp Lys Ala Pro Gly Gln Leu Glu Cys Glu Thr Ala
 1650 1655 1660
 Ile Ala Ala Leu Asn Ser Cys Leu Arg Asp Leu Asp Gln Ala Ser Leu
 1665 1670 1675 1680
 Ala Ala Val Ser Gln Gln Leu Ala Pro Arg Glu Gly Ile Ser Gln Glu
 1685 1690 1695
 Ala Leu His Thr Gln Met Leu Thr Ala Val Gln Glu Ile Ser His Leu
 1700 1705 1710
 Ile Glu Pro Leu Ala Asn Ala Ala Arg Ala Glu Ala Ser Gln Leu Gly
 1715 1720 1725
 His Lys Val Ser Gln Met Ala Gln Tyr Phe Glu Pro Leu Thr Leu Ala
 1730 1735 1740
 Ala Val Gly Ala Ala Ser Lys Thr Leu Ser His Pro Gln Gln Met Ala
 1745 1750 1755 1760
 Leu Leu Asp Gln Thr Lys Thr Leu Ala Glu Ser Ala Leu Gln Leu Leu
 1765 1770 1775
 Tyr Thr Ala Lys Glu Ala Gly Gly Asn Pro Lys Gln Ala Ala His Thr
 1780 1785 1790
 Gln Glu Ala Leu Glu Glu Ala Val Gln Met Met Thr Glu Ala Val Glu
 1795 1800 1805
 Asp Leu Thr Thr Thr Leu Asn Glu Ala Ala Ser Ala Ala Gly Val Val
 1810 1815 1820
 Gly Gly Met Val Asp Ser Ile Thr Gln Ala Ile Asn Gln Leu Asp Glu
 1825 1830 1835 1840
 Gly Pro Met Gly Glu Pro Glu Gly Ser Phe Val Asp Tyr Gln Thr Thr
 1845 1850 1855
 Met Val Arg Thr Ala Lys Ala Ile Ala Val Thr Val Gln Glu Met Val
 1860 1865 1870
 Thr Lys Ser Asn Thr Ser Pro Glu Glu Leu Gly Pro Leu Ala Asn Gln
 1875 1880 1885
 Leu Thr Ser Asp Tyr Gly Arg Leu Ala Ser Glu Ala Lys Pro Ala Ala
 1890 1895 1900
 Val Ala Ala Glu Asn Glu Glu Ile Gly Ser His Ile Lys His Arg Val
 1905 1910 1915 1920
 Gln Glu Leu Gly His Gly Cys Ala Ala Leu Val Thr Lys Ala Gly Ala
 1925 1930 1935
 Leu Gln Cys Ser Pro Ser Asp Ala Tyr Thr Lys Lys Glu Leu Ile Glu
 1940 1945 1950
 Cys Ala Arg Arg Val Ser Glu Lys Val Ser His Val Leu Ala Ala Leu
 1955 1960 1965
 Gln Ala Gly Asn Arg Gly Thr Gln Ala Cys Ile Thr Ala Ala Ser Ala
 1970 1975 1980
 Val Ser Gly Ile Ile Ala Asp Leu Asp Thr Thr Ile Met Phe Ala Thr
 1985 1990 1995 2000
 Ala Gly Thr Leu Asn Arg Glu Gly Thr Glu Thr Ser Ala Asp His Arg
 2005 2010 2015
 Glu Gly Ile Leu Lys Thr Ala Lys Val Leu Val Glu Asp Thr Lys Val
 2020 2025 2030
 Leu Val Gln Asn Ala Ala Gly Ser Gln Glu Lys Leu Ala Gln Ala Ala

2035				2040				2045			
Gln Ser Ser Val	Ala Thr	Ile Thr	Arg Leu	Ala Asp	Val Val	Lys Leu					
2050		2055		2060							
Gly Ala Ala Ser	Leu Gly	Ala Glu	Asp Pro	Glu Thr	Gln Val	Val Leu					
2065		2070		2075		2080					
Ile Asn Ala Val	Lys Asp	Val Ala	Lys Ala	Leu Gly	Asp Leu	Ile Ser					
	2085		2090		2095						
Ala Thr Lys Ala	Ala Ala	Gly Lys	Val Gly	Asp Asp	Pro Ala	Val Trp					
	2100		2105		2110						
Gln Leu Lys Asn	Ser Ala	Lys Val	Met Val	Thr Asn	Val Thr	Ser Leu					
	2115		2120		2125						
Leu Lys Thr Val	Lys Ala	Val Glu	Asp Glu	Ala Thr	Lys Gly	Thr Arg					
	2130		2135		2140						
Ala Leu Glu Ala	Thr Thr	Glu His	Ile Arg	Gln Glu	Leu Ala	Val Phe					
2145		2150		2155		2160					
Cys Ser Pro Glu	Pro Pro	Ala Lys	Thr Ser	Thr Pro	Glu Asp	Phe Ile					
	2165		2170		2175						
Arg Met Thr Lys	Gly Ile	Thr Met	Ala Thr	Ala Lys	Ala Val	Ala Ala					
	2180		2185		2190						
Gly Asn Ser Cys	Arg Gln	Glu Asp	Val Ile	Ala Thr	Ala Asn	Leu Ser					
	2195		2200		2205						
Arg Arg Ala Ile	Ala Asp	Met Leu	Arg Ala	Cys Lys	Glu Ala	Ala Tyr					
	2210		2215		2220						
His Pro Glu Val	Ala Pro	Asp Val	Arg Leu	Arg Ala	Leu His	Tyr Gly					
2225		2230		2235		2240					
Arg Glu Cys Ala	Asn Gly	Tyr Leu	Glu Leu	Leu Asp	His Val	Leu Leu					
	2245		2250		2255						
Thr Leu Gln Lys	Pro Ser	Pro Glu	Leu Lys	Gln Gln	Leu Thr	Gly His					
	2260		2265		2270						
Ser Lys Arg Val	Ala Gly	Ser Val	Thr Glu	Leu Ile	Gln Ala	Ala Glu					
	2275		2280		2285						
Ala Met Lys Gly	Thr Glu	Trp Val	Asp Pro	Glu Asp	Pro Thr	Val Ile					
	2290		2295		2300						
Ala Glu Asn Glu	Leu Leu	Gly Ala	Ala Ala	Ala Ile	Glu Ala	Ala Ala					
2305		2310		2315		2320					
Lys Lys Leu Glu	Gln Leu	Lys Pro	Arg Ala	Lys Pro	Lys Glu	Ala Asp					
	2325		2330		2335						
Glu Ser Leu Asn	Phe Glu	Glu Gln	Ile Leu	Glu Ala	Ala Lys	Ser Ile					
	2340		2345		2350						
Ala Ala Ala Thr	Ser Ala	Leu Val	Lys Ala	Ala Ser	Ala Ala	Gln Arg					
	2355		2360		2365						
Glu Leu Val Ala	Gln Gly	Lys Val	Gly Ala	Ile Pro	Ala Asn	Ala Leu					
	2370		2375		2380						
Asp Asp Gly Gln	Trp Ser	Gln Gly	Leu Ile	Ser Ala	Ala Arg	Met Val					
2385		2390		2395		2400					
Ala Ala Ala Thr	Asn Asn	Leu Cys	Glu Ala	Ala Asn	Ala Val	Gln					
	2405		2410		2415						
Gly His Ala Ser	Gln Glu	Lys Leu	Ile Ser	Ser Ala	Lys Gln	Val Ala					
	2420		2425		2430						
Ala Ser Thr Ala	Gln Leu	Leu Val	Ala Cys	Lys Val	Lys Ala	Asp Gln					
	2435		2440		2445						
Asp Ser Glu Ala	Met Lys	Arg Leu	Gln Ala	Ala Gly	Asn Ala	Val Lys					
	2450		2455		2460						
Arg Ala Ser Asp	Asn Leu	Val Lys	Ala Ala	Gln Lys	Ala Ala	Ala Phe					

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2465                2470                2475                2480
Glu Glu Gln Glu Asn Glu Thr Val Val Val Lys Glu Lys Met Val Gly
                2485                2490                2495
Gly Ile Ala Gln Ile Ile Ala Ala Gln Glu Glu Met Leu Arg Lys Glu
                2500                2505                2510
Arg Glu Leu Glu Glu Ala Arg Lys Lys Leu Ala Gln Ile Arg Gln Gln
                2515                2520                2525
Gln Tyr Lys Phe Leu Pro Ser Glu Leu Arg Asp Glu His
                2530                2535                2540

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<210> 1703
<211> 346
<212> DNA
<213> Homo sapiens

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<400> 1703
ggatcccgag gagaaaaatc ctctgttact tcatgggtca tgtgactgag aatcttttta
60
ggaatctgtg atggagaaga atgactcttc ttcttctctg agtcctgtag taatgcattc
120
ctgtctctac ctttctccat gactgctgcc tggctctgtcc tagccttgct ctgatccaca
180
ctgagctggc cttgagcagg gtgcacactg tacatgaaga caatggctgg tttctcactg
240
gactctcctt tcgctctgtg gaaccagtga tggcgctgaa ctggaggaag aggcagcatg
300
tgaatgactg tgccatccat ggccaccaag ttccctttct ctgcgt
346

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<210> 1704
<211> 106
<212> PRT
<213> Homo sapiens

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<400> 1704
Met Asp Gly Thr Val Ile His Met Leu Pro Leu Pro Pro Val Gln Arg
1          5          10          15
His His Trp Phe Thr Glu Ala Lys Gly Glu Ser Ser Glu Lys Pro Ala
20         25         30
Ile Val Phe Met Tyr Arg Cys Asp Pro Ala Gln Gly Gln Leu Ser Val
35         40         45
Asp Gln Ser Lys Ala Arg Thr Asp Gln Ala Ala Val Met Glu Lys Gly
50         55         60
Arg Ala Glu Asn Ala Leu Leu Gln Asp Ser Glu Lys Lys Arg Ser His
65         70         75         80
Ser Ser Pro Ser Gln Ile Pro Lys Lys Ile Leu Ser His Met Thr His
85         90         95
Glu Val Thr Glu Asp Phe Ser Pro Arg Asp
100        105

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<210> 1705
<211> 377
<212> DNA
<213> Homo sapiens

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<400> 1705
 gtgcaccttt tctcaggact cgctcagaag gtccttctgg gaggacaatg gacaagacta
 60
 aaccatcaaa tccattctca atgggtcaaa ttccaaatct tcttgaaggg ctggcttcta
 120
 ctgggtctcc aatcgagttg cagaaagga tacaggggtg agcaagtta tttaatcctg
 180
 gttttggctg gaaccaaatt ccacaagttc aaaccttgaa gaattctcaa ggttctattc
 240
 ataatttagt gaggtctgga gttactgttg aaaggaaagt taatgtaggg gcacaaggag
 300
 cttttaactc tgccttgca ccacagatgg aatttccac agttcctcca tacaaccctc
 360
 cttccttcgg agctagc
 377

<210> 1706
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1706
 Met Asp Lys Thr Lys Pro Ser Asn Pro Phe Ser Met Gly Gln Ile Pro
 1 5 10 15
 Asn Phe Pro Glu Gly Leu Ala Ser Thr Gly Ala Pro Ile Glu Leu Gln
 20 25 30
 Lys Gly Ile Gln Gly Gly Ala Ser Leu Phe Asn Pro Gly Phe Gly Trp
 35 40 45
 Asn Gln Asn Pro Gln Val Gln Thr Leu Lys Asn Ser Gln Gly Ser Ile
 50 55 60
 His Asn Leu Val Arg Ser Gly Val Thr Val Glu Arg Lys Val Asn Val
 65 70 75 80
 Gly Ala Gln Gly Ala Phe Asn Ser Ala Pro Ala Pro Gln Met Glu Phe
 85 90 95
 Pro Thr Val Pro Pro Tyr Asn Pro Ser Ser Phe Gly Ala Ser
 100 105 110

<210> 1707
 <211> 427
 <212> DNA
 <213> Homo sapiens

<400> 1707
 nnttcggtga acccgagacc cggacgcagc gccgataccc atgtgcgccc agtactacgc
 60
 catcacgccca agcagtgct catcatcggg gccgggctag ccggcatgga ggctgcgcga
 120
 gttctcagcg aacgcgcaca cgaacctctc atcgtcgagg ccagcgacca cattggcgga
 180
 gtcatecttg cgggtggtca accttccttc aaggaggacg acctagctct gctggagtg
 240
 taccgcacca ccctggagga gttgggcgtg gagattcgac tcaacaccac cgtaacggct
 300

gattcttatcg cttccttcg ggccgatacac gtcgtcctgg cgaccggatc gagggccggt
 360
 cgactcgacc taggtgatga tgccaagggtc attgacgcca ccgacgtctt gctcaaccgc
 420
 gacgcgt
 427

<210> 1708
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1708
 Xaa Ser Val Asn Pro Lys Pro Gly Arg Ser Ala Asp Thr His Val Arg
 1 5 10 15
 Pro Val Leu Arg His His Ala Lys Arg Val Leu Ile Ile Gly Ala Gly
 20 25 30
 Leu Ala Gly Met Glu Ala Ala Arg Val Leu Ser Glu Arg Ala His Glu
 35 40 45
 Pro Leu Ile Val Glu Ala Ser Asp His Ile Gly Gly Val Ile Leu Ala
 50 55 60
 Gly Gly Gln Pro Ser Phe Lys Glu Asp Asp Leu Ala Leu Leu Glu Trp
 65 70 75 80
 Tyr Arg Thr Thr Leu Glu Glu Leu Gly Val Glu Ile Arg Leu Asn Thr
 85 90 95
 Thr Val Thr Ala Asp Leu Ile Ala Ser Phe Gly Ala Asp His Val Val
 100 105 110
 Leu Ala Thr Gly Ser Arg Pro Arg Leu Asp Leu Gly Asp Asp Ala
 115 120 125
 Lys Val Ile Asp Ala Thr Asp Ala Leu Leu Asn Arg Asp Ala
 130 135 140

<210> 1709
 <211> 446
 <212> DNA
 <213> Homo sapiens

<400> 1709
 acgcgtgaag gggaccagga ggttggaac agaccattgc aatggaaatg atgatttaga
 60
 ctgttctttt ctgactgatg actgggagtc agggaagatg aatgcagagt ctgtgatcac
 120
 ctctctttcc agccacatca tatctcagcc tcctggagga aactcccata gcttgtctct
 180
 tcagteccag ttgacagctt ctgaacgttt ccaagagaat agttcggatc attcagaaac
 240
 cagggtgttg caagaggtct tctttcaggc aatctgctt gctgtgtgct taatcatttc
 300
 tgcattgtga agatgggtta tgggagaaa attagccagt gtcttcacat gctcattgat
 360
 gataaactga gcttatgtga aatcattggt tctcagcctt gccagctatt tcaaaaccac
 420
 tgcctgtgct cggtttgtca aaattt
 446

<210> 1710
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 1710
 Met Asn Ala Glu Ser Val Ile Thr Ser Ser Ser Ser His Ile Ile Ser
 1 5 10 15
 Gln Pro Pro Gly Gly Asn Ser His Ser Leu Ser Leu Gln Ser Gln Leu
 20 25 30
 Thr Ala Ser Glu Arg Phe Gln Glu Asn Ser Ser Asp His Ser Glu Thr
 35 40 45
 Arg Leu Leu Gln Glu Val Phe Phe Gln Ala Ile Leu Leu Ala Val Cys
 50 55 60
 Leu Ile Ile Ser Ala Cys Ala Arg Trp Val Met Gly Glu Ile Leu Ala
 65 70 75 80
 Ser Val Phe Thr Cys Ser Leu Met Ile Thr Val Ala Tyr Val Lys Ser
 85 90 95
 Leu Phe Leu Ser Leu Ala Ser Tyr Phe Lys Thr Thr Ala Cys Ala Arg
 100 105 110
 Phe Val Lys Ile
 115

<210> 1711
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1711
 nggggggattc atgttagtat ttgtcagaaa aggccttttga aagagccaaa ttaaaaagag
 60
 cactagaaca tgaacaggga aagcagagga aatacttgta gaaagtattt ttacagctc
 120
 cctcaatata attcagtaat gtctattcct ggtgagaagt ctgtccgcac acacagcatc
 180
 agccaagcag cagaagcagt ggtgtctggg gggctgggaa gtttttcccc caaataccca
 240
 ccccatgcac tgcccagtc ccagacccca aagactttgt cctgcgcetca cgcacctttt
 300
 gcaggctcac actgtctgtg tgcgcaagag gtagcgacag gagacaatgg ggaaagagct
 360
 gaaggaggca aacaaggcca gggggaaagc ctacctcgag gcacagaggg gccccaagat
 420
 ggatat
 426

<210> 1712
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 1712
 Met Asn Arg Glu Ser Arg Gly Asn Thr Cys Arg Lys Tyr Phe Leu Gln

```

1           5           10           15
Leu Pro Gln Tyr Asn Ser Val Met Phe Ile Pro Gly Glu Lys Ser Val
20           25           30
Arg Thr His Ser Ile Ser Gln Ala Ala Glu Ala Val Val Ser Gly Gly
35           40           45
Leu Gly Ser Phe Ser Pro Lys Tyr Pro Pro His Ala Leu Pro Ser Pro
50           55           60
Gln Thr Pro Lys Thr Leu Ser Ser Pro His Ala Pro Phe Ala Gly Ser
65           70           75           80
His Cys Leu Cys Ala Gln Glu Val Ala Thr Gly Asp Asn Gly Glu Arg
85           90           95
Ala Glu Gly Gly Lys Gln Gly Gln Gly Glu Ser Leu Pro Arg Gly Thr
100          105          110
Glu Gly Pro Gln Asp Gly Tyr
115

```

<210> 1713
 <211> 328
 <212> DNA
 <213> Homo sapiens

```

<400> 1713
tctagaaagg tttatttcat gggccaaggc ttgtgtttcc aaagccagga agggctgaag
60
ccagaattgg ccctggctgc ttgccacaga gtctggccgg gggaccctgg acctcagcag
120
ggctcatgatg aggtcagctt tggaggagca gggccagcgt gtctgcttt ctgctcctgg
180
aatgagcctc actccctccc tgctcaaggc agcccttcac ccagccgccc ggacaggtgc
240
cctgtgccac ctgccatccc tgggattctc catctcagtg agtgctccct ggggcctggg
300
aacgcacctg gctggtgact cctggggg
328

```

<210> 1714
 <211> 99
 <212> PRT
 <213> Homo sapiens

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<400> 1714
Met Gly Gln Gly Leu Cys Phe Gln Ser Gln Glu Gly Leu Lys Pro Glu
1           5           10           15
Leu Ala Leu Ala Ala Cys His Arg Val Trp Pro Gly Asp Pro Gly Pro
20           25           30
Gln Gln Gly His Asp Glu Val Ser Phe Gly Gly Ala Gly Pro Ala Cys
35           40           45
Pro Ala Phe Cys Ser Trp Asn Glu Pro His Ser Leu Pro Ala Gln Gly
50           55           60
Ser Pro Ser Pro Ser Arg Arg Asp Arg Cys Pro Val Pro Pro Ala Ile
65           70           75           80
Pro Gly Ile Leu His Leu Ser Glu Cys Ser Leu Gly Pro Gly Asn Ala
85           90           95
Ser Gly Trp

```

<210> 1715
 <211> 489
 <212> DNA
 <213> Homo sapiens

<400> 1715
 gttgccacg atgggcccga tttgtacatc ccggtatttc gtgttcgggtg tgggtgtaaaa
 60
 gatgccccat gtgtgacatt ctgtggatag ttattgttag cattatttga caagtcttag
 120
 aaatcgatcc acccaggcgt gtagctgcgg tatttcatca gagttgatcg ttgcgatgag
 180
 ttgatcatgg cctgtcatgg cgtagtcttc tacgtcgtaa agtatgagac aatccacggg
 240
 aatatgggtg tttttggcca actcggaagc cgggggtgtcg ggggaagtcgg tcctctgaag
 300
 gtatgggcct gtccaatga cgacgtgtgc tgggtccatg aggagtccgt ccaagggttcg
 360
 aactcattac cgtcgaatac gacgtgtcg ccacgcggcg tgctgaatcg aatcctcaaa
 420
 gtgtatccgt actcgggtgc gcgcaacagg tgcctaacct cagcgctagt gggctgtgca
 480
 ctgacgcgt
 489

<210> 1716
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 1716
 Met Ala Cys His Gly Val Val Phe Tyr Val Val Lys Tyr Glu Thr Ile
 1 5 10 15
 His Gly Asn Met Val Phe Phe Gly Gln Leu Gly Ser Arg Gly Val Gly
 20 25 30
 Glu Val Gly Pro Cys Lys Val Trp Ala Cys Pro Asn Asp Asp Val Cys
 35 40 45
 Trp Val His Glu Glu Phe Val Gln Gly Ser Asn Ser Leu Pro Ser Asn
 50 55 60
 Thr Thr Leu Ser Pro Ser Ala Val Ser Asn Arg Ile Leu Lys Val Tyr
 65 70 75 80
 Pro Tyr Ser Val Ser Arg Asn Arg Cys Leu Thr Ser Ala Leu Val Gly
 85 90 95
 Cys Ala Leu Thr Arg
 100

<210> 1717
 <211> 312
 <212> DNA
 <213> Homo sapiens

<400> 1717

nggcatacaa cggagtaaaa accacatcaa cagaagtggga aacaggccca gagagcgtga
 60
 gaggtttctg gtttcaagaa ggcacactga gtcctctgcac ccgatgcctc tccttcccca
 120
 aatccccactg gaatacacag agagacataa aaacaaggag tgtcctgtag cagagcagcc
 180
 aggctggctc atgagacaga gggagcagtc ttctgggaga catggctctt gctgctgctg
 240
 atcagccaac agatccatgg aaagcaagg gcccttctcc ggaggcttcc tggggcctgc
 300
 catgaatgtg tc
 312

<210> 1718

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1718

Met	Ala	Gly	Pro	Arg	Lys	Pro	Pro	Glu	Lys	Gly	Pro	Leu	Leu	Ser	Met
1			5					10					15		
Asp	Leu	Leu	Ala	Asp	Pro	Gln	Gln	Gln	Glu	Pro	Cys	Leu	Pro	Glu	Asp
		20					25					30			
Cys	Ser	Leu	Cys	Leu	Met	Ser	Gln	Pro	Gly	Cys	Ser	Ala	Thr	Gly	His
	35					40					45				
Ser	Leu	Phe	Leu	Cys	Leu	Ser	Val	Tyr	Ser	Ser	Gly	Ile	Trp	Gly	Arg
	50				55					60					
Arg	Gly	Ile	Gly	Cys	Arg	Asp	Ser	Val	Cys	Leu	Leu	Glu	Thr	Arg	Asn
65					70				75					80	
Leu	Ser	Arg	Ser	Leu	Gly	Leu	Phe	Pro	Leu	Leu	Leu	Met	Trp	Phe	Leu
			85					90					95		
Leu	Arg	Cys	Met	Pro											
			100												

<210> 1719

<211> 404

<212> DNA

<213> Homo sapiens

<400> 1719

tgcacccac ggcctgccca tttttgtctg ggaccgcaga ccgtatgctg ccctcgaag
 60
 tcagagacaa tccaaccggc ctgcaaaact gcggtcttgc ccggggcaac gtcgtagggt
 120
 ccaacagttt ctccaacctc ataggttagaa gaagtgcctat agctgctgga aatggagatg
 180
 tggatcacat cgagcagtgga gaagtcaatg cctgccgaaa ccgaccagtt ctcgtcttta
 240
 gtttctgtga tggatcgctg gaccggctgc ggagtgtctg tgagtgggaa atcgctcacgt
 300
 cccagcagag ccatcgaagt agctgcgcac cacatgaacg ggctgtccgt gtcacccgga
 360
 ttcgagcagg gagcacccat tgggtgngtgg tgtccccggg ggtt
 404

<210> 1720
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 1720
 Met Gly Ala Pro Cys Ser Asn Pro Gly Asp Thr Asp Ser Pro Phe Met
 1 5 10 15
 Trp Cys Ala Ala Thr Ser Met Ala Leu Leu Gly Arg Asp Asp Phe Gln
 20 25 30
 Leu Asn Asp Thr Pro Gln Pro Val Thr Arg Ser Ile Thr Glu Thr Lys
 35 40 45
 Thr Lys Asn Trp Ser Val Ser Ala Gly Ile Asp Phe Pro Leu Leu Asp
 50 55 60
 Val Ile His Ile Ser Ile Ser Ser Tyr Ser Thr Ser Ser Thr Tyr
 65 70 75 80
 Glu Val Gly Glu Thr Val Gly Pro Tyr Asp Val Ala Pro Gly Lys Thr
 85 90 95
 Ala Val Leu Gln Ala Gly Trp Ile Val Ser Asp Phe Glu Gly Gln His
 100 105 110
 Thr Val Cys Gly Pro Asp Lys Lys Trp Gln Gly Arg Gly Asp
 115 120 125

<210> 1721
 <211> 529
 <212> DNA
 <213> Homo sapiens

<400> 1721
 ccatggccac cctttcagga cagagctgcc ctccccatgc tggaggagcc acagggcctg
 60
 gtcgctgtgg cttcagcctc ccagctcctc ctgtcctctg ctgggcactt gtaatgtcca
 120
 ggcactccct gcttggatca ggggatctgg gtttcatctt cccagctcct cctgtcctct
 180
 gctgggcacc tgtgatgtcc aggcactccc tgcttgatt gggggatctg ggtttcatct
 240
 tcccagctcc tccgtgcctc cgcctgggac ctgtgatgtc caggcactcc ctgcttggat
 300
 cgggggggtct ggggtttgtg ctatacttgg tgctcccttt cactcaggcc ccttcttgac
 360
 tctgcagagc taccctctgc catctctttc acgcgggcct cctgcagtct ctgtgctcac
 420
 cctgtgactc tgcttccggt gttgtcaaat gggggatcac ccaggaccgc caccactggg
 480
 tcgtgtgcag gtttctgggg tggcagagtg cggatgagtg ggcacgcgt
 529

<210> 1722
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 1722

```

Met Ala Thr Leu Ser Gly Gln Ser Cys Pro Ser His Ala Gly Gly Ala
 1           5           10           15
Thr Gly Pro Gly Arg Cys Gly Phe Ser Leu Pro Ala Pro Pro Val Leu
           20           25           30
Cys Trp Ala Leu Val Met Ser Arg His Ser Leu Leu Gly Ser Gly Asp
           35           40           45
Leu Gly Phe Ile Phe Pro Ala Pro Pro Val Leu Cys Trp Ala Pro Val
           50           55           60
Met Ser Arg His Ser Leu Leu Gly Leu Gly Asp Leu Gly Phe Ile Phe
65           70           75           80
Pro Ala Pro Pro Val Leu Arg Trp Ala Pro Val Met Ser Arg His Ser
           85           90           95
Leu Leu Gly Ser Gly Gly Leu Gly Phe Val Leu Tyr Leu Val Leu Pro
           100           105           110
Phe Thr Gln Ala Pro Ser
           115

```

<210> 1723

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1723

```

acgcgtttga agctggatgc atggatatcc agcgccgccca tcgggtcaaa tggggtgacg
60
ctgcctctga tgggtaccgg ggcgtagcga tctaccttac cgttgatgtc gacgctcgcc
120
ggtttggcct ggcggtgtc aatggtgccca atcttcccg tgaattgttg aatggcagtg
180
gcaaagttgg gcgtgaggct gaagtcggcg aagttggccg agccatcatt gatcgcaacc
240
tgcccaatgt gaatgccagc tggcttctct ttgctggccg ccggtgtctc tgttgccagt
300
gtcggccggg tgcgggatca gcaagtcacg gatgttggtg gggcggtcat cggtgatcgc
360
tgcattcaat a
371

```

<210> 1724

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1724

```

Met Asp Ile Gln Arg Arg His Arg Val Lys Trp Val Asp Ala Ala Leu
 1           5           10           15
Asp Gly His Arg Gly Val Ala Ile Tyr Leu Thr Val Asp Val Asp Ala
           20           25           30
Arg Arg Phe Gly Leu Ala Ala Val Asn Gly Ala Asn Leu Pro Val Glu
           35           40           45
Leu Leu Asn Gly Ser Gly Lys Val Gly Arg Glu Ala Glu Val Gly Glu
50           55           60
Val Gly Arg Ala Ile Ile Asp Arg Asn Leu Pro Asn Val Asn Ala Gln

```

65		70		75		80									
Trp	Leu	Leu	Phe	Ala	Gly	Arg	Arg	Leu	Ser	Cys	Cys	Gln	Cys	Arg	Pro
			85						90					95	
Gly	Ala	Gly	Ser	Ala	Ser	His	Arg	Cys	Trp	Trp	Gly	Gly	His	Arg	
			100					105					110		

<210> 1725

<211> 807

<212> DNA

<213> Homo sapiens

<400> 1725

```

ngtgcacctg gtatggtgcc ctctgggtct aagcctgtcc ttgtacacac tcacactttg
60
atttgaagtg acctcttccc tctgagcctt ctggtgtcca actctcccct tctctaggac
120
catgcagctg tggaggccga gaggcagaag atgtcagccc ttgtgcgagg gctgcagagg
180
gagctggagg agacttcaga ggagacaggg cattggcaga gtatgttcca gaagaacaa
240
gaggatctta gagccaccaa gcaggaactc ctgcagctgc gaatggagaa ggaggagatg
300
gaagaggagc ttggagagaa gatagaggtc ttgcagaggg aattagagca ggcccagagc
360
agtgtctggg ataactcgcca ggttgagggt ctcaagaagg agctgctccg gacacaggag
420
gagcttaagg aactgcaggc agaacggcag agccaggagg tggctggggc acaccgggac
480
cgggagttgg agaagcagct gccggtcctg agggctcagg ctgacgcagg tggggagctg
540
gaagaacaga acctccagct acaaaagacc ctccagcaat tgcgacagga ctgtgaagag
600
gcttccaagg ctaagatggt ggcccaggca gaggcaacag tgctggggca gcggcggggc
660
gcagtggaga cgacgcttcg ggagacccag gaggaaaatg acgaattccg ccggcgcatc
720
ctgggttttg agcagcagct gaaggagact cagggtcttg tggatggttg ggaagcggtg
780
gaggcacgac tacgggacaa gctgcag
807

```

<210> 1726

<211> 230

<212> PRT

<213> Homo sapiens

<400> 1726

```

Asp His Ala Val Leu Glu Ala Glu Arg Gln Lys Met Ser Ala Leu Val
1          5          10          15
Arg Gly Leu Gln Arg Glu Leu Glu Glu Thr Ser Glu Glu Thr Gly His
20          25          30
Trp Gln Ser Met Phe Gln Lys Asn Lys Glu Asp Leu Arg Ala Thr Lys
35          40          45
Gln Glu Leu Leu Gln Leu Arg Met Glu Lys Glu Glu Met Glu Glu Glu

```

```

      50              55              60
Leu Gly Glu Lys Ile Glu Val Leu Gln Arg Glu Leu Glu Gln Ala Arg
65              70              75              80
Ala Ser Ala Gly Asp Thr Arg Gln Val Glu Val Leu Lys Lys Glu Leu
      85              90              95
Leu Arg Thr Gln Glu Glu Leu Lys Glu Leu Gln Ala Glu Arg Gln Ser
      100              105              110
Gln Glu Val Ala Gly Arg His Arg Asp Arg Glu Leu Glu Lys Gln Leu
      115              120              125
Ala Val Leu Arg Val Glu Ala Asp Arg Gly Arg Glu Leu Glu Glu Gln
      130              135              140
Asn Leu Gln Leu Gln Lys Thr Leu Gln Gln Leu Arg Gln Asp Cys Glu
145              150              155              160
Glu Ala Ser Lys Ala Lys Met Val Ala Glu Ala Glu Ala Thr Val Leu
      165              170              175
Gly Gln Arg Arg Ala Ala Val Glu Thr Thr Leu Arg Glu Thr Gln Glu
      180              185              190
Glu Asn Asp Glu Phe Arg Arg Arg Ile Leu Gly Leu Glu Gln Gln Leu
      195              200              205
Lys Glu Thr Arg Gly Leu Val Asp Gly Gly Glu Ala Val Glu Ala Arg
      210              215              220
Leu Arg Asp Lys Leu Gln
225              230

```

<210> 1727

<211> 474

<212> DNA

<213> Homo sapiens

<400> 1727

```

aaccaactct ccacaacatc gccagaaaca gtcgctgccca agaggctcca ccatgtttta
60
gcagcttcag aagacaaaga taagatgaaa aaggaagttt tacaaagctc aaggacatt
120
atgcaatcca aatcagcttg cgaaattaaa caaagtcacc aagaatgtag tacccaacaa
180
acacaacaga agaagtattt ggagcagttg cacttgcccc aaagcaaacc aatttcccc
240
aatttcaaag ttaaaacat caaacttcca actctagatc atacattaaa tgaaacagac
300
cacagctatg aaagtcataa acagcaatct gagattgatg ttcaaacctt taccaaaaaa
360
caatatctga aaaccaagaa aactgaagca agcactgaat gtatgcataa gcaatctctg
420
gctgaaagac attatcagtt acctaagaag gagaaaaagag tgacagtaca attg
474

```

<210> 1728

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1728

Met Lys Lys Glu Val Leu Gln Ser Ser Arg Asp Ile Met Gln Ser Lys

```

      1           5           10           15
Ser Ala Cys Glu Ile Lys Gln Ser His Gln Glu Cys Ser Thr Gln Gln
      20           25           30
Thr Gln Gln Lys Lys Tyr Leu Glu Gln Leu His Leu Pro Gln Ser Lys
      35           40           45
Pro Ile Ser Pro Asn Phe Lys Val Lys Thr Ile Lys Leu Pro Thr Leu
      50           55           60
Asp His Thr Leu Asn Glu Thr Asp His Ser Tyr Glu Ser His Lys Gln
      65           70           75           80
Gln Ser Glu Ile Asp Val Gln Thr Phe Thr Lys Lys Gln Tyr Leu Lys
      85           90           95
Thr Lys Lys Thr Glu Ala Ser Thr Glu Cys Ser His Lys Gln Ser Leu
      100          105          110
Ala Glu Arg His Tyr Gln Leu Pro Lys Lys Glu Lys Arg Val Thr Val
      115          120          125
Gln Leu
      130

```

<210> 1729

<211> 470

<212> DNA

<213> Homo sapiens

<400> 1729

```

acgcgtgact cgccataaca ttgctgacac gttttccacg gcaagggagg catcatgacg
60
aggatcgacg tgtggctgtg gtcggtgccg gtctataagt cccggctcgt ggctaccgcc
120
gccgtcaagg gcggccacat tcgcctcaat ggagaccggg ttaaacctc ccaacgacgtg
180
aaaccggcgg ataccgtcac catccacacc cccggatggg accgggtcct caaggctcatc
240
aacccgatca cgaaaagagt cggcgccaaa ctgcggtcgc aggcttacga agatctgtca
300
nngccccccc acccgcttac ctctctgnet cccctcgccc gccgcgacgg tggggctgga
360
cgaccaccca agaaggatcg tcgcgagatc gatcggtccc gaggccggga ctctcgctat
420
tgaggactct tcgcccggcc caacacacca cggtctcgcg ccgaattggc
470

```

<210> 1730

<211> 131

<212> PRT

<213> Homo sapiens

<400> 1730

```

His Val Phe His Gly Lys Gly Gly Ile Met Thr Arg Ile Asp Val Trp
      1           5           10           15
Leu Trp Ser Val Arg Val Tyr Lys Ser Arg Ser Leu Ala Thr Ala Ala
      20           25           30
Val Lys Gly Gly His Ile Arg Leu Asn Gly Asp Pro Val Lys Pro Ser
      35           40           45
His Asp Val Lys Pro Gly Asp Thr Val Thr Ile His Thr Pro Gly Trp

```

```

      50              55              60
Asp Arg Val Leu Lys Val Ile Asn Pro Ile Thr Lys Arg Val Gly Ala
65              70              75              80
Lys Leu Ala Val Glu Ala Tyr Glu Asp Leu Ser Xaa Pro Pro Asp Pro
      85              90              95
Pro Thr Ser Leu Xaa Pro Leu Ala Arg Arg Asp Arg Gly Ala Gly Arg
      100              105              110
Pro Thr Lys Lys Asp Arg Arg Glu Ile Asp Arg Leu Arg Gly Arg Asp
      115              120              125
Ser Arg Tyr
130

<210> 1731
<211> 534
<212> DNA
<213> Homo sapiens

<400> 1731
agcgctccct gcctgctgct gggcggaggg aaggcggcaa gagctgcgga gccctcggaa
60
gagcttcag gaacctgcg ctgtgggata aaggaatgag gttcagaaag gggcagggag
120
ttgcccgcag ccgcaccgca cgtcttcagc ccgaccgttg tctgacctc tctgtcccg
180
ccctgcacca gtctaccat ggccttctgg acacagctga tgctgctgct ctggaagaat
240
ttcatgtatc gccggagaca gccggtccag ctctggtcgc aattgctgtg gcctctcttc
300
ctcttcttca tcctggtggc tgttcgccac tcccaccgcg ccctggagca ccatgaatgc
360
cacttcccaa acaagccact gccatcggcg ggcaccgtgc cctggctcca ggggtctc
420
tgtaaatgtga acaacacctg ctttcgcgag ctgacaccgg gcgaggagcc cgggcgcctg
480
agcaacttca acgactccct ggtctccggc ctgctacgtc ggagagaggg tgga
534

<210> 1732
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1732
Met Ala Phe Trp Thr Gln Leu Met Leu Leu Trp Lys Asn Phe Met
1              5              10              15
Tyr Arg Arg Arg Gln Pro Val Gln Leu Leu Val Glu Leu Leu Trp Pro
      20              25              30
Leu Phe Leu Phe Phe Ile Leu Val Ala Val Arg His Ser His Pro Pro
      35              40              45
Leu Glu His His Glu Cys His Phe Pro Asn Lys Pro Leu Pro Ser Ala
      50              55              60
Gly Thr Val Pro Trp Leu Gln Gly Leu Ile Cys Asn Val Asn Asn Thr
65              70              75              80
Cys Phe Pro Gln Leu Thr Pro Gly Glu Glu Pro Gly Arg Leu Ser Asn

```

85 90 95
 Phe Asn Asp Ser Leu Val Ser Arg Leu Leu Arg Arg Arg Glu Ala Gly
 100 105 110
 <210> 1733
 <211> 409
 <212> DNA
 <213> Homo sapiens
 <400> 1733
 acgcgtgatg gccgatccga ctgtgcccgg tcacgacccg cggcgtccga gtcctgaccc
 60
 ggacatgccg tggctgatcc gcgacatcac cctcggcaac aacgtgatcg cgggcagcac
 120
 gggcaactgc accctctgcg tcgaggacta ctcgcgcagg tacgcggcga ggatcctcaa
 180
 catcgtctcc gacggcaacg tctcgcagcg cgcacgcggc gcacagccag cgtggctggg
 240
 tgggtgtggtc gcggggatca gcgaactccg atccgtacgt attctccagc ctcgacgtt
 300
 accggggcgc cactgggtttt taggaccttc gctcgggttc gatcgatggc gtgctgtcac
 360
 cgcgcccgga gcgctgctcc cgggcattga tctcaaggcg gtcacgagg
 409
 <210> 1734
 <211> 134
 <212> PRT
 <213> Homo sapiens
 <400> 1734
 Met Ala Asp Pro Thr Val Pro Gly His Asp Pro Arg Arg Pro Ser Pro
 1 5 10 15
 Asp Pro Asp Met Pro Trp Leu Ile Arg Asp Ile Thr Leu Gly Asn Asn
 20 25 30
 Val Ile Ala Gly Ser Thr Gly Asn Cys Thr Leu Cys Val Glu Asp Tyr
 35 40 45
 Ser Arg Arg Tyr Ala Ala Arg Ile Leu Asn Ile Val Ser Asp Gly Asn
 50 55 60
 Val Leu Gln Arg Ala Ser Ala Ala Gln Pro Ala Trp Leu Val Gly Val
 65 70 75 80
 Val Ala Gly Ile Ser Glu Leu Arg Ser Val Arg Ile Leu Gln Pro Arg
 85 90 95
 Arg Leu Pro Gly Asp His Trp Phe Leu Gly Pro Ser Leu Gly Leu Asp
 100 105 110
 Arg Trp Arg Ala Val Thr Ala Ala Gly Ala Leu Leu Pro Gly Ile Asp
 115 120 125
 Leu Lys Ala Val Thr Arg
 130
 <210> 1735
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 1735
 ggcgccatgg tcatcagcat catgtgttcg gcgcccgcgtg cacgaatgtt cgtgcgatca
 60
 agcgcgcctt ttagttcgac gcacggtaaa gcccgctgcgc atcgatgtag gccaggaccg
 120
 cgtcaggcac caggaaacgt accgacttcc cgctggccgg cagttgacgg atctgggttg
 180
 cggacacgcg aagcggggtc tgccagacga atgcaatatt cccgttcggc ccggtcaggg
 240
 ccaagggggtc acttaccgac cgcgcggcca gcaggttgcg caaggcatcc ggcggttcgc
 300
 tggcggcatc cgggcgttgc aaaaccagga tgtggcaatg ct
 342

<210> 1736
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 1736
 Met Val Ile Ser Ile Met Cys Ser Ala Pro Ala Ala Arg Met Phe Val
 1 5 10 15
 Arg Ser Ser Ala Pro Phe Ser Ser Thr His Gly Lys Ala Arg Ala His
 20 25 30
 Arg Cys Arg Pro Gly Pro Arg Gln Ala Pro Gly Asn Val Pro Thr Ser
 35 40 45
 Arg Trp Pro Ala Val Asp Gly Ser Gly Trp Arg Thr Pro Gln Ala Gly
 50 55 60
 Ser Ala Arg Arg Met Gln Tyr Ser Arg Ser Ala Arg Ser Gly Pro Arg
 65 70 75 80
 Gly His Leu Pro Thr Ala Arg Pro Ala Gly Cys Ala Arg His Pro Ala
 85 90 95
 Val Arg Trp Arg His Pro Gly Val Ala Lys Pro Gly Cys Gly Asn Ala
 100 105 110

<210> 1737
 <211> 506
 <212> DNA
 <213> Homo sapiens

<400> 1737
 acgogtgttc accatgacct ggaccgcccc gcggcccgac gggtcgagcg cggaggagtc
 60
 ggacgagacg actgtgttg tccctgccat ctcagcgccc caccgggtacg acgtgcaggc
 120
 gtccggcgcc cagtcacct cccaccacgg cgaccgggtg gcgcggttgc acctcaacca
 180
 aggcagctacc acggcgaagg tcacgatcac cctgcgctaa ccttcaagc gtcttcagca
 240
 ccgacctata agtctccag acacttttac gaccggccct ccccttggg gtggggcccc
 300
 tcttttctgt gtcgtgggat gcacctggca gcaccacctc cgcccccat ggagaacagt
 360

aggtatcctc gcagggtact acggccaagg catatttgac gttccacgct tgccactgcc
 420
 gtcttagggc catactgccg ccacgcagct gagacggtga ccaatcgggt aaggtgactg
 480
 gttgccgtag tccatgcgag gccggc
 506

<210> 1738
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1738
 Met Ala Leu Arg Arg Gln Trp Gln Ala Trp Asn Val Lys Tyr Ala Leu
 1 5 10 15
 Ala Val Val Pro Cys Glu Asp Thr Tyr Cys Ser Pro Trp Gly Pro Glu
 20 25 30
 Val Val Leu Pro Gly Ala Ser His Asp Thr Lys Arg Thr Gly Pro Thr
 35 40 45
 Pro Arg Gly Arg Ala Gly Arg Lys Ser Val Trp Glu Thr Tyr Arg Ser
 50 55 60
 Val Leu Lys Thr Leu Glu Gly Leu Ala Gln Gly Asp Arg Asp Leu Arg
 65 70 75 80
 Arg Gly Thr Ala Leu Val Glu Val Gln Pro Arg His Pro Val Ala Trp
 85 90 95
 Val Gly Gly Asp Val Gly Ala Gly Arg Leu His Val Val Pro Val Gly
 100 105 110
 Arg

<210> 1739
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 1739
 cgcgttattg aaaatgctgc tttttttact aaattaggac agcgtttaat cggcgcatta
 60
 catcaagtga cggttgatgg atttgtttac cgtgttgata tgcggttacg cccttttgga
 120
 gaggctgggc cattgggttag cagctttaat tcaatagagg actattatca aaccatcggt
 180
 cgagagtggg agtggttatgc catgggttaa gcccggtgta ttggtgttga ggacgagtat
 240
 aaacaagcgt tagaaaggat gtttaagcct ttcgtattta gacgtttacat tgattttgat
 300
 gctattgatt ctttgcgaaa aatgaaaacg atgatcagtg ctgaagttcg tcgcaagggg
 360
 ttaaaagaca atattaagtt gggaatggga gggatccgtg aaattgaatt tgtggctcaa
 420

<210> 1740
 <211> 140
 <212> PRT

<213> Homo sapiens

<400> 1740

```

Arg Val Ile Glu Asn Ala Ala Phe Phe Thr Lys Leu Gly Gln Arg Leu
 1             5             10             15
Ile Gly Ala Leu His Gln Val Thr Val Asp Gly Phe Val Tyr Arg Val
                20             25             30
Asp Met Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Ser Thr
    35             40             45
Phe Asn Ser Ile Glu Asp Tyr Tyr Gln Thr His Gly Arg Glu Trp Glu
 50             55             60
Cys Tyr Ala Met Val Lys Ala Arg Val Ile Gly Val Glu Asp Glu Tyr
 65             70             75             80
Lys Gln Ala Leu Glu Arg Met Leu Arg Pro Phe Val Phe Arg Arg Tyr
            85             90             95
Ile Asp Phe Ser Ala Ile Asp Ser Leu Arg Lys Met Lys Thr Met Ile
        100             105             110
Ser Ala Glu Val Arg Arg Lys Gly Leu Lys Asp Asn Ile Lys Leu Gly
    115             120             125
Met Gly Gly Ile Arg Glu Ile Glu Phe Val Ala Gln
    130             135             140

```

<210> 1741

<211> 378

<212> DNA

<213> Homo sapiens

<400> 1741

```

nnacgcgctgc aggtgattca ggccgacgcc actgaccgcc tggctcctca cagtctcaat
60
gggcaggtgc acgtcgctgc ctccaacccg cctacgtgc cagccggcgc cgtggaggac
120
accgagacgg cccagcacga gccacgggtg gcgctctatg gcggggggccc ggacgggtga
180
gagattccga ttgacgtcct gngtgcgctc agtcgcgctg ctgccaccgg cggagtgcctc
240
gtcatggagc acgaccacga gcagggggcg ctgctgccgg cggcgccttc gtgagccggg
300
ttcaagcagg ccgagaccgg tcaggacctc accggccgcg accgetacct gcgcgcggtg
360
cgtaaacccc gctggtag
378

```

<210> 1742

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1742

```

Xaa Arg Val Glu Val Ile Gln Ala Asp Ala Thr Asp Pro Leu Val Leu
 1             5             10             15
His Ser Leu Asn Gly Gln Val Asp Val Val Val Ser Asn Pro Pro Tyr
    20             25             30
Val Pro Ala Gly Ala Val Glu Asp Thr Glu Thr Ala Gln His Glu Pro

```

[illegible]

atggatgtgg ccaacttcg gcgggtgccc cgcattgccc tctacggcac ggcccagccc
1380
agcgccaagg ccctggggag catcctggcc tacctgacgg acgccaagag gaggtgcgg
1440
aaggttgtct gggtagacct tcgggaggag gccgtgttg agtgtgacgg gcacacctac
1500
agcctgcggt ggctggggcc ccctgtggct cctgaccagc tggagacctt ggaggccacg
1560
ctgaaggccc atctaagcga gcctccccc ggcaaggagg gcccctgac ctacaggttc
1620
cagacctgcc ttacctgca ggaggtcttc agccagcacc gcaggccctg tcttgccctc
1680
acctaccacc gcatcccat gccggacttc tgtgcccccc gagaggagga ctttgaccag
1740
ctgctggagg ccctgcgggc cgcctctctc aaggaccacg gcactggctt cgtgttcacg
1800
tgccctcagc gccaggggccg taccacaact gcgatggttg tggctgtcct ggcctcttg
1860
cacatcaag gcttccccga ggtgggtgag gaggagctcg tgagtgtgcc tgatgccaag
1920
ttcactaagg gtgaatttca ggtagtaatg aaggtggtgc agctgctacc cgatggggac
1980
cgtgtgaaga aggaggtgga cgcagcgtcg gacactgtca gcgagaccat gacgcccag
2040
cactaccacc tcggggagat catcatctgc acctaccgcc aggcgaaggc agcgaagag
2100
gcgcaggaaa tcgggaggct gcagctgcgg agcctgcagt acttgagcgc ctatgtctgc
2160
ctgattctct tcaacgcgta cctccacctg gagaaggccg actcctggca gaggcccttc
2220
agcacctgga tcgaggagggt ggcatcgaag gctggcatct acgagatcct taacgagctg
2280
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2340
caggagcaga gctgcagcct cgagccctct gcccgcagg acttgctgta gggggcctta
2400
ctccctgtcc cccaccacc agggccccc gcaggccttg ggtgtctgag gtgctcttg
2460
ctgggagcgg ccctgagggg tgctggcctt gaaatgatc cccacttcc tggagagact
2520
gagcggaggt gggagccttt ttagaaagaa ctttttatag gacagggaga cagcacagcc
2580
atcccttgca aaccaccaag gtgtgtggct gacctccagg gaggagcact cactggagtg
2640
ctcacaagggt gcacactgct gtgtgtacct tgcagacagg ccggcgctca gcctccaagg
2700
ggctcactcc ccagttgcc aaacactgtg gatctctctg tctctctctc cctctctca
2760
gattggcctg gcagccctg gcacagagca gacctgcca ctggtagctc ccacttctc
2820
tactctctgt gctctgcat tgccgctccc cttcttgctg cccaagcact gccctcgggc
2880
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2940

gcagcttcac ccagttttct ggactctcat gcccccatct ccgacctggg agacttcagg
 3000
 aatgacaacc taccagcctt ggtggggctg gcaggatggt ggaggtttct caaggagctg
 3060
 gagacttcag ggagcccttc tcatggggag gaaagagctt ccagggggcg aacgcagcac
 3120
 agaggaagag gctgtctcca cttgtctggg aaactgggca ggaggcacag aggaagccaa
 3180
 ggctctggag tgcaggtccc ccggcatctc tctctgtccc ggagcccgat gatggcctgg
 3240
 tgccccacc tgctgcagca ggagcccaaa ggagtgtctg ctgaggggtg ttgctggggg
 3300
 ggtcctcatg gacagtggag tgtgcaaggg tgcactgagg gtggtgggag gggatcacct
 3360
 ggggttcagg ccatccttgc tgagcatctt tgagcctgcc ttccgggtgg agcagaaaaa
 3420
 gccagaccct gctgagttag aggtgtctgg gatccactgt ttccacacag cgggaaggct
 3480
 gctgggaaca ggtggcagag aagtgccatg ttgctgttga gccttgcagc tcttcagct
 3540
 ggggactggt gcttgcagaa acccaggagc tgaacagtga ggagggtgct caccttgcct
 3600
 ggctcactgg gaccaggaaa gcctgtcttt ggttaggctc gtgtacttct gcagaaaaaa
 3660
 aaaaaaagga tgtgtcattg gtcagtatat ttgaaaaagg gaggaggccg aagttgttcc
 3720
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 3780
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 3840
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 3900
 gatcctttgt gttctcatgg ttggtcttga ctttcagctg tgttgggacc actggctgat
 3960
 cacatcacct ctctgcctca gtttcccatc ctgtaaaatg ggagaataat acttgcctac
 4020
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 4080
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 4121

<210> 1744

<211> 796

<212> PRT

<213> Homo sapiens

<400> 1744

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1				5					10					15	
Lys	Ala	His	Tyr	Thr	Leu	Gly	Arg	Leu	Ser	Asp	Asn	Thr	Pro	Glu	His
				20				25					30		
Tyr	Leu	Val	Gln	Gly	Arg	Tyr	Phe	Leu	Val	Arg	Asp	Val	Thr	Glu	Lys
		35					40				45				
Met	Asp	Val	Leu	Gly	Thr	Val	Gly	Ser	Cys	Gly	Ala	Pro	Asn	Phe	Arg

50					55					60				
Gln Val	Gln Gly	Gly Leu	Thr Val	Phe Gly	Met Gly	Gln Pro	Ser Leu							
65		70			75		80							
Ser Gly	Phe Arg	Arg Val	Leu Gln	Lys Leu	Gln Lys	Asp Gly	His Arg							
		85			90		95							
Glu Cys	Val Ile	Phe Cys	Val Arg	Glu Glu	Pro Val	Leu Phe	Leu Arg							
		100			105		110							
Ala Asp	Glu Asp	Phe Val	Ser Tyr	Thr Pro	Arg Asp	Lys Gln	Asn Leu							
		115			120		125							
His Glu	Asn Leu	Gln Gly	Leu Gly	Pro Gly	Val Arg	Val Glu	Ser Leu							
		130			135		140							
Glu Leu	Ala Ile	Arg Lys	Glu Ile	His Asp	Phe Ala	Gln Leu	Ser Glu							
		145			150		155							
Asn Thr	Tyr His	Val Tyr	His Asn	Thr Glu	Asp Leu	Trp Gly	Glu Pro							
		165			170		175							
His Ala	Val Ala	Ile His	Gly Glu	Asp Asp	Leu His	Val Thr	Glu Glu							
		180			185		190							
Val Tyr	Lys Arg	Pro Leu	Phe Leu	Gln Pro	Thr Tyr	Arg Tyr	His Arg							
		195			200		205							
Leu Pro	Leu Pro	Glu Gln	Gly Ser	Pro Leu	Glu Ala	Gln Leu	Asp Ala							
		210			215		220							
Phe Val	Ser Val	Leu Arg	Glu Thr	Pro Ser	Leu Leu	Gln Leu	Arg Asp							
		225			230		235							
Ala His	Gly Pro	Pro Pro	Ala Leu	Val Phe	Ser Cys	Gln Met	Gly Val							
		245			250		255							
Gly Arg	Thr Asn	Leu Gly	Met Val	Leu Gly	Thr Leu	Ile Leu	Leu His							
		260			265		270							
Arg Ser	Gly Thr	Thr Ser	Gln Pro	Glu Ala	Ala Pro	Thr Gln	Ala Lys							
		275			280		285							
Pro Leu	Pro Met	Glu Gln	Phe Gln	Val Ile	Gln Ser	Phe Leu	Arg Met							
		290			295		300							
Val Pro	Gln Gly	Arg Arg	Met Val	Glu Glu	Val Asp	Arg Ala	Ile Thr							
		305			310		315							
Ala Cys	Ala Glu	Leu His	Asp Leu	Lys Glu	Val Val	Leu Glu	Asn Gln							
		325			330		335							
Lys Lys	Leu Glu	Gly Ile	Arg Pro	Glu Ser	Pro Ala	Gln Gly	Ser Gly							
		340			345		350							
Ser Arg	His Ser	Val Trp	Gln Arg	Ala Leu	Trp Ser	Leu Glu	Arg Tyr							
		355			360		365							
Phe Tyr	Leu Ile	Leu Phe	Asn Tyr	Tyr Leu	His Glu	Gln Tyr	Pro Leu							
		370			375		380							
Ala Phe	Ala Leu	Ser Phe	Ser Arg	Trp Leu	Cys Ala	His Pro	Glu Leu							
		385			390		395							
Tyr Arg	Leu Pro	Val Thr	Leu Ser	Ser Ala	Gly Pro	Val Ala	Pro Arg							
		405			410		415							
Asp Leu	Ile Ala	Arg Gly	Ser Leu	Arg Glu	Asp Asp	Leu Val	Ser Pro							
		420			425		430							
Asp Ala	Leu Ser	Thr Val	Arg Glu	Met Asp	Val Ala	Asn Phe	Arg Arg							
		435			440		445							
Val Pro	Arg Met	Pro Ile	Tyr Gly	Thr Ala	Gln Pro	Ser Ala	Lys Ala							
		450			455		460							
Leu Gly	Ser Ile	Leu Ala	Tyr Leu	Thr Asp	Ala Lys	Arg Arg	Leu Arg							
		465			470		475							
Lys Val	Val Trp	Val Ser	Leu Arg	Glu Glu	Ala Val	Leu Glu	Cys Asp							

[illegible]

<210> 1745

<211> 426

<212> DNA

<213> Homo sapiens

<400> 1745

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ntcatgaaaa  ttaaaaaaatg  gcttggtgta  gcagcccttg  ctacagtcgc  aggtttggct
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120
actgttaacc  gtacggttc   tgaagaaaaa  cgttgggaca  aaatccaaga  attggttaaa
180
aaagcggta  tactttgga   atttacggag  ttcacaggct  actcacaacc  aaacaaggca
240

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actgctgatg gcgaagtaga ttggaacgct ttccaacact ataactttctt gaacaactgg
 300
 aacaaagaaa acgggaaaga ccttgtagcg attgcagata cttacatctc tccaatccgt
 360
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 420
 tcgcga
 426

<210> 1746
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1746
 Xaa Met Lys Ile Lys Lys Trp Leu Gly Val Ala Ala Leu Ala Thr Val
 1 5 10 15
 Ala Gly Leu Ala Leu Ala Ala Cys Gly Asn Ser Glu Lys Lys Ala Asp
 20 25 30
 Asn Ala Thr Thr Ile Lys Ile Ala Thr Val Asn Arg Ser Gly Ser Glu
 35 40 45
 Glu Lys Arg Trp Asp Lys Ile Gln Glu Leu Val Lys Lys Asp Gly Ile
 50 55 60
 Thr Leu Glu Phe Thr Glu Phe Thr Gly Tyr Ser Gln Pro Asn Lys Ala
 65 70 75 80
 Thr Ala Asp Gly Glu Val Asp Leu Asn Ala Phe Gln His Tyr Asn Phe
 85 90 95
 Leu Asn Asn Trp Asn Lys Glu Asn Gly Lys Asp Leu Val Ala Ile Ala
 100 105 110
 Asp Thr Tyr Ile Ser Pro Ile Arg Leu Tyr Ser Gly Leu Asn Gly Ser
 115 120 125
 Asp Asn Lys Tyr Thr Lys Val Glu Ala Gly Val Cys Ser Arg
 130 135 140

<210> 1747
 <211> 373
 <212> DNA
 <213> Homo sapiens

<400> 1747
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 atcacgcccc ctgaaggcgt gttggaggca cgggcggggt cgctcctcaa ggacggcacg
 120
 tggcacatca tgtaccagta cgaaccacac gcggatgggc acggcctctg gggacatgtc
 180
 acttccccca acttctctcc cttaaactgg acagacggag aagacattct ggttccagag
 240
 ggcgaggaaa ccgacctgtg ggcaggttct gttattagca acgctggaaa agtgacgtg
 300
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 360
 caaagctacg cgt
 373

<210> 1748
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1748
 Met Val Thr His Arg Pro Glu Leu His Ile Thr Ala Pro Glu Gly Val
 1 5 10 15
 Leu Glu Ala Pro Ala Gly Ser Leu Leu Lys Asp Gly Thr Trp His Ile
 20 25 30
 Met Tyr Gln Tyr Glu Pro His Ala Asp Gly His Gly Leu Trp Gly His
 35 40 45
 Val Thr Ser Pro Asn Phe Ser Pro Phe Asn Trp Thr Asp Gly Glu Asp
 50 55 60
 Ile Leu Val Pro Glu Gly Glu Glu Thr Asp Leu Trp Ala Gly Ser Val
 65 70 75 80
 Ile Ser Asn Ala Gly Lys Val Thr Leu Phe Phe Thr Ser Val Lys Gly
 85 90 95
 Asp Xaa Asp Gly Asn Pro Ser Gly Arg Cys Arg Arg Arg Gln Ser Tyr
 100 105 110
 Ala

<210> 1749
 <211> 853
 <212> DNA
 <213> Homo sapiens

<400> 1749
 cccagcaggc aaagagagag gcctccctgg ctctcagtggt caggggagcc gcgttccctc
 60
 ccagggctgg agcagaggac cacaaggcag cagaaagcgc ggggtccagat gagggccagg
 120
 aaggggagga gagtggggc caagaacgag ccttaaggga gcagtcctaa gctggagcca
 180
 cccagggctg ggtctgggag tctctcagtg ccaactgtcc caggttaggg ggcttgccct
 240
 gctctctcca gggccagtct ctgtgtgtgg ggactcagcc cgtggccgac agatgccatc
 300
 caggatgtac aaggtgcagc caaggcaggc catgcagggg ccgggcctgt ctgcagctgg
 360
 tggatgcctg tgggcatggc ttctctggg gacccattc ctgtcagtag caaccctggc
 420
 agtgctccga gcggtcttag acaactttgg tcataggaac tctggagggt ggttctggct
 480
 atctgaggtg gctactcaac aggtttgagg cccacagca acagaagtcc aggacccatc
 540
 aggttgcttc agaagcccta agactgatga gctggagcgc gcatttgaga gaagcctcgc
 600
 acccactgtg tactggcccc gctcaggccg gcctggcaca ccgttgccctg ctggcggctc
 660
 tcatggggaa gcgcctgggc actggggatt gcttgtgggc cactcaactc ttggggcagt
 720

ggccgtaacc ctagtgttgc tgaggccctt atgtcccctt atgttctctg tactggagct
 780
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 840
 aggacactga gga
 853

<210> 1750
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1750
 Glu Lys Pro Arg Thr His Cys Val Leu Ala Pro Leu Arg Pro Ala Trp
 1 5 10 15
 His Thr Val Ala Cys Trp Arg Leu Ser Trp Gly Ser Ala Trp Ala Leu
 20 25 30
 Gly Ile Ala Cys Gly Pro Leu Asn Ser Trp Gly Ser Gly Arg Asn Pro
 35 40 45
 Ser Leu Pro Glu Ala Leu Met Ser Pro Tyr Val Pro Gly Thr Gly Ala
 50 55 60

<210> 1751
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 1751
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 gacgatgccg ttgtcgagaa ggccatggcg acgaccgggg tctccgagct tactgatagg
 120
 gcatgggtctt ccctgtcagg aggagagagg caacgggtac agctggctcg tgccttggca
 180
 caggagcccc agatcttatt tcttgacgag ccgacaaatc accttgactt gccacaccag
 240
 atcgacctcc tggagcgggt ccgaggactc ggccctgacga cggtcaccgt cattcatgatc
 300
 ctgcacttgg ctgccgccta cgccgacgac ctcactcgtg tcgactcggg tcgcatggtt
 360
 gctggcggac cgccgagcac agtgctgacg cctggccttg tccgtgacca ctttgggtgtc
 420
 gacggtgagg tttggctctc ctgagggcgc ggcttcacct ggaacgggct gcagacatga
 480
 cgacgcgtat cgcagtatcc ctccgatggg acgacgccat tgacttgagc c
 531

<210> 1752
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1752
 Gly Arg Ile Pro His Leu Gly Arg Trp Arg Met Gly Asn Phe Ser Arg

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      1           5           10           15
Arg  Gln Gly His Asp Asp Ala Val Val Glu Lys Ala Met Ala Thr Thr
      20           25           30
Gly Val Ser Glu Leu Thr Asp Arg Ala Trp Ser Ser Leu Ser Gly Gly
      35           40           45
Glu Arg Gln Arg Val Gln Leu Ala Arg Ala Leu Ala Gln Glu Pro Glu
      50           55           60
Ile Leu Phe Leu Asp Glu Pro Thr Asn His Leu Asp Leu Pro His Gln
      65           70           75           80
Ile Asp Leu Leu Glu Arg Val Arg Gly Leu Gly Leu Thr Thr Val Thr
      85           90           95
Val Ile His Asp Leu Asp Leu Ala Ala Ala Tyr Ala Asp Asp Leu Ile
      100          105          110
Val Leu Asp Ser Gly Arg Met Val Ala Gly Gly Pro Ala Ser Thr Val
      115          120          125
Leu Thr Pro Gly Leu Val Arg Asp His Phe Gly Val Asp Gly Glu Val
      130          135          140
Trp Ser Ser Ser Arg Arg Gly Phe Thr Trp Asn Gly Leu Gln Thr
      145          150          155

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<210> 1753

<211> 920

<212> DNA

<213> Homo sapiens

<400> 1753

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tgggaccoga tggtctctggg gactcagggc cgctctgtgc tggacaggga ttccaaggac
120
acacagacca ggatcagcca aaagggccgc cgtctgcagc ccccggggac tcctcgggcc
180
ccaccccaga gaagggcccg gaaacagctg aacccctgcc ggggcaccga gagagtggac
240
cctgggtctg aggggggtgac tctgaagttt cagataaagc cggactccag cctgcagatc
300
atccccacgt acagcctgcc ctgcagtagc cgttctcagg aatccccctg agatgctgtt
360
ggggggccntg cagccatccc agagggcacc gagggccact cagcaggcag cgaggccctg
420
gagccccgcg cctgtgcttc ctgtcggacc cagaggaccc cgctctggag agacgttgaa
480
gatgggaccc ttctctgcaa cgcctgtggg atcaggtaca agaaatacgg cactcgctgc
540
tccagctgct ggctggtgcc caggaaaaat gtccagccca agaggctatg tggcagatgt
600
ggagtgtccc tggaccccat tcaggaaggt taaaccacgc ttcacctgc tgagctgtgc
660
cttctgcctc cgtttcacca gtgggagaat gggcagaagc agctctccta ggaggattgg
720
ggaaagagcc ggctgcctc ctctctgcc tctccagatt caaggatccc gggggaagac
780
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840

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cagagggcccc ctcaggagac gctctcagga aggatgagca ttgttacagc agggacaata
 900
 aagtacagag atatgccgag
 920

<210> 1754
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 1754
 Glu Thr Val Glu Arg Leu Gly Gln Ser Pro Ala Gln Asp Thr Pro Val
 1 5 10 15
 Leu Gly Pro Cys Trp Asp Pro Met Ala Leu Gly Thr Gln Gly Arg Leu
 20 25 30
 Leu Leu Asp Arg Asp Ser Lys Asp Thr Gln Thr Arg Ile Ser Gln Lys
 35 40 45
 Gly Arg Arg Leu Gln Pro Pro Gly Thr Pro Ser Ala Pro Pro Gln Arg
 50 55 60
 Arg Pro Arg Lys Gln Leu Asn Pro Cys Arg Gly Thr Glu Arg Val Asp
 65 70 75 80
 Pro Gly Phe Glu Gly Val Thr Leu Lys Phe Gln Ile Lys Pro Asp Ser
 85 90 95
 Ser Leu Gln Ile Ile Pro Thr Tyr Ser Leu Pro Cys Ser Ser Arg Ser
 100 105 110
 Gln Glu Ser Pro Ala Asp Ala Val Gly Gly Xaa Ala Ala Ile Pro Glu
 115 120 125
 Gly Thr Glu Gly His Ser Ala Gly Ser Glu Ala Leu Glu Pro Arg Arg
 130 135 140
 Cys Ala Ser Cys Arg Thr Gln Arg Thr Pro Leu Trp Arg Asp Ala Glu
 145 150 155 160
 Asp Gly Thr Leu Leu Cys Asn Ala Cys Gly Ile Arg Tyr Lys Lys Tyr
 165 170 175
 Gly Thr Arg Cys Ser Ser Cys Trp Leu Val Pro Arg Lys Asn Val Gln
 180 185 190
 Pro Lys Arg Leu Cys Gly Arg Cys Gly Val Ser Leu Asp Pro Ile Gln
 195 200 205
 Glu Gly
 210

<210> 1755
 <211> 437
 <212> DNA
 <213> Homo sapiens

<400> 1755
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 ggagcaatca gaaatgatca aggagaatcc ttgatacgaa ctgcattcca gtgtcttcag
 120
 ttggttgatga cagattttct accaacaatg ccttgactt gcctgcaaat agttgttagat
 180
 gttgcaggta gctttggcct ccataaccaa gaactcaat ttagtttaac ttcaatagggt
 240

ttattgtgga atatttcaga ttattttttc caaagagggg aaactattga aaaagaacta
 300
 aataaggaag aggcagcaca gcaaaagcag gcagaagaga aaggagtgtg tttaaactgg
 360
 ccattccacc ctgcaccgcc atttgattgc ttgtggttat gtctttatgc aaaattgggt
 420
 gaactatgtg tggatcc
 437

<210> 1756

<211> 126

<212> PRT

<213> Homo sapiens

<400> 1756

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Phe	Gln	Cys	Leu	Gln	Leu	Val	Val	Thr	Asp	Phe	Leu	Pro	Thr	Met	Pro
			20					25					30		
Cys	Thr	Cys	Leu	Gln	Ile	Val	Val	Asp	Val	Ala	Gly	Ser	Phe	Gly	Leu
			35				40					45			
His	Asn	Gln	Glu	Leu	Asn	Ile	Ser	Leu	Thr	Ser	Ile	Gly	Leu	Leu	Trp
	50				55					60					
Asn	Ile	Ser	Asp	Tyr	Phe	Phe	Gln	Arg	Gly	Glu	Thr	Ile	Glu	Lys	Glu
	65				70					75				80	
Leu	Asn	Lys	Glu	Glu	Ala	Ala	Gln	Gln	Lys	Gln	Ala	Glu	Glu	Lys	Gly
			85						90					95	
Val	Val	Leu	Asn	Arg	Pro	Phe	His	Pro	Ala	Pro	Pro	Phe	Asp	Cys	Leu
			100					105					110		
Trp	Leu	Cys	Leu	Tyr	Ala	Lys	Leu	Gly	Glu	Leu	Cys	Val	Asp		
			115				120					125			

<210> 1757

<211> 1297

<212> DNA

<213> Homo sapiens

<400> 1757

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 gcgcacagca tccatggcac caaccctcaa tatctggttg agaagatcat tcgaacgcga
 120
 atctatgagt ccaagtactg gaaagaggag tgctttggac ttacagctga actttagtgc
 180
 gataaagcca tggagttaag gtttgggggt ggcgtctatg gtggcaacat aaaaccaaca
 240
 ccctttctgt gtttaacctt gaagatgctt caaattcaac ccgagaagga tatcattgta
 300
 gagtttatca aaaatgaaga tttcaagtat gtccgcatgc tggggggcact ttacatgagg
 360
 ctgacaggca ctgaattga ttgctacaag tacttggaac ctttgtacaa tgactatcga
 420
 aaaatcaaga gccagaaccg aaatggggag tttgaattga tgcagtgtga tgagtttatt
 480

gatgaactat tgcacagtga gagagtctgt gatatcattc tgccccgact acagaaacgc
 540
 tatgtattag aggaagctga gcaactggag cctcgagtta gtgctctgga agaggacatg
 600
 gatgatgtgg agtccagtga agaggaagaa gaggaggatg agaagttgga aagagtgcc
 660
 tcacctgac accgccggag aagctaccga gacttggaca agccccgtcg ctctcccaca
 720
 ctgcgctaca ggaggagtag gagccggtct cccagaaggc ggagtcgatc tcccaaaagg
 780
 agaagccctc cccctcgccg agaaaggcat cggagcaaga gtccaagacg tcaccgcagc
 840
 aggtcccgag atcgccggca cagatcccg tccaagtccc caggctcatca cgtagtacac
 900
 agacacagga gccactcaaa gtctcccgaa aggtctaaga agagccacaa gaagagccgg
 960
 agagggaatg agtaatggac tcagtttggg tttagtccac atggcctcct gtggatataa
 1020
 ggatatctgt atgtggaagg attaatctc cccccaggga gctataagaa tatttttagtt
 1080
 tttttcttat caagtttctc aacctttatt tttaatgaag gagggtgctga gttttgtatc
 1140
 tttttaatca taatcaacat cagtttttga cccaactaac cttgactgta ttcaaactta
 1200
 tgagagtata aaggatctgg aggttgggga tatgactgac aaggaaaggc tgtggccacc
 1260
 tgatgaccct ttcccttttt attaaaccgg acacacc
 1297

<210> 1758

<211> 312

<212> PRT

<213> Homo sapiens

<400> 1758

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Pro	Gln	Tyr	Leu	Val	Glu	Lys	Ile	Ile	Arg	Thr	Arg	Ile	Tyr	Glu	Ser
			20					25					30		
Lys	Tyr	Trp	Lys	Glu	Glu	Cys	Phe	Gly	Leu	Thr	Ala	Glu	Leu	Val	Val
			35				40					45			
Asp	Lys	Ala	Met	Glu	Leu	Arg	Phe	Val	Gly	Gly	Val	Tyr	Gly	Gly	Asn
	50					55				60					
Ile	Lys	Pro	Thr	Pro	Phe	Leu	Cys	Leu	Thr	Leu	Lys	Met	Leu	Gln	Ile
	65				70				75					80	
Gln	Pro	Glu	Lys	Asp	Ile	Ile	Val	Glu	Phe	Ile	Lys	Asn	Glu	Asp	Phe
			85						90				95		
Lys	Tyr	Val	Arg	Met	Leu	Gly	Ala	Leu	Tyr	Met	Arg	Leu	Thr	Gly	Thr
			100				105						110		
Ala	Ile	Asp	Cys	Tyr	Lys	Tyr	Leu	Glu	Pro	Leu	Tyr	Asn	Asp	Tyr	Arg
		115					120					125			
Lys	Ile	Lys	Ser	Gln	Asn	Arg	Asn	Gly	Glu	Phe	Glu	Leu	Met	His	Val
	130				135					140					
Asp	Glu	Phe	Ile	Asp	Glu	Leu	Leu	His	Ser	Glu	Arg	Val	Cys	Asp	Ile

```

145          150          155          160
Ile Leu Pro Arg Leu Gln Lys Arg Tyr Val Leu Glu Glu Ala Glu Gln
          165          170          175
Leu Glu Pro Arg Val Ser Ala Leu Glu Glu Asp Met Asp Asp Val Glu
          180          185          190
Ser Ser Glu Glu Glu Glu Glu Asp Glu Lys Leu Glu Arg Val Pro
          195          200          205
Ser Pro Asp His Arg Arg Arg Ser Tyr Arg Asp Leu Asp Lys Pro Arg
          210          215          220
Arg Ser Pro Thr Leu Arg Tyr Arg Arg Ser Arg Ser Arg Ser Pro Arg
          225          230          235
Arg Arg Ser Arg Ser Pro Lys Arg Arg Ser Pro Ser Pro Arg Arg Glu
          245          250          255
Arg His Arg Ser Lys Ser Pro Arg Arg His Arg Ser Arg Ser Asp
          260          265          270
Arg Arg His Arg Ser Arg Ser Lys Ser Pro Gly His His Arg Ser His
          275          280          285
Arg His Arg Ser His Ser Lys Ser Pro Glu Arg Ser Lys Lys Ser His
          290          295          300
Lys Lys Ser Arg Arg Gly Asn Glu
305          310

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<210> 1759

<211> 324

<212> DNA

<213> Homo sapiens

<400> 1759

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ggcctgggca gacacaatta ttgtcggaaat ccagatgggtg atgccagacc ttgggtgccat
120
gtgatgaagg accgaaagct gacgtgggaa tactgtgaca tgtccccatg ctccacctgt
180
ggcctgaggc agtgcaaacg gcctcagttt agaactaaag gaggactcta cacagacatc
240
acctcacacc cttggcaggc tgccatcttt gtcagcaaca agagggtctcc tggagagaga
300
ttcctttgtg gaggggtgct gatc
324

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<210> 1760

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1760

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Asn Ser Ile Val Leu Met Gly Lys Ser Tyr Thr Ala Trp Arg Thr Asn
1          5          10          15
Ser Gln Ala Leu Gly Leu Gly Arg His Asn Tyr Cys Arg Asn Pro Asp
          20          25          30
Gly Asp Ala Arg Pro Trp Cys His Val Met Lys Asp Arg Lys Leu Thr
          35          40          45
Trp Glu Tyr Cys Asp Met Ser Pro Cys Ser Thr Cys Gly Leu Arg Gln

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      50              55              60
Cys Lys Arg Pro Gln Phe Arg Thr Lys Gly Gly Leu Tyr Thr Asp Ile
65              70              75              80
Thr Ser His Pro Trp Gln Ala Ala Ile Phe Val Ser Asn Lys Arg Ser
      85              90              95
Pro Gly Glu Arg Phe Leu Cys Gly Gly Val Leu Ile
      100              105

<210> 1761
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1761
ngcgatctcg gctcactaca acctcgggtga cagagcgaga ctctatccca aaaaaataaa
60
aataaaaatc aactggagaa ggaaatgggg ttggggagca tctctgta atataaaggc
120
agccattcat ttaggagag gaggtagaag gaaatgctgt ttgtcgatgg ttcctttcca
180
gagaggaaga gaggagaaag gaagagcggg gagcaggtgg ggagcccga gtaagaccgc
240
acagtggggc caggtggtct tgcaccctgt attcccactt tggctggggc agcccagagt
300
ccaggccagc aggtaatgcc ccagccatgc ccactcgggc ctattggatc c
351

<210> 1762
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1762
Met Ala Gly Ala Leu Pro Ala Gly Leu Asp Ser Gly Leu Pro Gln Pro
1              5              10              15
Lys Trp Glu Tyr Arg Val Gln Asp His Leu Ala Pro Leu Trp Gly Leu
      20              25              30
Thr Ala Gly Ser Pro Pro Ala Pro Arg Ser Ser Phe Leu Leu Ser Ser
      35              40              45
Ser Leu Glu Lys Asn His Arg Gln Thr Ala Phe Pro Ser Thr Ser Ser
      50              55              60
Pro Thr Met Asn Gly Cys Leu Tyr Ile Phe Arg Gly Cys Ser Pro Thr
65              70              75              80
Pro Phe Pro Ser Pro Val Asp Phe Tyr Phe Tyr Phe Phe Gly Ile Glu
      85              90              95
Ser Arg Ser Val Thr Glu Val Val Val Ser Arg Asp Arg
      100              105

<210> 1763
<211> 356
<212> DNA
<213> Homo sapiens

<400> 1763

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gcgcgccggg ggcgcgatgt ggagcgggca cttaccggtt tcatggccaa gacaggcgag
 60
 actcagagtc ttttcaaaga tgacgtcagc acattttccat tgattgtctc cagacctttc
 120
 accatcccct acctgacagc ttttcttccg tctgaactgg agatgcaaca aatggaagag
 180
 acagattcct cggagcagga tgaacagaca gacacagaga acctgtctct tcatatcagc
 240
 atggaggatt ctggagccga gaaagagaac acctctgtcc tgcagcagaa cccctccttg
 300
 tcgggtagcc ggaatgggga ggagaacatc atcgataacc cttatctgcg accggg
 356

<210> 1764

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1764

Ala	Arg	Arg	Gly	Arg	Asp	Val	Glu	Arg	Ala	Leu	Thr	Arg	Phe	Met	Ala
1				5					10					15	
Lys	Thr	Gly	Glu	Thr	Gln	Ser	Leu	Phe	Lys	Asp	Asp	Val	Ser	Thr	Phe
			20					25					30		
Pro	Leu	Ile	Ala	Ala	Arg	Pro	Phe	Thr	Ile	Pro	Tyr	Leu	Thr	Ala	Leu
		35					40					45			
Leu	Pro	Ser	Glu	Leu	Glu	Met	Gln	Gln	Met	Glu	Glu	Thr	Asp	Ser	Ser
		50				55					60				
Glu	Gln	Asp	Glu	Gln	Thr	Asp	Thr	Glu	Asn	Leu	Ala	Leu	His	Ile	Ser
				70					75					80	
Met	Glu	Asp	Ser	Gly	Ala	Glu	Lys	Glu	Asn	Thr	Ser	Val	Leu	Gln	Gln
				85					90					95	
Asn	Pro	Ser	Leu	Ser	Gly	Ser	Arg	Asn	Gly	Glu	Glu	Asn	Ile	Ile	Asp
				100				105					110		
Asn	Pro	Tyr	Leu	Arg	Pro										
															115

<210> 1765

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1765

cggccgcatt cttcgtgact gggtccccgc cgccggtgca aaagtgtcag gaaataccag
 60
 tcatgactat gtttagccgc acctctctgc agtatgcgat cgttctggga gcgctggggc
 120
 gtgcggtctt ggcgtctctg gccatgtcga gtgcgacgga ggccaatcag gcggaatgtg
 180
 cccaggccag gccaggcatt attgcggcgg cgccggtgtg cgtggatgtc gagggcgggc
 240
 tgctgcggct ctccaccag cgcgacgggg tgattcagga tgtgccgggt aaggaaggac
 300
 agcgggtcaa agccggcgat atcctcgccg cgctcgacaa tcgcccggaa ctgacgc
 357

<210> 1766
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 1766
 Met Thr Met Phe Ser Arg Thr Ser Leu Gln Tyr Ala Ile Val Leu Ala
 1 5 10 15
 Ala Leu Gly Gly Ala Gly Leu Ala Leu Trp Ala Met Ser Ser Ala Thr
 20 25 30
 Glu Ala Asn Gln Ala Glu Ile Ala Gln Ala Arg Pro Gly Ile Ile Ala
 35 40 45
 Ala Ala Arg Gly Val Val Asp Val Glu Gly Gly Leu Leu Arg Leu Ser
 50 55 60
 Thr Gln Arg Asp Gly Val Ile Gln Asp Val Pro Val Lys Glu Gly Gln
 65 70 75 80
 Arg Val Lys Ala Gly Asp Ile Leu Ala Ala Leu Asp Asn Arg Arg Glu
 85 90 95
 Leu Ile

<210> 1767
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 1767
 nnnccgccgac ggccgccatg acgcaccgca ttgacgtgaa ccaggggcgac gatgcccaacc
 60
 ccggccaaca cgccaggctg cttgacgccc ccagccaacc cgacgaacgc cccaccaaga
 120
 acgagcccga gccatccccg gccaatcaac gccagacgta tggccacaac gaggcgacg
 180
 agggacaaac ccacctggag tccgtcgttg tgcattgcccc ccaccacgct caacgtcgct
 240
 aatggacagc acaccgccag ccagagggca tgatccggat cgggtccggc gtacgcn
 297

<210> 1768
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1768
 Met Pro Thr Pro Ala Asn Thr Pro Gly Cys Leu Thr Pro Pro Ala Asn
 1 5 10 15
 Pro Thr Asn Ala Pro Pro Arg Thr Ser Pro Ser His Pro Arg Pro Ile
 20 25 30
 Asn Ala Arg Arg Met Ala Thr Thr Ser Ala Thr Arg Asp Lys Pro Thr
 35 40 45
 Trp Ser Pro Ser Leu Cys Met Pro Pro Thr Thr Leu Asn Val Val Asn
 50 55 60
 Gly Gln His Thr Ala Ser Gln Arg Ala

65

70

<210> 1769
 <211> 474
 <212> DNA
 <213> Homo sapiens

<400> 1769
 caccatgctg gctcgggttcg acgcattcgg gtgggtgagt ctgttctcgt caccgacggg
 60
 cagggtcatg ccgttcgtgg ccctgccatt gaggtgacga aagggtcagt tagcgtcgag
 120
 accgttgaga tcttccatac tcccgcgacc acgcatcgat gggctgcctg ccaggcattg
 180
 ccgaagtccg atagagctga gctggcgggtg gcgacctca ccgagatggg agttcacgaa
 240
 atcctcgcct ggcaggctga tcggagcadc gtgcgatgga agggcgacaa gcaagccaag
 300
 ggctgtcgga ggtggcaagc ggctgccctg gaggccacca aacagtctcg acgttttctt
 360
 gtgccacagg tagaactagc gcaaaccctg gaagttgtta agcggatttg caatgccccg
 420
 gccgcctacg ttttgcacga gtcggccagt gaaccgctgg tgcacagga gctc
 474

<210> 1770
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 1770
 His His Ala Gly Ser Val Arg Arg Ile Arg Val Gly Glu Ser Val Leu
 1 5 10 15
 Val Thr Asp Gly Gln Gly His Ala Val Arg Gly Pro Ala Ile Glu Val
 20 25 30
 Thr Lys Gly Ser Val Ser Val Glu Thr Val Glu Ile Leu His Thr Pro
 35 40 45
 Ala Thr Thr His Arg Trp Val Ala Val Gln Ala Leu Pro Lys Ser Asp
 50 55 60
 Arg Ala Glu Leu Ala Val Ala Thr Leu Thr Glu Met Gly Val His Glu
 65 70 75 80
 Ile Leu Ala Trp Gln Ala Asp Arg Ser Ile Val Arg Trp Lys Gly Asp
 85 90 95
 Lys Gln Ala Lys Gly Val Ala Arg Trp Gln Ala Ala Ala Arg Glu Ala
 100 105 110
 Thr Lys Gln Ser Arg Arg Phe Leu Val Pro Gln Val Glu Leu Ala Gln
 115 120 125
 Thr Arg Glu Val Val Lys Arg Ile Cys Asn Ala Gln Ala Ala Tyr Val
 130 135 140
 Leu His Glu Ser Ala Ser Glu Pro Leu Val His Gln Glu Leu
 145 150 155

<210> 1771
 <211> 287

<212> DNA

<213> Homo sapiens

<400> 1771

acgcgtgatg ggtaattcta atacatgcaa agaattatct ctgcaagtat actcagatat
 60
 taataacagc ggggtgtcgca gaggaagaag cctgggagaa tgggaagtcat ggaaggagag
 120
 caacaggctt ctcaactctgt gccatgagca tgtgctagcc atggagacac tctgcatgtt
 180
 acctagaact gctgattcat tgctctggaa ttattcagct attcaagacc cagtgaataa
 240
 cagcaagcag ctttcattca tacacacaca tgtgcatcca tgtgcac
 287

<210> 1772

<211> 93

<212> PRT

<213> Homo sapiens

<400> 1772

Met	Gly	Asn	Ser	Asn	Thr	Cys	Lys	Glu	Leu	Ser	Leu	Gln	Val	Tyr	Ser
1				5				10				15			
Asp	Ile	Asn	Asn	Ser	Gly	Cys	Arg	Arg	Gly	Arg	Ser	Leu	Gly	Glu	Trp
			20				25					30			
Lys	Ser	Gly	Lys	Glu	Ser	Asn	Arg	Leu	Leu	Thr	Leu	Cys	His	Glu	His
		35					40					45			
Val	Leu	Ala	Met	Glu	Thr	Leu	Cys	Met	Leu	Pro	Arg	Thr	Ala	Asp	Ser
	50					55				60					
Leu	Leu	Trp	Asn	Tyr	Ser	Ala	Ile	Gln	Asp	Pro	Val	Lys	Tyr	Ser	Lys
65				70					75						80
Gln	Leu	Ser	Phe	Ile	His	Thr	His	Val	His	Pro	Cys	Ala			
				85					90						

<210> 1773

<211> 393

<212> DNA

<213> Homo sapiens

<400> 1773

accggtgagt tctacgtccc ggtaaccac ctcgagggtg aacaggcgca cctcgagctc
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 ttcgattctc cgcttaacga gtacgcagcg atgggatttg agtacggcta ctctgttgcc
 120
 cgtccggatt ctctggtatt gtgggaagcc caattcggcg atttcaccaa cggtgccacc
 180
 acgatcatcg atgagttcat cgctctggct ggctccaagt ggggtcagaa gtcgggagtc
 240
 gtgctgtctg tgcgcacagg ttacgaaggt caggggcctg atcactcgct ggcccgtctg
 300
 gagcgcttcc tcaatctatg cagtgaagac gctttggccg tctgccagcc ctcgaccccc
 360
 gcaagctaca gccatttatt gcgtcagcac gcg
 393

<210> 1774
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 1774
 Thr Gly Glu Phe Tyr Val Pro Val Asn His Leu Gly Gly Glu Gln Ala
 1 5 10 15
 His Leu Asp Val Phe Asp Ser Pro Leu Asn Glu Tyr Ala Ala Met Gly
 20 25 30
 Phe Glu Tyr Gly Tyr Ser Val Ala Arg Pro Asp Ser Leu Val Leu Trp
 35 40 45
 Glu Ala Gln Phe Gly Asp Phe Thr Asn Gly Ala Gln Thr Ile Ile Asp
 50 55 60
 Glu Phe Ile Ala Ser Ala Gly Ser Lys Trp Gly Gln Lys Ser Gly Val
 65 70 75 80
 Val Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His Ser
 85 90 95
 Ser Ala Arg Leu Glu Arg Phe Leu Asn Leu Cys Ser Glu Asp Ala Leu
 100 105 110
 Ala Val Cys Gln Pro Ser Thr Pro Ala Ser Tyr Ser His Leu Leu Arg
 115 120 125
 Gln His Ala
 130

<210> 1775
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 1775
 nncctccgag cagctctccg gggcagaccc cagctgcaag ccacagcccg gccctggtaa
 60
 cgggagggca tcgctaggga ggggtggggc ggcccggtt cgatgcagcc atgtgggagg
 120
 gccactctca gagaccccc gccttccttg ccacccccac ccagagggg aagctggagc
 180
 tgggaggctg cagacccagg ccaaggtgtg gccagggctg gctttcttgg gaggtttga
 240
 gcatcctgct tcctggccac ccagctcttg ggctgctgtc aactcttgat ttgtagacat
 300
 cactccagcc tetggcctgt caccctgaac ctccccatg tctgtgtctt ttctcactgg
 360
 aacaccggt
 369

<210> 1776
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1776
 Arg Glu Gly Ile Ala Arg Glu Gly Trp Gly Gly Pro Ala Ser Met Gln

```

      1           5           10           15
Pro Cys Gly Arg Ala Thr Leu Arg Asp Pro Pro Ser Leu Pro Pro
      20
Pro Pro Gln Arg Gly Ser Trp Ser Trp Glu Ala Ala Asp Pro Gly Gln
      35
Gly Val Ala Arg Ala Gly Phe Leu Gly Arg Leu
      50           55

<210> 1777
<211> 370
<212> DNA
<213> Homo sapiens

<400> 1777
agcttccttat cactatcctt tagtgctttt tggctcacct tagcggtaat gctccatcaa
60
gaatatgggtt ttggtagtgc aactcgggga ttttttggcc tcgctgggtgc cgccggagct
120
ttagcagcac cactgtccgg taaactaaca gataaacaag gaccgacacg ggtcacgcag
180
ctgggtgctgt ccttagttgt cgtctctttc gcacatctagt tgttattgccc ttacttcagt
240
atcagtagccc aagttataat gattattggt gctaccatag tgtttgacct tgggtgttcag
300
gcggcactta ttgctcatca aaccttagtg tataacattg actctaccgc tcgtgggacgc
360
cttaacgcgt
370

<210> 1778
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1778
Ser Phe Leu Ser Leu Ser Phe Ser Ala Phe Trp Ser Thr Leu Ala Val
1           5           10           15
Met Leu His Gln Glu Tyr Gly Phe Gly Ser Ala Thr Ala Gly Phe Phe
      20
Gly Leu Ala Gly Ala Ala Gly Ala Leu Ala Ala Pro Leu Ser Gly Lys
      35
Leu Thr Asp Lys Gln Gly Pro Thr Arg Val Thr Gln Leu Gly Ala Ala
      50           55           60
Leu Val Val Val Ser Phe Ala Ser Met Leu Leu Leu Pro Tyr Phe Ser
      65           70           75           80
Ile Ser Thr Gln Val Ile Met Ile Ile Val Ala Thr Ile Val Phe Asp
      85           90           95
Phe Gly Val Gln Ala Ala Leu Ile Ala His Gln Thr Leu Val Tyr Asn
      100           105           110
Ile Asp Ser Thr Ala Arg Gly Arg Leu Asn Ala
      115           120

<210> 1779
<211> 345

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<212> DNA

<213> Homo sapiens

<400> 1779

ccatgtgtgt gtatatgtctc gtgtgtgatg gtatgtatat gtgtatatgt gnnatatatgt
 60
 atacacgtgt gttatgggtgt gtatatatgt atatacgtgt gtgtatatat atgtatatgg
 120
 gtatgtgtgt gcatgtgcgt atgggtgtgt atatgtgtat atatgtaggt gtgtatatct
 180
 gggaatatat ggggtgtgt atgtgtgtat aggtttttat atgtggggaa atatttaaac
 240
 ctgtgtatat tggaaatgtgt gtgtatatgt gtgtatatat ggnggtgtgt atgtacatgt
 300
 atgtgtgtat atatgtgtgt atatacgtag gtgtgcatat gtgtg
 345

<210> 1780

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1780

Pro Cys Val Cys Ile Cys Ser Cys Val Met Val Cys Ile Cys Val Tyr
 1 5 10 15
 Val Xaa Ile Cys Ile His Val Cys Tyr Gly Val Tyr Ile Cys Ile Tyr
 20 25 30
 Val Cys Val Tyr Ile Cys Ile Trp Val Cys Val Cys Met Cys Val Trp
 35 40 45
 Val Cys Ile Cys Val Tyr Met
 50 55

<210> 1781

<211> 349

<212> DNA

<213> Homo sapiens

<400> 1781

nacgcgtcat gctaaatttt gccctttatg gcaacatttt cgtcagaaca agcgggaagag
 60
 aagctactat ccaagtttca tacgccgggtt aaaagaaaac atgatgatac gagatcatct
 120
 gatgtgaaca caacgcaaac tggttcaagc gccacgcca ttacacctgt acccttactg
 180
 cccagtgcac aagagcccag ttatctttgc cagtgggtgcg ctccccagac acgaaagcac
 240
 aagacatggg aggggtgatgc tattcttata ttgcatggaa ataaaaactac ttgttcgcta
 300
 cgatccgcac atgatggcag catgctagtgc acgaatgctg ccttcgcga
 349

<210> 1782

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1782

```

Met Ala Thr Phe Ser Ser Glu Gln Ala Glu Glu Lys Leu Leu Ser Lys
 1           5           10           15
Phe His Thr Pro Val Lys Arg Lys His Asp Asp Thr Arg Ser Ser Asp
          20           25           30
Val Asn Thr Thr Gln Thr Gly Ser Ser Ala Thr Pro Ile Thr Pro Val
          35           40           45
Pro Leu Leu Pro Ser Ala Gln Glu Pro Ser Tyr Leu Cys Gln Trp Cys
          50           55           60
Ala Pro Gln Thr Arg Lys His Lys Thr Trp Glu Gly Asp Ala Ile Leu
65          70           75           80
Ile Leu His Gly Asn Lys Thr Thr Cys Ser Leu Arg Ser Ala His Asp
          85           90           95
Gly Ser Met Leu Val Thr Asn Ala Ala Phe Arg
          100          105

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<210> 1783

<211> 1829

<212> DNA

<213> Homo sapiens

<400> 1783

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gtgcacgact tcgacgccag cctctcgggc atcgggcagg aactggggcgc cggcgcttac
60
agcatgagtg atgtcttggc attgccatt ttcaagcagg aagattccag cttccattg
120
gatggtgaaa cagagcacc accctttcag tatgtgatgt gtgctgcaac gtcaccagca
180
gtaaaactgc atgatgaaac gcttacttat ttgaaccaag gtcagtcata tgaaaatcgg
240
atgtcggata atcggaataat gggatgatatg cctgagatca atggaaaatt agtaaaagac
300
atcataaggg ttgtattcca tgacagacgg ctacaataca cagagcatca gcaacttgaa
360
ggatggaagt ggaatcgccc aggagacaga cttcttgatt tagatattcc aatgtctgtg
420
ggaataattg acacaaggac gaatccaggc cagttaaatg cggttgaaatt tctgtgggac
480
ccagcaaaac gcacctctgc ttctattcag gtacactgca tcagcacaga atttactcca
540
cggaagcagc gaggtgaaaa gggagtgcgc tttaggatcc aggttgacac ctttaagcag
600
aatgaaaaatg gagaatacac agatcatcta cactcagcta gctgccaaat caaagttttt
660
aagcctaaag gtgcagacag gaaacaaaaa actgaccgag agaagatgga gaagagaaca
720
gctcatgaaa aagaaaagta tcagccgtcc tatgatacca caatcctcac agagatgagg
780
cttgagccta taattgaaga tgcagttgaa catgagcaga aanaagtcca gcaagcggac
840
tttgccgcag actacggtga ttctctggca aagcgaggga gttgttctcc gtggcccgat
900

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gccccacag cctatgtgaa taacagccct tccccagcgc ccactttcac ctccccacag
 960
 cagagcactt gcagtgctcc agacagcaat tcttcttccc caaatcatca gggagatgga
 1020
 gcttcacaga cctctgggtga acaaatcag ccttcagcta cgatccagga aacacagcaa
 1080
 tggctgctca aaaacagatt ctcttcctac acaagactgt tctctaattt ttcaggtgcc
 1140
 gacttattaa aactgacaaa ggaggattta gttcaaattt gtgggtgcgc cgatggaatt
 1200
 cggctctata attcactgaa gtcaaggctcg gttgacccc gtttaacat ctatgtctgc
 1260
 cgggagcagc caagcagcac agtgctgcaa gggcagcagc aagctgcaag cagtgcgaagc
 1320
 gagaatggca gtggggcacc ctatgtttat catgcaatct acttggaaga aatgattgcc
 1380
 tcagaagttg ctgaaaaact tgcgctgggtg ttttaatatcc ctctccacca aattaatcag
 1440
 gtttacagac aggggtccac cggtattcac attcttggtta gtgacaggt aaatcaaacc
 1500
 atttggtttt ccttttcaga ctggtattta cttttatata tgtaattgta gaactgtaga
 1560
 aaaattctgt gacctctttt gaaaataact atgagaatca ttttcagaga gttgggaatc
 1620
 actttggaag aacttataac caagagtttc aggcaccta gtgataatat ggaatacaag
 1680
 ccaaggaaaa ctggtcttagc ctccccccag ccttttagga tgcagccaat cactggggca
 1740
 ctctagggat agtggcaggc tttggccctt tttatgaggt gagtactggt atgtgttttc
 1800
 cttttgtcta ttatttgatg actaattta
 1829

<210> 1784

<211> 514

<212> PRT

<213> Homo sapiens

<400> 1784

Val	His	Asp	Phe		Ala	Ser	Leu	Ser	Gly	Ile	Gly	Gln	Glu	Leu	Gly
1				5					10					15	
Ala	Gly	Ala	Tyr	Ser	Met	Ser	Asp	Val	Leu	Ala	Leu	Pro	Ile	Phe	Lys
			20					25					30		
Gln	Glu	Asp	Ser	Ser	Leu	Pro	Leu	Asp	Gly	Glu	Thr	Glu	His	Pro	Pro
		35				40						45			
Phe	Gln	Tyr	Val	Met	Cys	Ala	Ala	Thr	Ser	Pro	Ala	Val	Lys	Leu	His
	50				55				60						
Asp	Glu	Thr	Leu	Thr	Tyr	Leu	Asn	Gln	Gly	Gln	Ser	Tyr	Glu	Ile	Arg
65				70				75						80	
Met	Leu	Asp	Asn	Arg	Lys	Met	Gly	Asp	Met	Pro	Glu	Ile	Asn	Gly	Lys
			85					90					95		
Leu	Val	Lys	Ser	Ile	Ile	Arg	Val	Val	Phe	His	Asp	Arg	Arg	Leu	Gln
		100					105						110		
Tyr	Thr	Glu	His	Gln	Gln	Leu	Glu	Gly	Trp	Lys	Trp	Asn	Arg	Pro	Gly

[illegible]

<210> 1785

<211> 381

<212> DNA

<213> Homo sapiens

<400> 1785

atcacggacg cagaggagaa agggctgatt actccaggcg tgagtgttct gattgaacca
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 actacggcga acacagggcat tggactggcc tttatggctg ctgccaaggg ctacaaactt
 120
 acaactacaa tgcctgcctc catgagcatg gagaggagga tcatattgaa ggcttttggg
 180
 gctgaacttg tccttactga cccactcttg ggaatgaaag gagctgtcaa gaaagcggaa
 240
 gagatacaag caaagacacc caactcgtac atccttcaac aatttgaaaa tccagctaac
 300
 ccaaagattc actatgagac tactgggcct gaaatctgga aagctacagc aggaaaaaatt
 360
 gatggccttg tatctggtat c
 381

<210> 1786

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1786

Ile	Thr	Asp	Ala	Glu	Glu	Lys	Gly	Leu	Ile	Thr	Pro	Gly	Val	Ser	Val
1				5				10					15		
Leu	Ile	Glu	Pro	Thr	Ser	Gly	Asn	Thr	Gly	Ile	Gly	Leu	Ala	Phe	Met
			20				25					30			
Ala	Ala	Ala	Lys	Gly	Tyr	Lys	Leu	Thr	Leu	Thr	Met	Pro	Ala	Ser	Met
			35				40				45				
Ser	Met	Glu	Arg	Arg	Ile	Ile	Leu	Lys	Ala	Phe	Gly	Ala	Glu	Leu	Val
	50				55				60						
Leu	Thr	Asp	Pro	Leu	Leu	Gly	Met	Lys	Gly	Ala	Val	Lys	Lys	Ala	Glu
65				70					75					80	
Glu	Ile	Gln	Ala	Lys	Thr	Pro	Asn	Ser	Tyr	Ile	Leu	Gln	Gln	Phe	Glu
			85						90					95	
Asn	Pro	Ala	Asn	Pro	Lys	Ile	His	Tyr	Glu	Thr	Thr	Gly	Pro	Gly	Ile
			100					105					110		
Trp	Lys	Ala	Thr	Ala	Gly	Lys	Ile	Asp	Gly	Leu	Val	Ser	Gly	Ile	
			115				120						125		

<210> 1787

<211> 294

<212> DNA

<213> Homo sapiens

<400> 1787

gtgcacacag caattcaata tgccaagaca ccagggttgc gcagagaaaag atttaattgt
 60
 aggggtcacct aacaaggaga tgagaacaaa ctttaaatct atctctctaa ggaatttggg
 120
 cttcggtttt ttaagggtta gaatgggcca aaacatggac attattgatt ggtcaaagag
 180

tacagggtca tgggaacctgg agatgaaaaa gccatattct catgctgac ctgttcctct
 240
 gtggaaggtc ttcaaattgg ttgccggaat aaaagatctg tcaaacatct tagg
 294

<210> 1788

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1788

Met Pro Arg His Gln Val Ala Ala Glu Lys Asp Leu Ile Val Gly Ser
 1 5 10 15
 Pro Asn Lys Glu Met Arg Thr Asn Phe Lys Ser Ile Ser Leu Arg Asn
 20 25 30
 Leu Asp Phe Gly Phe Leu Arg Phe Arg Met Gly Gln Asn Met Asp Ile
 35 40 45
 Ile Asp Trp Ser Lys Ser Thr Gly Ser Trp Asn Leu Glu Met Lys Lys
 50 55 60
 Pro Tyr Ser His Ala Asp Pro Val Pro Leu Trp Lys Val Phe Lys Leu
 65 70 75 80
 Val Ala Gly Ile Lys Asp Leu Ser Asn Ile Leu
 85 90

<210> 1789

<211> 353

<212> DNA

<213> Homo sapiens

<400> 1789

ttccacacata caccacgcg gcatgtcctg acagagatgc acaccctag cacatattca
 60
 cacacacaga catgccacac ccgccatcc cccacactc gtacacgccc accaccctc
 120
 gcaggcacac atgcacacac gcgcgcgcac acgcacacac acccccgcc cggaacggcc
 180
 gacctgctcc cgggggtctc tcccgcaggc aggtctcctc gccgagtctc cgaaaagggg
 240
 cggctcgtggc ggccctggcg ccagctggg caacgcttcg tggatatctca ccgcttctct
 300
 ctgttgtgcc cagcgcgccg actgaagatc cggatcttca gtccttggcg cgc
 353

<210> 1790

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1790

Met His Thr Pro Ser Thr Tyr Ser His Thr Gln Thr Cys His Thr Pro
 1 5 10 15
 Pro Ser Pro His Thr Arg Thr Arg Pro Pro Pro Leu Ala Gly Thr His
 20 25 30
 Ala His Thr Arg Ala His Thr His Thr His Pro Gln Pro Gly Pro Ala

```

      35              40              45
Asp Leu Leu Pro Gly Val Ser Pro Ala Gly Arg Ser Pro Arg Arg Val
 50              55              60
Ser Glu Lys Gly Arg Ser Trp Arg Pro Trp Arg Pro Ala Gly Gln Arg
 65              70              75              80
Phe Val Val Ser His Arg Phe Ser Leu Leu Cys Pro Ala Pro Arg Leu
      85              90              95
Lys Ile Arg Ile Phe Ser Pro Trp Arg
      100              105

```

<210> 1791

<211> 355

<212> DNA

<213> Homo sapiens

<400> 1791

```

aaatttcagt tagagattag ggaaaataaa gatgttattt tttcccatcc tagtttacag
 60
acccccccaga aacccactca tggattctcc cgagtccttg gacctggctc agacaccctt
120
gctttggatc aagccaatgc atgtatcccc taacacaccc atgctttatg tggtcctctg
180
ccctccctgc tcaggggact gcttggttaac ttcattgggt tggggacata tatattatag
240
gagagagaca gagaaaaaga aagagaggaa atgttattct ccttgctctgt atctgtatct
300
ccaactccgat tccattccc tctgctgctc tctctctct cctcccttca cgcgt
355

```

<210> 1792

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1792

```

Met Leu Phe Phe Pro Ile Leu Val Tyr Arg Pro Pro Arg Asn Pro Leu
 1              5              10              15
Met Asp Ser Pro Glu Ser Leu Asp Leu Ala Gln Thr Pro Leu Leu Trp
      20              25              30
Ile Lys Pro Met His Val Ser Pro Asn Thr Pro Met Leu Tyr Val Val
      35              40              45
Pro Ala Pro Pro Cys Ser Gly Asp Cys Leu Leu Thr Ser Leu Gly Trp
      50              55              60
Gly His Ile Tyr Tyr Arg Arg Glu Thr Glu Lys Lys Lys Glu Arg Lys
 65              70              75              80
Cys Tyr Ser Pro Cys Leu Tyr Leu Tyr Leu His Ser Asp Ser His Ser
      85              90              95
Leu Cys Cys Ser Pro Leu Ser Pro Pro Phe Thr Arg
      100              105

```

<210> 1793

<211> 510

<212> DNA

<213> Homo sapiens

<400> 1793
 tgggttccag cccgtagatg accttggcct gggaggcctt ccgaaggcca caccatatac
 60
 caccctctcg gagctctctg cttaccagtc gcccaaaagag cttgtccccc cagcagccag
 120
 agtcagccag acccttagca aacaccatag gggatcatctc aatctcttct ccaattcac
 180
 cttcttctct ggagatgaat cctgacaaca cctcagggtc gaggcagaag tcggtggagg
 240
 ccgagccgtg ctcattgtgg atggtgcacc gatacacacc gcagctctacg ggggaggcct
 300
 gcacgatggc caaggccgcc ggcccctcat cccctgcgtc cctgccacc tcgccactg
 360
 ggcgctgatc cttggcccat gtcaagactg agtcactaag aatgttgaaa aactggcacc
 420
 acagcttcag gctaccggag gcatcaggaa actgctccac ccgaatcttc cggatcacct
 480
 gtggggcttt cagcaggtct ttggctttcc
 510

<210> 1794
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 1794
 Met Thr Leu Ala Trp Glu Ala Phe Arg Arg Pro His Pro Tyr Pro Pro
 1 5 10 15
 Pro Arg Ser Ser Ser Leu Thr Ser Arg Pro Lys Ser Leu Ser Pro Gln
 20 25 30
 Gln Pro Glu Ser Ala Arg Pro Leu Ala Asn Thr Ile Gly Val Ile Ser
 35 40 45
 Ile Ser Ser Pro Thr Ser Pro Ser Ser Leu Glu Met Asn Pro Asp Asn
 50 55 60
 Thr Ser Gly Leu Arg Gln Lys Ser Val Glu Ala Glu Pro Cys Ser Leu
 65 70 75 80
 Trp Met Val His Arg Tyr Thr Pro Gln Ser Thr Gly Glu Ala Cys Thr
 85 90 95
 Met Ala Lys Ala Ala Gly Pro Ser Ser Pro Ala Leu Leu Pro Thr Ser
 100 105 110
 Pro Thr Gly Arg
 115

<210> 1795
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 1795
 ctatgctctg agtcacttct ccaagcattc ctttctgttc ttccttccct gggctgatca
 60
 ttccaagaag tcctacattc cagaaaaactt gagaggtgct tcttctctgg aagccccttt
 120

tcttttctgt gagctcaggg agcattctac atacctcagc tgtgtctgct atcttttgc
 180
 taattatcaa tctttccata taaacagtaa aggaccacag tttattcatc agattcccca
 240
 tccaaacctg cacctgcata cataaacgca ctggataaat gtaccgcagt agacagaggc
 300
 tctccagggt gagagctcca tgagggcacc aatttttgtc tgtttagctg tgtcctcaaa
 360
 gcaaggaagg gttgatccgg tctaga
 386

<210> 1796
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 1796
 Met Gln Val Gln Val Trp Met Gly Asn Leu Met Asn Lys Leu Trp Ser
 1 5 10 15
 Phe Thr Val Tyr Met Glu Arg Leu Ile Ile Lys Gln Lys Ile Ala Asp
 20 25 30
 Thr Ala Glu Val Cys Arg Met Leu Pro Glu Leu Thr Glu Lys Lys Arg
 35 40 45
 Gly Phe Gln Arg Arg Ser Thr Ser Gln Val Phe Trp Asn Val Gly Leu
 50 55 60
 Leu Glu Met Ile Ser Pro Gly Lys Glu Glu Gln Lys Gly Met Leu Gly
 65 70 75 80
 Glu Val Thr Gln Ser Ile
 85

<210> 1797
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 1797
 aagcttcact atgttgccca ttccatgggc ggcgtgctgg tgcgtgacct gctggcggac
 60
 cggaatttgc cgatgtcatt gatcaggtea tetgtctggg ctgcgccgag cagggctcgc
 120
 gtgccgctaa tttgttggcg ccatttgctg gcggcgcatc cgtaaaatgg tgtatcacag
 180
 cgactatgtg atgcgcgttg cgccacgccc cggcagcgcg cggtggagcg ccatacaactc
 240
 acagatggac aacctggtgt tgccggtgac ctcggaatt ttaccgggaa tgacctatgt
 300
 ggcgggtgat tacctggggc attgttcggt attgtacagc ccacgcgt
 348

<210> 1798
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1798

```

Met Gly Gly Val Leu Val Arg Asp Leu Leu Ala Asp Arg Asn Leu Pro
 1           5           10           15
Met Ser Leu Ile Arg Ser Ser Val Trp Ala Arg Arg Ser Arg Ala Arg
          20           25           30
Val Pro Leu Ile Cys Trp Arg His Leu Leu Ala Ala His Pro Ser Asn
          35           40           45
Gly Val Ser Gln Arg Leu Cys Asp Ala Ala Cys Ala His Ala Arg Gln
          50           55           60
Arg Ala Leu Glu Arg His Gln Leu Thr Asp Gly Gln Pro Gly Val Ala
65          70          75          80
Gly Asp Leu Gly Asn Phe Thr Gly Asn Asp Pro Cys Gly Gly Gly Leu
          85          90          95
Pro Gly Ala Leu Phe Val Ile Val Gln Pro Thr Arg
          100          105

```

<210> 1799

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1799

```

acgcgtcgcc tcctgctggg cgggattttc cttgctgtag ttaaccaaac caccggcgtc
60
aataccgcga tgtattacgc gcccaagggt ttggagttcg caggaatgag caccaggcgc
120
tcgattattt cagaggtggc taatggagtc atgtctgtta ttggtgccgc tgcaggcttg
180
tggctcatcg aacggtttga tcgtcgtcac ctgcttatct tcgagtgcac ggcggctcgg
240
gtgtgtctcc ttggtattgc ggctactttc gggctggcaa ttgctctcca tgtgggtcaa
300
ggggtaccga agtgggcgcc tattctcgtg ctgctcctga tgagtattct catgcttata
360
gtgcac
366

```

<210> 1800

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1800

```

Thr Arg Arg Leu Leu Val Gly Ile Phe Leu Ala Val Val Asn Gln
 1           5           10           15
Thr Thr Gly Val Asn Thr Val Met Tyr Tyr Ala Pro Lys Val Leu Glu
          20           25           30
Phe Ala Gly Met Ser Thr Gln Ala Ser Ile Ile Ser Glu Val Ala Asn
          35           40           45
Gly Val Met Ser Val Ile Gly Ala Ala Ala Gly Leu Trp Leu Ile Glu
          50           55           60
Arg Phe Asp Arg Arg His Leu Leu Ile Phe Asp Val Thr Ala Val Gly
65          70          75          80
Val Cys Leu Leu Gly Ile Ala Ala Thr Phe Gly Leu Ala Ile Ala Pro

```

```

      85              90              95
His Val Gly Gln Gly Val Pro Lys Trp Ala Pro Ile Leu Val Leu Val
      100              105              110
Leu Met Ser Ile Phe Met Leu Ile Val His
      115              120

```

<210> 1801

<211> 597

<212> DNA

<213> Homo sapiens

<400> 1801

```

aattttctcct tcggtgacta cttcaagaac gaggccattc agtacgcatg ggagctcgtc
60
actaagccgg cagaacaggg cggattgggt ttcgatcctg ccagcatctg ggtgacggtc
120
cttggacctg ggtttcaccc tgactatccg gagggcgaca ttgaggcgcg cgaggcggtg
180
cgtgctgcgg gtatccctga cgagcagatt cagggtcgct cccttaagga caactactgg
240
catatggggg ttcccggccc cggcgggccc tgctcggaaa tctacatcga tcgtggccca
300
gcctatggtc ccgacggtgg tccagaagca gatgaggacc gttaccttga gatctggaac
360
ctcgtatttc agaccgagga tctctcagcg gtgcgcgcta aagatgacct cgacatcgca
420
ggcccatctg gcagccttaa catcgacact ggtgccggtc tcgaacgtat tgccctaccta
480
ctccaggggc tcgacaatat gtacgagact gaccaggtat tccctgtcat tgagaaagcg
540
tccgagatgt cgggcaagcg gtacggcggt cgccacgacg acgacgtccg actacgc
597

```

<210> 1802

<211> 199

<212> PRT

<213> Homo sapiens

<400> 1802

```

Asn Phe Ser Phe Gly Asp Tyr Phe Lys Asn Glu Ala Ile Gln Tyr Ala
  1              5              10              15
Trp Glu Leu Val Thr Lys Pro Ala Glu Gln Gly Gly Leu Gly Phe Asp
      20              25              30
Pro Ala Ser Ile Trp Val Thr Val Leu Gly Pro Gly Phe His Pro Asp
      35              40              45
Tyr Pro Glu Gly Asp Ile Glu Ala Arg Glu Ala Trp Arg Ala Ala Gly
      50              55              60
Ile Pro Asp Glu Gln Ile Gln Gly Arg Ser Leu Lys Asp Asn Tyr Trp
      65              70              75              80
His Met Gly Val Pro Gly Pro Gly Gly Pro Cys Ser Glu Ile Tyr Ile
      85              90              95
Asp Arg Gly Pro Ala Tyr Gly Pro Asp Gly Gly Pro Glu Ala Asp Glu
      100              105              110
Asp Arg Tyr Leu Glu Ile Trp Asn Leu Val Phe Glu Thr Glu Asp Leu

```

```

      115              120              125
Ser Ala Val Arg Ala Lys Asp Asp Phe Asp Ile Ala Gly Pro Leu Arg
      130              135              140
Ser Leu Asn Ile Asp Thr Gly Ala Gly Leu Glu Arg Ile Ala Tyr Leu
      145              150              155              160
Leu Gln Gly Val Asp Asn Met Tyr Glu Thr Asp Gln Val Phe Pro Val
      165              170              175
Ile Glu Lys Ala Ser Glu Met Ser Gly Lys Arg Tyr Gly Val Arg His
      180              185              190
Asp Asp Asp Val Arg Leu Arg
      195

```

<210> 1803

<211> 708

<212> DNA

<213> Homo sapiens

<400> 1803

```

ccccacaaga tggccgcatc ggtggatggg gaagtgcctg aggaggcac acctaaggac
60
ctcatcctgg cctcatctc cgagatcgcc accggtgggg gacaaggcca tatggtcgag
120
tatcgcgggc aggccatcga gaagatgtcg atggagggtc gcatgacgat ctgcaatatg
180
tcgattgagt ggggagctcg cgctggcatg gttgcttctg atgagaccac cttcacctac
240
ctcaaaggatc gtccgcacgc tccgctgtgt gcacagtggg acaaggctgt cgcgtactgg
300
cgcaactctgc gtactgacga cgatgcgacc tttagcgtg agatccatgt ggacgcctcg
360
aatctcgccc ccttcgttac ctggggtacc aaccggggc agggatcccc ctaggcgggt
420
gtggtgccgg ccgtcgaaga ctttgaggac gaggtagctc gcagcgcage gtttgaggta
480
catggatttg accccgacga gatcggttcc cggtttgctg acatcttttc caataactct
540
gcgaacaacg gcttggtact ggctcaggtt gatcccaagg tcgtcggaga gttgtgggac
600
tttgcggagc agcatcctgg tgacgagctc accctctccc tcgagaatcg gacgattaac
660
cttcgggtc gcacgacctc cccgttccat attgatgacg tcacgcgt
708

```

<210> 1804

<211> 236

<212> PRT

<213> Homo sapiens

<400> 1804

```

Pro Thr Thr Met Ala Val Met Val Asp Gly Glu Val Pro Glu Glu Val
1              5              10              15
Thr Pro Lys Asp Leu Ile Leu Ala Leu Ile Ser Glu Ile Gly Thr Gly
20              25              30
Gly Gly Gln Gly His Met Val Glu Tyr Arg Gly Glu Ala Ile Glu Lys

```


ctggaaggtt cgategccgt cgtggatcg ctggtacagt ggctgcgcga caacctcaag
 720
 atgttcgaga cgcggccgca aatcgaagcc ctcgcccaaca ccgtcgcgga caatgggtggc
 780
 gcctactttt tgccggcctt ctctggcctg ttccgcgcgt actggcgctcc gga
 833

<210> 1806

<211> 277

<212> PRT

<213> Homo sapiens

<400> 1806

Xaa	Ala	Val	Val	Trp	Asp	Lys	Asn	Thr	Gly	Glu	Pro	Val	Tyr	Asn	Ala
1				5					10					15	
Ile	Val	Trp	Gln	Asp	Thr	Arg	Thr	Gln	Lys	Ile	Cys	Asn	Glu	Leu	Ala
			20					25					30		
Gly	Asp	Lys	Gly	Ala	Asp	Arg	Tyr	Lys	Glu	Ile	Cys	Gly	Leu	Gly	Leu
		35				40					45				
Ser	Thr	Tyr	Phe	Ser	Gly	Pro	Lys	Val	Lys	Trp	Ile	Leu	Asp	Asn	Val
50					55					60					
Glu	Gly	Ala	Arg	Ala	Arg	Ala	Glu	Ala	Gly	Asp	Leu	Leu	Phe	Gly	Asn
65				70					75					80	
Met	Asp	Thr	Trp	Val	Leu	Trp	Asn	Leu	Thr	Gly	Gly	Thr	Asn	Gly	Gly
			85						90				95		
Val	His	Ile	Thr	Asp	Pro	Thr	Asn	Ala	Ser	Arg	Thr	Met	Leu	Met	Asp
			100				105						110		
Val	Arg	Lys	Leu	Gln	Trp	Asp	Asp	Ser	Met	Cys	Glu	Val	Met	Gly	Ile
		115				120						125			
Pro	Lys	Ser	Met	Leu	Pro	Glu	Ile	Lys	Ser	Ser	Ser	Glu	Ile	Tyr	Gly
		130			135					140					
Tyr	Gly	Arg	Lys	Asn	Gly	Leu	Leu	Ile	Asp	Thr	Pro	Ile	Ser	Gly	Ile
145				150					155					160	
Leu	Gly	Asp	Gln	Gln	Ala	Ala	Thr	Phe	Gly	Gln	Ala	Cys	Phe	Gln	Lys
			165				170						175		
Gly	Met	Ala	Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Met	Leu	Met	Asn
		180					185						190		
Thr	Gly	Glu	Glu	Ala	Ile	Phe	Ser	Glu	Asn	Gly	Leu	Leu	Thr	Thr	Val
		195				200						205			
Cys	Tyr	Lys	Ile	Gly	Asp	Gln	Pro	Thr	Val	Tyr	Ala	Leu	Glu	Gly	Ser
		210			215					220					
Ile	Ala	Val	Ala	Gly	Ser	Leu	Val	Gln	Trp	Leu	Arg	Asp	Asn	Leu	Lys
225				230						235				240	
Met	Phe	Glu	Thr	Ala	Pro	Gln	Ile	Glu	Ala	Leu	Ala	Asn	Thr	Val	Glu
			245					250					255		
Asp	Asn	Gly	Gly	Ala	Tyr	Phe	Val	Pro	Ala	Phe	Ser	Gly	Leu	Phe	Ala
		260					265						270		
Pro	Tyr	Trp	Arg	Pro											
				275											

<210> 1807

<211> 420

<212> DNA

<213> Homo sapiens

<400> 1807
 nnntatcggc aaggtggctcg aaatggctct tgactatgtc aacggtgaca cgtgcgccgc
 60
 gaccgcccc ttcatttgtc gtttgacgtc gacgcgatgg accctagcgt gggccccgagc
 120
 acaggcacac cgggtgcgtgg tgggtctcaca ttccgagaag gccactacat atgcgaggcg
 180
 gttagctgaga ccggctcgtt ggtggctatg gatatggtag aagtcaaccc ccatcttgaa
 240
 aagcatgcgg ctgagcagac gatcgccgtg ggttgttccc tcattcgttc ggcgctgggg
 300
 gagacgcttc tgtaatgggt gcatgatggg ccgggtgggtcc atagccatgc atagacactc
 360
 cgggcgctga tatgatgagt gacatagcac gtacgataaa tctcggtttt gagcacgcgt
 420

<210> 1808

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1808

His	Val	Arg	Arg	Asp	Arg	Pro	Ile	His	Leu	Ser	Phe	Asp	Val	Asp	Ala
1				5					10				15		
Met	Asp	Pro	Ser	Ser	Val	Ala	Pro	Ser	Thr	Gly	Thr	Pro	Val	Arg	Gly
			20					25					30		
Leu	Thr	Phe	Arg	Glu	Gly	His	Tyr	Ile	Cys	Glu	Ala	Val	Ala	Glu	Thr
		35					40				45				
Gly	Ser	Leu	Val	Ala	Met	Asp	Met	Val	Glu	Val	Asn	Pro	His	Leu	Glu
		50			55					60					
Lys	His	Ala	Ala	Glu	Gln	Thr	Ile	Ala	Val	Gly	Cys	Ser	Leu	Ile	Arg
65				70				75					80		
Ser	Ala	Leu	Gly	Glu	Thr	Leu	Leu								
				85											

<210> 1809

<211> 340

<212> DNA

<213> Homo sapiens

<400> 1809

nnaccggtga tcgcacggt gagcctcggc gcgatgcgcy tggtcgacct tcgccatcgc
 60
 cagaccggtg tcacgcatgc gtatcgccctc gggcatggca gcctcctcgt gatgcggggc
 120
 cccacccagg ccgaatggca gcacgcgctg ccgaaagcgc cgggtgtgca gggcgagcgc
 180
 gtgaacctga cgttttcggcg cgtgatgccg gtcggtatgg gccggtaaca accggcgctg
 240
 ccgaggtgcc cggatcgccg ggcgattcgc gccccgtttt cgcgattcat gcgcgatcga
 300
 tacgggcagg cggtcgcatg tgcggcacgt tgccgcacgn
 340

<210> 1810
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 1810
 Xaa Pro Val Ile Ala Ser Val Ser Leu Gly Ala Met Arg Val Phe Asp
 1 5 10 15
 Leu Arg His Arg Gln Thr Gly Val Thr His Ala Tyr Arg Leu Gly His
 20 25 30
 Gly Ser Leu Leu Val Met Arg Gly Pro Thr Gln Ala Glu Trp Gln His
 35 40 45
 Arg Val Pro Lys Ala Pro Gly Val Gln Gly Glu Arg Val Asn Leu Thr
 50 55 60
 Phe Arg Arg Val Met Pro Val Gly Met Gly Arg
 65 70 75

<210> 1811
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 1811
 nnacgcgtgc taggaatagc catggactca tcatcagata catgctggat ttatacttca
 60
 ctgggtggat tgtatgagct gctcgtaaaa gatgaggctc gcgatatgtg gcatttgttg
 120
 ctgaaacggt gcgactttga gaaggcacta acattttgtc gtgatgagac gtgtcggaag
 180
 cagggtactgg aaaagaaggc cgtgcactg ctacacgcag gtcagctcat ggaggccgtc
 240
 gagtgctatg ctcaggccca gacaccggcc tttgaacagg ttgtgctttc tttgatggac
 300
 gtctgtgccg acaaggcatt gcgtcgatat gtcagactgc gtctcgacaa gatgccgaaa
 360
 caagctcgcg tgccctcgtct catgctgggt acttggtcct tgaattgta tgtggccggc
 420
 attcaagcgc atgaaccac ctccgaacat tatcagacac ttttgcgtgga agcccaggag
 480
 acacttgagc ggcacatcatga
 500

<210> 1812
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 1812
 Xaa Arg Val Leu Gly Ile Ala Met Asp Ser Ser Ser Asp Thr Cys Trp
 1 5 10 15
 Ile Tyr Thr Ser Leu Gly Gly Leu Tyr Glu Leu Leu Val Lys Asp Glu
 20 25 30
 Ala Arg Asp Met Trp His Leu Leu Leu Lys Arg Cys Asp Phe Glu Lys

```

      35              40              45
Ala Leu Thr Phe Cys Arg Asp Glu Thr Cys Arg Lys Gln Val Leu Glu
  50              55              60
Lys Lys Gly Asp Ala Leu Leu His Ala Gly Gln Leu Met Glu Ala Val
  65              70              75              80
Glu Cys Tyr Ala Gln Ala Gln Thr Pro Ala Phe Glu Gln Val Val Leu
      85              90              95
Ser Leu Met Asp Val Cys Ala Asp Lys Ala Leu Arg Arg Tyr Val Arg
      100              105              110
Leu Arg Leu Asp Lys Met Pro Lys Gln Ala Arg Val Pro Arg Leu Met
      115              120              125
Leu Ala Thr Trp Leu Ile Glu Leu Tyr Val Ala Ala Ile Gln Ala His
      130              135              140
Glu Pro Thr Ser Glu His Tyr Gln Thr Leu Leu Leu Glu Ala Gln Glu
  145              150              155              160
Thr Leu Glu Arg His His
      165

```

<210> 1813

<211> 426

<212> DNA

<213> Homo sapiens

<400> 1813

```

tctagagccg ttgtgatcgg tatccatggg tggatggggg tcatctcgat ggaggagtgt
  60
gtcctgaggg gtggcagtga cctggtaggg gtgcctgcgg cgctgcggct tgcgatcgct
  120
ggttctcggg gatgactctc ggtgaatat agatctgcta agacgtcatt agattcgctt
  180
ggcgcttggt tgggaacggg tgtgaagcag cttctgatg gatgtatttt tgcgttggtg
  240
aataagggtt caatattaat tgaatatggc gctagatgct ggtttaggat cagttgacgt
  300
ccgctgtaga tcctccctat ggtcattctg gggccaggcg ctccgccagc tggccatcgc
  360
aacaatgggt tggcgaaggg ttatgaggtg agtatggctg agcaagtctg tggacaggcg
  420
tctaca
  426

```

<210> 1814

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1814

```

Met Thr Ile Gly Arg Ile Tyr Ser Gly Arg Gln Leu Ile Leu Asn Gln
  1              5              10              15
His Leu Ala Pro Tyr Ser Ile Asn Ile Glu Thr Leu Phe Asn Asn Ala
      20              25              30
Lys Ile His Pro Ser Glu Gly Cys Phe Thr Pro Val Pro Asn Gln Ala
      35              40              45
Pro Ser Glu Ser Asn Asp Val Leu Ala Asp Leu Tyr Ser Ser Glu Ser

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      50              55              60
His Pro Arg Glu Pro Ala Ile Ala Ser Arg Asp Ala Ala Gly Thr Pro
65              70              75              80
Thr Arg Ser Leu Pro Pro Leu Arg Thr His Ser Ser Ile Glu Met Asn
      85              90              95
Pro Ile Gln Pro Trp Ile Pro Ile Thr Thr Ala Leu
      100              105

```

<210> 1815
 <211> 303
 <212> DNA
 <213> Homo sapiens

```

<400> 1815
ggcgccacaca tggctacgct cgcaccgcgg cacaaggtaa gccgtagcgg cgggatcgag
60
cgccaggcgg cgcattctcgg catggagcgc gatcagttcg gccatcatcg cgctcgtcggg
120
cgtgccgac tcgaggggca acgcccgcgc gagccgcgaa gccagatcgg gcacgcgcgat
180
ccgcacgcca tcggcaaatt cgcgagtgat gacgagcaag ggccgcctgg tctcctcgcc
240
ccggttccag cagtgggaaca cgttcgcctc gggcagacgg cggcgcacgg cgatcacggg
300
acc
303

```

<210> 1816
 <211> 98
 <212> PRT
 <213> Homo sapiens

```

<400> 1816
Met Ala Thr Leu Ala Pro Arg His Lys Val Ser Arg Ser Gly Gly Ile
1      5      10      15
Glu Arg Gln Ala Ala His Leu Gly Met Glu Arg Asp Gln Phe Gly His
      20      25      30
His Arg Val Val Gly Arg Ala Asp Leu Glu Gly Gln Arg Arg Ala Glu
      35      40      45
Pro Arg Ser Gln Ile Gly Gln Arg Asp Pro Pro Ala Ile Gly Lys Phe
      50      55      60
Ala Ser Asp Asp Glu Gln Gly Pro Pro Gly Leu Arg Pro Val Pro
65      70      75      80
Ala Val Glu His Val Arg Leu Gly Gln Thr Gly Gly Ile Gly Asp His
      85      90      95
Gly Thr

```

<210> 1817
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 1817

nncagcttgc aagaccgcgg ccacacagtg tacatcttaa catcacattt cgaatgcgtcg
 60
 catgcgcttg agcccacacg cgaatggcaca cttcagggtca ttcacgcaaa gacatggatc
 120
 ccgcgcctct tatttcacat gctgcatctg cgaatggccat tgcagcagct tttttctctt
 180
 gtgatgcagg tcgtggtagc agcgtatgga tcgtcactcg cagcgcactt gccgcagtgc
 240
 tacagggcgt gacgcatgtc ccgtcaaaact cgtctccaga cgtgtttgtt attgaccaac
 300
 ttccagcagc gatacccccta atcaaaactcc tgtgtgggag cgtgtcatgc tactactgtc
 360
 acttccctga caaagaaatc agcgtgctgc tggctcgaca gcgaggcagc cgt
 413

<210> 1818

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1818

Xaa	Ser	Leu	Gln	Asp	Arg	Gly	His	Thr	Val	Tyr	Ile	Leu	Thr	Ser	His
1				5					10					15	
Phe	Asp	Ala	Ser	His	Ala	Phe	Glu	Pro	Thr	Arg	Asp	Gly	Thr	Leu	Gln
			20					25					30		
Val	Ile	His	Ala	Lys	Thr	Trp	Ile	Pro	Arg	Ser	Leu	Phe	His	Met	Leu
			35				40					45			
His	Leu	Arg	Trp	Pro	Phe	Ala	Ala	Val	Phe	Ser	Leu	Val	Met	Gln	Val
	50				55					60					
Val	Val	Ala	Ala	Tyr	Gly	Ser	Ser	Leu	Ala	Arg	His	Leu	Pro	His	Val
65					70					75				80	
Tyr	Arg	Ala													

<210> 1819

<211> 343

<212> DNA

<213> Homo sapiens

<400> 1819

ggatccaaga gtggggcatc aggaacatgc catggttgctc gtggtgctgg aatgagaaca
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 atcacaagac agataggcct tggcatgcatc caacagatga acactgtttg ccttgaatgc
 120
 aaaggatcag gtgagatcat aagtgacaag gacaaatgcc caagctgtaa aggaacaaca
 180
 gtatgccagg agaagaaggt gttagaggtt catgtggaga aaggaatgca acataaccaa
 240
 aagattgtat tccaggttca ggctgatgaa gctcctgata cgggtacagg agacattgtt
 300
 tttgtcttgc aacttaaaga ccatccaaaa ttttaagagga tgt
 343

<210> 1820

<211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1820
 Gly Ser Lys Ser Gly Ala Ser Gly Thr Cys His Gly Cys Arg Gly Ala
 1 5 10 15
 Gly Met Arg Thr Ile Thr Arg Gln Ile Gly Leu Gly Met Ile Gln Gln
 20 25 30
 Met Asn Thr Val Cys Pro Glu Cys Lys Gly Ser Gly Glu Ile Ile Ser
 35 40 45
 Asp Lys Asp Lys Cys Pro Ser Cys Lys Gly Asn Lys Val Val Gln Glu
 50 55 60
 Lys Lys Val Leu Glu Val His Val Glu Lys Gly Met Gln His Asn Gln
 65 70 75 80
 Lys Ile Val Phe Gln Gly Gln Ala Asp Glu Ala Pro Asp Thr Gly Thr
 85 90 95
 Gly Asp Ile Val Phe Val Leu Gln Leu Lys Asp His Pro Lys Phe Lys
 100 105 110
 Arg Met

<210> 1821
 <211> 285
 <212> DNA
 <213> Homo sapiens

<400> 1821
 aagcttgagt tcagcaagat cttggaggct attaaggcaa acttcaacga caagttcga
 60
 gaggtcggga agaagtgggg aggtggcatc atgggatcca agtcgcaggc caagaccaag
 120
 gccccggaaa agttgctcgc caaggaggcc gccacgcgga tgacctagat tgtctactgc
 180
 tgtgtctgcc ctgtagtttg acggggaaga actgatgaac tcgtattgtg gttttccgaa
 240
 tctagtttca tatgtttctg tccaccagac catgtttaga agctt
 285

<210> 1822
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1822
 Lys Leu Glu Phe Ser Lys Ile Leu Glu Ala Ile Lys Ala Asn Phe Asn
 1 5 10 15
 Asp Lys Phe Asp Glu Val Gly Lys Lys Trp Gly Gly Gly Ile Met Gly
 20 25 30
 Ser Lys Ser Gln Ala Lys Thr Lys Ala Arg Glu Lys Leu Leu Ala Lys
 35 40 45
 Glu Ala Ala Gln Arg Met Thr
 50 55

<210> 1823
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 1823
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 60
 tggggcgtgg tcgataagct ctgcatggcc aactatcagc aaaagcgcga tccggccccc
 120
 tgtgagcaga tttatatgcc gcagggtaaa gcgcagggct ttagcgtgct gcaaaacccc
 180
 cgttatccct atcatttcct tctgggtgcc acggcgccgc ttcccgcat tgaaagcccc
 240
 ctgctgctgg ccggagagcg aacggactat ttggctatg catggctgat cggttacccg
 300
 ctggccgcgc agtatggcgg gccgggtgcc gacgacaggc tgggcatggc gatcaactcc
 360
 gcttacggcc gcagccagaa ccaattg
 387

<210> 1824
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1824
 Xaa Trp Leu Leu Leu Gly Val Leu Ser Leu Thr Gly Cys Ala Arg
 1 5 10 15
 Ser Asp Ala Leu Trp Gly Val Val Asp Lys Leu Cys Met Ala Asn Tyr
 20 25 30
 Gln Gln Lys Arg Asp Pro Ala Pro Cys Glu Gln Ile Tyr Met Pro Gln
 35 40 45
 Gly Lys Ala Gln Gly Phe Ser Val Leu Gln Asn Pro Arg Tyr Pro Tyr
 50 55 60
 His Phe Ile Leu Val Pro Thr Ala Pro Leu Ser Gly Ile Glu Ser Pro
 65 70 75 80
 Leu Leu Leu Ala Gly Glu Arg Thr Asp Tyr Phe Gly Tyr Ala Trp Leu
 85 90 95
 Met Arg Tyr Arg Leu Ala Ala Glu Tyr Gly Gly Pro Val Pro Asp Asp
 100 105 110
 Arg Leu Gly Met Ala Ile Asn Ser Ala Tyr Gly Arg Ser Gln Asn Gln
 115 120 125
 Leu

<210> 1825
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 1825
 gtgcacggac gaccgcgcac agggactcgt gtgccgcgca tgggacgacg gcgatgcgtg
 60

tgcgtgcata ccgctgctct ggcaggctgt gcgtgctgatt gtcgccgaca catcgccggc
 120
 ttggcagctc gtgattgggc gcctaggcac catgtcgag gccgacatgg acatgtgggc
 180
 gtctgctcctc gatacgcgcg acccttctct ctctcggtgg gccttgtgtg cctggagcgc
 240
 gatgcctggc ctacgggcac gcgatgcac ggtggtctac ctgtcggaca tgccgctggg
 300
 tctggcctca ggtgcgtggc cgatccgctg gcctcgctcg gcgttatgtg tctgccggcg
 360
 cctatgccat tcattctgtg cagctacgtc acctggctga tctcgacgcg gct
 413

<210> 1826

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1826

Met	Gly	Arg	Arg	Cys	Val	Cys	Val	His	Thr	Ala	Ala	Leu	Ala	Gly
1			5					10				15		
Arg	Ala	Cys	Asp	Cys	Arg	Arg	His	Ile	Gly	Gly	Leu	Ala	Arg	Asp
		20					25				30			
Trp	Ala	Pro	Arg	His	His	Val	Ala	Gly	Arg	His	Gly	His	Val	Gly
	35					40					45			
Val	Pro	Arg	Tyr	Ala	Arg	Pro	Phe	Leu	Leu	Ser	Val	Gly	Leu	Val
	50				55					60				
Leu	Glu	Arg	Asp	Ala	Trp	Pro	Thr	Gly	Thr	Arg	Cys	Ile	Gly	Gly
65				70				75				80		
Pro	Val	Gly	His	Ala	Ala	Gly	Ser	Gly	Leu	Arg	Cys	Val	Ala	Asp
			85					90				95		
Arg	Ala	Ser	Leu	Gly	Val	Met	Cys	Leu	Pro	Ala	Pro	Met	Pro	Phe
			100				105					110		
Ser	Cys	Ser	Tyr	Val	Thr	Trp	Leu	Ile	Ser	Thr	Arg			
			115				120							

<210> 1827

<211> 345

<212> DNA

<213> Homo sapiens

<400> 1827

ctggccaact ggggtgccga cctgttcatg aagcgcgtcg aagccgacca ggaatggtcg
 60
 ctgttctgac cgcgctggt gccggagttc accgacctgt tgcggcaagc cttcgaagcc
 120
 gcctacctgc aggcgcaagc gcagggcaag gccaaaccga cgatctctgc ccgcaagctg
 180
 tacgcccgcga tgatgcgtac gctggccgag accggcaagc gctggatgac cttcaaggac
 240
 aagtgcgaac gcgccagcaa ccagaccctg cgtccgggca acgtgatcca cctgtccaac
 300
 ctgtgcaccg aaatcctgga agtcaacttc aacgatgaaa ccgcg
 345

<210> 1828
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1828
 Leu Ala Asn Trp Val Pro Asp Leu Phe Met Lys Arg Val Glu Ala Asp
 1 5 10 15
 Gln Glu Trp Ser Leu Phe Asp Pro Arg Val Val Pro Glu Phe Thr Asp
 20 25 30
 Leu Phe Gly Glu Ala Phe Glu Ala Ala Tyr Leu Gln Ala Glu Ala Gln
 35 40 45
 Gly Lys Ala Asn Arg Thr Ile Ser Ala Arg Lys Leu Tyr Ala Arg Met
 50 55 60
 Met Arg Thr Leu Ala Glu Thr Gly Asn Gly Trp Met Thr Phe Lys Asp
 65 70 75 80
 Lys Cys Asn Arg Ala Ser Asn Gln Thr Leu Arg Pro Gly Asn Val Ile
 85 90 95
 His Leu Ser Asn Leu Cys Thr Glu Ile Leu Glu Val Thr Ser Asn Asp
 100 105 110
 Glu Thr Ala
 115

<210> 1829
 <211> 4457
 <212> DNA
 <213> Homo sapiens

<400> 1829
 attccaatgg ttgtgtctga ttttgatctt ccagaccaac agatagaaat acttcagagt
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 tctgactcgg gatgttcaca gtccctctgct ggggacaact tgagttacga agttgatcct
 120
 gaaaccgtga atgcccaaga ggattctcaa atgcccaagg aaagctcccc agatgatgat
 180
 gttaacacagg tagtatttga cctgatattgt aaagttgtaa gtggcctcga agtggaaatct
 240
 gcatcagtta catctcaatt agaaattgaa gctatgcccc caaagtgcag tgatatagat
 300
 ccagatgaag agacgattaa aattgaagat gactccattc gagagagtca gaatgctttg
 360
 ctgagtaatg aaagttctca gtttctgtct gtgtctgcag agggaggcca tgagtgtgtg
 420
 gcaaatggaa tctccaggaa tagctcctca ccttgtattt caggaaccac acacactctt
 480
 catgactctt ctgttgcttc catagaaacc aaatctagac aaaggagtca cagtagtatt
 540
 caattcagct tcaaagaaaa attatcagaa aaagtttcgg agaaggaaac aatagttaag
 600
 gagtcaggta aacaaccagg agcaaaacct aaagtaaaac ttgccagaaa aaaggatgat
 660
 gacaagaaaa aatcttcaaa tgaaaaactc aaacaaacca gtgtattctt cagtgatggg
 720

ctggatttag agaactggta tagctgtgga gagggagaca ttctgaaat tgagagtgc
780
atgggttctc caggatctcg aaaatctccc aatttcaaca ttcatcctct ctatcaacat
840
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900
aaagccatct tgaactaa ccctatagct ttgtaaatg ccatttcaac tactagtgt
960
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tctgttatgg gcaagattt ttatagtcac attccagtgg actcaaatca taacttccgg
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1200
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1260
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1920
gccattatcc attactgttt gttggatcca actacacagt atcaccaact tttggtcagt
1980
gtagaccaga aacacttgtt tgaagcacgc agtggatcc tctcaatcct tcatatgac
2040
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2160
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2340

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2400
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2760
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3840
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3900
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3960

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 4020
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 4080
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 4140
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 4200
 cgttgtatag ttttcccttt tttgtatgta acagaacaca tttcagattg tatttaattt
 4260
 aaatatttgt atataagagc aaatgtctga atgtggcctg aatcaagttt aaatatttgt
 4320
 ggctcatact gattatgggtg cctaagagag ctatatatat acacatgtaa agtccattgt
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 4440
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 4457

<210> 1830

<211> 1377

<212> PRT

<213> Homo sapiens

<400> 1830

Ile Pro Met Val Val Ser Asp Phe Asp Leu Pro Asp Gln Gln Ile Glu
 1 5 10 15
 Ile Leu Gln Ser Ser Asp Ser Gly Cys Ser Gln Ser Ser Ala Gly Asp
 20 25 30
 Asn Leu Ser Tyr Glu Val Asp Pro Glu Thr Val Asn Ala Gln Glu Asp
 35 40 45
 Ser Gln Met Pro Lys Glu Ser Ser Pro Asp Asp Val Gln Gln Val
 50 55 60
 Val Phe Asp Leu Ile Cys Lys Val Val Ser Gly Leu Glu Val Glu Ser
 65 70 75 80
 Ala Ser Val Thr Ser Gln Leu Glu Ile Glu Ala Met Pro Pro Lys Cys
 85 90 95
 Ser Asp Ile Asp Pro Asp Glu Glu Thr Ile Lys Ile Glu Asp Asp Ser
 100 105 110
 Ile Arg Gln Ser Gln Asn Ala Leu Leu Ser Asn Glu Ser Ser Gln Phe
 115 120 125
 Leu Ser Val Ser Ala Glu Gly Gly His Glu Cys Val Ala Asn Gly Ile
 130 135 140
 Ser Arg Asn Ser Ser Ser Pro Cys Ile Ser Gly Thr Thr His Thr Leu
 145 150 155 160
 His Asp Ser Ser Val Ala Ser Ile Glu Thr Lys Ser Arg Gln Arg Ser
 165 170 175
 His Ser Ser Ile Gln Phe Ser Phe Lys Glu Lys Leu Ser Glu Lys Val
 180 185 190
 Ser Glu Lys Glu Thr Ile Val Lys Glu Ser Gly Lys Gln Pro Gly Ala
 195 200 205
 Lys Pro Lys Val Lys Leu Ala Arg Lys Lys Asp Asp Asp Lys Lys Lys
 210 215 220
 Ser Ser Asn Glu Lys Leu Lys Gln Thr Ser Val Phe Phe Ser Asp Gly

```

225                230                235                240
Leu Asp Leu Glu Asn Trp Tyr Ser Cys Gly Glu Gly Asp Ile Ser Glu
                245                250                255
Ile Glu Ser Asp Met Gly Ser Pro Gly Ser Arg Lys Ser Pro Asn Phe
                260                265                270
Asn Ile His Pro Leu Tyr Gln His Val Leu Leu Tyr Leu Gln Leu Tyr
                275                280                285
Asp Ser Ser Arg Thr Leu Tyr Ala Phe Ser Ala Ile Lys Ala Ile Leu
                290                295                300
Lys Thr Asn Pro Ile Ala Phe Val Asn Ala Ile Ser Thr Thr Ser Val
305                310                315                320
Asn Asn Ala Tyr Thr Pro Gln Leu Ser Leu Leu Gln Asn Leu Leu Ala
                325                330                335
Arg His Arg Ile Ser Val Met Gly Lys Asp Phe Tyr Ser His Ile Pro
                340                345                350
Val Asp Ser Asn His Asn Phe Arg Ser Ser Met Tyr Ile Glu Ile Leu
                355                360                365
Ile Ser Leu Cys Leu Tyr Tyr Met Arg Ser His Tyr Pro Thr His Val
370                375                380
Lys Val Thr Ala Gln Asp Leu Ile Gly Asn Arg Asn Met Gln Met Met
385                390                395                400
Ser Ile Glu Ile Leu Thr Leu Leu Phe Thr Glu Leu Ala Lys Val Ile
                405                410                415
Glu Ser Ser Ala Lys Gly Phe Pro Ser Phe Ile Ser Asp Met Leu Ser
                420                425                430
Lys Cys Lys Val Gln Lys Val Ile Leu His Cys Leu Leu Ser Ser Ile
                435                440                445
Phe Ser Ala Gln Lys Trp His Ser Glu Lys Met Ala Gly Lys Asn Leu
450                455                460
Val Ala Val Glu Glu Gly Phe Ser Glu Asp Ser Leu Ile Asn Phe Ser
465                470                475                480
Glu Asp Glu Phe Asp Asn Gly Ser Thr Leu Gln Ser Gln Leu Leu Lys
                485                490                495
Val Leu Gln Arg Leu Ile Val Leu Glu His Arg Val Met Thr Ile Pro
                500                505                510
Glu Glu Asn Glu Thr Gly Phe Asp Phe Val Val Ser Asp Leu Glu His
515                520                525
Ile Ser Pro His Gln Pro Met Thr Ser Leu Gln Tyr Leu His Ala Gln
530                535                540
Pro Ile Thr Cys Gln Gly Met Phe Leu Cys Ala Val Ile Arg Ala Leu
545                550                555                560
His Gln His Cys Ala Cys Lys Met His Pro Gln Trp Ile Gly Leu Ile
                565                570                575
Thr Ser Thr Leu Pro Tyr Met Gly Lys Val Leu Gln Arg Val Val Val
                580                585                590
Ser Val Thr Leu Gln Leu Cys Arg Asn Leu Asp Asn Leu Ile Gln Gln
595                600                605
Tyr Lys Tyr Glu Thr Gly Leu Ser Asp Ser Arg Pro Leu Trp Met Ala
610                615                620
Ser Ile Ile Pro Pro Asp Met Ile Leu Thr Leu Leu Glu Gly Ile Thr
625                630                635                640
Ala Ile Ile His Tyr Cys Leu Leu Asp Pro Thr Thr Gln Tyr His Gln
                645                650                655
Leu Leu Val Ser Val Asp Gln Lys His Leu Phe Glu Ala Arg Ser Gly

```

[illegible]

1090 1095 1100
 Tyr Gln Lys Tyr Leu Pro Asp Ile Gln Glu Arg Leu Val Glu Ser Leu
 1105 1110 1115 1120
 Arg Leu Pro Gln Val Pro Thr Leu His Ser Gln Val Phe Leu Phe Phe
 1125 1130 1135
 Arg Val Leu Leu Leu Arg Met Ser Pro Gln His Leu Thr Ser Leu Trp
 1140 1145 1150
 Pro Thr Met Ile Thr Glu Leu Val Gln Val Phe Leu Leu Met Glu Gln
 1155 1160 1165
 Glu Leu Thr Ala Asp Glu Asp Ile Ser Arg Thr Ser Gly Pro Ser Val
 1170 1175 1180
 Ala Gly Leu Glu Thr Thr Tyr Thr Gly Gly Asn Gly Phe Ser Thr Ser
 1185 1190 1195 1200
 Tyr Asn Ser Gln Arg Trp Leu Asn Leu Tyr Leu Ser Ala Cys Lys Phe
 1205 1210 1215
 Leu Asp Leu Ala Leu Ala Leu Pro Ser Glu Asn Leu Pro Gln Phe Gln
 1220 1225 1230
 Met Tyr Arg Trp Ala Phe Ile Pro Glu Ala Ser Asp Asp Ser Gly Leu
 1235 1240 1245
 Glu Val Arg Arg Gln Gly Ile His Gln Arg Glu Phe Lys Pro Tyr Val
 1250 1255 1260
 Val Arg Leu Ala Lys Leu Leu Arg Lys Arg Ala Lys Lys Asn Pro Glu
 1265 1270 1275 1280
 Glu Asp Asn Ser Gly Arg Thr Leu Gly Trp Glu Pro Gly His Leu Leu
 1285 1290 1295
 Leu Thr Ile Cys Thr Val Arg Ser Met Glu Gln Leu Leu Pro Phe Phe
 1300 1305 1310
 Asn Val Leu Ser Gln Val Phe Asn Ser Lys Val Thr Ser Arg Cys Gly
 1315 1320 1325
 Gly His Ser Gly Ser Pro Ile Leu Tyr Ser Asn Ala Phe Pro Asn Lys
 1330 1335 1340
 Asp Met Lys Leu Glu Asn His Lys Pro Cys Ser Ser Lys Ala Arg Gln
 1345 1350 1355 1360
 Lys Ile Glu Glu Met Val Glu Lys Asp Phe Leu Glu Gly Met Ile Lys
 1365 1370 1375
 Thr

<210> 1831
 <211> 508
 <212> DNA
 <213> Homo sapiens

<400> 1831
 nntcatgaaa ggagaggccg tatgcccatt gtcaaaactca gtgcgcagtt cgtgcgcgaa
 60
 gcggtttgcc cgcccggaaa atccaagggtg gactattacg acaacgcact caaagggttc
 120
 atcctggagg ctcgaccttc aggtggcaaaa acctttttacc tgcgctatca cgacagccac
 180
 ggcaagctgc gccaatgcaa gatcggtgat gctgctgcgg tcagctacga caaggccggg
 240
 cgaaggcca tgcggttcg ttggaagggtg gaatgggggg gcaatccatt ggaggagcgc
 300

caagccttgc gtgcggtacc gaccctggcc gagttcatcc gcgagaccta tgtgccgcac
 360
 atccacctgc accggaggaa ttttcagtcc acgctgagct tectcaagtg ccatgtctctg
 420
 ccgcgctttg gagccaagca cctggagcaa atcacgacca acatgctggc cgaggctcac
 480
 caggatctgc gcacgaaggg ctacgcgt
 508

<210> 1832
 <211> 169
 <212> PRT
 <213> Homo sapiens

<400> 1832
 Xaa His Glu Arg Arg Gly Arg Met Pro Ile Val Lys Leu Ser Ala Gln
 1 5 10 15
 Phe Val Arg Glu Ala Val Cys Pro Pro Gly Lys Ser Lys Val Asp Tyr
 20 25 30
 Tyr Asp Asn Ala Leu Lys Gly Phe Ile Leu Glu Ala Arg Pro Ser Gly
 35 40 45
 Gly Lys Thr Phe Tyr Leu Arg Tyr His Asp Ser His Gly Lys Leu Arg
 50 55 60
 Gln Cys Lys Ile Gly Asp Ala Ala Val Ser Tyr Asp Lys Ala Arg
 65 70 75 80
 Gln Lys Ala Met Arg Leu Arg Trp Lys Val Glu Trp Gly Gly Asn Pro
 85 90 95
 Leu Glu Glu Arg Gln Ala Leu Arg Ala Val Pro Thr Leu Ala Glu Phe
 100 105 110
 Ile Arg Glu Thr Tyr Val Pro His Ile His Leu His Arg Arg Asn Phe
 115 120 125
 Gln Ser Thr Leu Ser Phe Leu Lys Cys His Val Leu Pro Arg Phe Gly
 130 135 140
 Ala Lys His Leu Asp Glu Ile Thr Thr Asn Met Leu Ala Glu Ala His
 145 150 155 160
 Gln Asp Leu Arg Thr Lys Gly Tyr Ala
 165

<210> 1833
 <211> 430
 <212> DNA
 <213> Homo sapiens

<400> 1833
 acgcgtgcga tgttgaagga gcgcttcggc atcggggcatg cgacgctgca ggttgaactg
 60
 tccggtgcgc aggcagacga tgccgagcgc gccgctgct aagggtgcgc gtcgttcagt
 120
 ggccgaaaagc gccgatgac gcgtcgaaca gcgttactcc agccagcggg ccaaccaaca
 180
 gcataccagg gttgaaaccg atgatccacg ccgcgatgct ttctcggcgc gggtttggca
 240
 gcggcttggg ctcggcttcc cagcgttccg gcggcggcca gccattttgg aaatcgacga
 300

acatctccgg cgctcctgct gtcaggcgct gaaggtatcg aaagtcatgc gccgtgacaa
 360
 aggaagatcg gcgacacagg agccgaagcg ccgccgcctg caataagcgc gcgcgatcgc
 420
 aattgtcggn
 430

<210> 1834

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1834

Met	Arg	Arg	Cys	Arg	Leu	Asn	Cys	Pro	Val	Pro	Arg	Gln	Thr	Met	Pro
1			5						10					15	
Arg	Arg	Ala	Ala	Ala	Lys	Gly	Arg	Arg	Ser	Val	Ala	Gln	Ser	Gly	
		20					25					30			
Asp	Asp	Arg	Val	Glu	Gln	Arg	Tyr	Ser	Ser	Gln	Arg	Ala	Asn	Gln	Gln
	35					40					45				
His	His	Gln	Val	Glu	Thr	Asp	Asp	Pro	Arg	Arg	Asp	Ala	Phe	Ser	Ala
	50				55					60					
Arg	Val	Trp	Gln	Arg	Leu	Gly	Leu	Gly	Phe	Pro	Ala	Phe	Arg	Arg	Arg
65				70				75						80	
Pro	Ala	Ile	Leu	Glu	Ile	Asp	Glu	His	Leu	Arg	Arg	Ser	Cys	Cys	Gln
			85				90						95		
Ala	Leu	Lys	Val	Ser	Lys	Val	Met	Arg	Arg	Asp	Lys	Gly	Arg	Ser	Ala
			100				105						110		
Thr	Gln	Glu	Pro	Lys	Arg	Arg	Arg	Leu	Gln						
	115						120								

<210> 1835

<211> 677

<212> DNA

<213> Homo sapiens

<400> 1835

nataactcaag gactttgacg gcacccgagc ccggttgctc cctgaggcca tcataaaccc
 60
 cccagtggca ccctatgcta ctgtggcacc cagcacttta gccacacccc aggccacaggc
 120
 tctggcccgc cagcaggccc tgcagcatgc acagacctg gcccatgccc ctccccagac
 180
 gctgcagcac cctcagggtta tcccgcaccc ccaggcactg tcccaccctc agagcctcca
 240
 gcagcctcag ggccctgggcc accctcagcc catggcccaa acccagggct tggctccacc
 300
 tcaggccctg gctcaccagg gtctccagca cccccacaat cccttgctgc atggaggccg
 360
 gaagatgcca gactcagatg cccccccgaa tgtgaccgtg tctacctcaa ctatccccct
 420
 ttcaatggcg gccactctgc agcacagcca gcctccggac ctgagttaga tctgtcacca
 480
 gatcaaccag ttttgccaga cgagggcagg catcagcact acctcagtgt gtgagggccca
 540

gacgcgcaac ccagcccca ttatgcgag tctgctcatc aatgcaagca cccgggtgtc
 600
 gaccacagc gtccccacac caatgccttc atgtgtgggc aatcccatgg agcacacca
 660
 cgcgccacc gccgcgg
 677

<210> 1836

<211> 140

<212> PRT

<213> Homo sapiens

<400> 1836

Gly	His	His	Glu	Pro	Pro	Ser	Gly	Thr	Leu	Cys	Tyr	Cys	Gly	Thr	Gln
1				5				10						15	
His	Phe	Ser	Pro	Pro	Pro	Gly	Pro	Gly	Ser	Gly	Pro	Pro	Ala	Gly	Pro
			20					25					30		
Ala	Ala	Cys	Thr	Asp	Pro	Gly	Pro	Cys	Pro	Ser	Pro	Asp	Ala	Ala	Ala
		35					40					45			
Pro	Ser	Gly	Tyr	Pro	Ala	Thr	Pro	Gly	Thr	Val	Pro	Pro	Ser	Glu	Pro
		50				55				60					
Pro	Ala	Ala	Ser	Gly	Pro	Gly	Pro	Pro	Ser	Ala	His	Gly	Pro	Asn	Pro
65					70					75				80	
Gly	Leu	Gly	Pro	Pro	Ser	Gly	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Ala	Pro
			85					90						95	
Pro	Gln	Ser	Leu	Ala	Ala	Trp	Arg	Pro	Glu	Asp	Ala	Arg	Leu	Arg	Cys
			100					105					110		
Pro	Pro	Glu	Cys	Asp	Arg	Val	Tyr	Leu	Asn	Tyr	Pro	Pro	Phe	Asn	Gly
		115					120					125			
Gly	His	Ser	Ala	Ala	Gln	Pro	Ala	Ser	Gly	Pro	Glu				
		130					135				140				

<210> 1837

<211> 564

<212> DNA

<213> Homo sapiens

<400> 1837

nntctagaac actctgcccc tgaatctgta cgggattgt ttggcccgtc acgaactcgt
 60
 acggctgata tcaatatcac tgggttttct tcacagtatt taccgcccc ctatggacca
 120
 attgtcgagg acgtcaaaca aacctgggagc tgggaccac aggatctgac gattgtctca
 180
 acttctgctg atcacgacca taacctcga tatgcagtac agcatttcgg cgcaagcccg
 240
 accccgatcc agtaaccttc gataacgcga aagccggcac cccacataac tcggnctgac
 300
 accgaagtc ctgccaaagt tccatccgac ataggggagt taactaacgg aattatcaag
 360
 gggaaatcta ccccgtaac caaggccatc gcgattcaaa actggcttcg tgacagcgct
 420
 cgattccatt acgacatcaa cgcacccgaa ggtgacggct atcaggtact ggaaaacttc
 480

ctgctgcaca cccaccgcgg ttattgcatc catttcgcgg cgtcaatggc actcatggca
540

cgacttgaag gtattccgtc acgc
564

<210> 1838

<211> 84

<212> PRT

<213> Homo sapiens

<400> 1838

Xaa	Leu	Glu	His	Ser	Ala	Pro	Glu	Ser	Val	Pro	Gly	Leu	Phe	Gly	Pro
1				5					10					15	
Ser	Arg	Thr	Arg	Thr	Val	Asp	Ile	Asn	Ile	Thr	Gly	Phe	Ser	Ser	Gln
			20					25					30		
Tyr	Leu	Pro	Ala	Pro	Tyr	Gly	Pro	Ile	Ala	Ala	Asp	Val	Lys	Gln	Thr
			35					40					45		
Trp	Ala	Trp	Asp	Pro	Gln	Asp	Leu	Thr	Ile	Val	Ser	Thr	Ser	Ala	Asp
			50				55				60				
His	Asp	His	Asn	Leu	Arg	Tyr	Ala	Val	Gln	His	Phe	Gly	Ala	Ser	Pro
65					70					75				80	
Thr	Pro	Ile	Gln												

<210> 1839

<211> 300

<212> DNA

<213> Homo sapiens

<400> 1839

ncaatcaggc tgaacaccgc tgatatacacc cgctactttcc ccgtcaacgg aaaattttcc
60
gaagtccagg caaaggctta tcaggcgggtg ctggacgctg cagatgcggc atttaaggca
120
gccgttcctg gcaataaatt ccgcgacgtc catgctgcag cgatgaatgt tctgcctcc
180
cgcccttgagg actggggggt tatgcccgtc agcgcgaagg tcgctctttc ggacgagggc
240
gggcaacacc gtcgttggat gccgcacggc accagccacc atctagggct ggatgtgcac
300

<210> 1840

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1840

Xaa	Ile	Arg	Leu	Asn	Thr	Ala	Asp	Ile	Thr	Arg	Thr	Phe	Pro	Val	Asn
1				5					10					15	
Gly	Lys	Phe	Ser	Glu	Val	Gln	Ala	Lys	Ala	Tyr	Gln	Ala	Val	Leu	Asp
			20					25					30		
Ala	Ala	Asp	Ala	Ala	Phe	Lys	Ala	Ala	Val	Pro	Gly	Asn	Lys	Phe	Arg
			35					40					45		
Asp	Val	His	Ala	Ala	Ala	Met	Asn	Val	Leu	Ala	Ser	Arg	Leu	Glu	Asp


```

      50              55              60
Trp Gly Leu Met Pro Val Ser Ala Lys Val Ala Leu Ser Asp Glu Gly
65              70              75              80
Gly Gln His Arg Arg Trp Met Pro His Gly Thr Ser His His Leu Gly
      85              90              95
Leu Asp Val His
      100

```

```

<210> 1841
<211> 330
<212> DNA
<213> Homo sapiens

```

```

<400> 1841
nnctccaaga acgtcccga gtggggcccc agggcgctcg aactccccg cgggcccggt
60
gtcgcacccg tggctcagat cggcgggtccc ggtacgctag cccaatcgat ggtcgccccg
120
cgcgcgcggc cccatgtcgc ctgcatcgcc gtgcttnacg gggattgtcg ggcggtgagg
180
acggcgctgc tgatgagcaa gaatctgcgc gtgcaagggc tgccggctcg cagccgcgcg
240
cagcaactcg cgatgatcgc gggggctcgag gcgaacggca tccgtccgat cctcgaccag
300
catttccgc tcgaaaatct ccccgacgcg
330

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<210> 1842
<211> 110
<212> PRT
<213> Homo sapiens

```

```

<400> 1842
Xaa Ser Lys Asn Val Pro Glu Trp Gly Pro Arg Ala Leu Glu Leu Pro
1      5      10      15
Gly Gly Pro Gly Val Asp Pro Val Val Glu Ile Gly Gly Pro Gly Thr
20      25      30
Leu Ala Gln Ser Met Val Ala Pro Arg Val Gly Ala His Val Ala Leu
35      40      45
Ile Gly Val Leu Xaa Gly Asp Cys Arg Ala Val Arg Thr Ala Leu Leu
50      55      60
Met Ser Lys Asn Leu Arg Val Gln Gly Leu Pro Val Gly Ser Arg Ala
65      70      75      80
Gln Gln Leu Ala Met Ile Ala Gly Val Glu Ala Asn Gly Ile Arg Pro
85      90      95
Ile Leu Asp Gln His Phe Pro Leu Glu Asn Leu Pro Asp Ala
100      105      110

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<210> 1843
<211> 473
<212> DNA
<213> Homo sapiens

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<400> 1843

```

aagctttggc atctccagca aaagatgtgc tatttactga taccatcacc atgaaggcca
 60
 acagttttga gtccagatta acaccaagca ggttcataaa agccttaagt tatgcatcat
 120
 tagataaaga agattttattg agtcctatta atcaaaatac cctgcaacga tcttcctcag
 180
 tgccgtccat ggtgtccagt gccacatatg ggggttcaga tgattacatt ggtcttgcgc
 240
 tcccgggtga tataaatgat atattccagg taaaggatat tcctattttt cagacaaaaa
 300
 acataccacc acatgatgat cgaggtgcaa gagcatttgc ccatgatgca ggaggtcttc
 360
 catctggaac tggaggtctt gtaaaaaatt cttttcactt gctacgacag cagatgagtc
 420
 ttacggaaat aatgaattca atccattcag atgcctctcn cnnccnccnccc
 473

<210> 1844

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1844

Met	Lys	Ala	Asn	Ser	Phe	Glu	Ser	Arg	Leu	Thr	Pro	Ser	Arg	Phe	Met
1			5						10					15	
Lys	Ala	Leu	Ser	Tyr	Ala	Ser	Leu	Asp	Lys	Glu	Asp	Leu	Ser	Pro	
			20					25					30		
Ile	Asn	Gln	Asn	Thr	Leu	Gln	Arg	Ser	Ser	Ser	Val	Arg	Ser	Met	Val
			35				40					45			
Ser	Ser	Ala	Thr	Tyr	Gly	Gly	Ser	Asp	Asp	Tyr	Ile	Gly	Leu	Ala	Leu
			50			55					60				
Pro	Val	Asp	Ile	Asn	Asp	Ile	Phe	Gln	Val	Lys	Asp	Ile	Pro	Tyr	Phe
			65			70				75				80	
Gln	Thr	Lys	Asn	Ile	Pro	Pro	His	Asp	Asp	Arg	Gly	Ala	Arg	Ala	Phe
			85					90					95		
Ala	His	Asp	Ala	Gly	Gly	Leu	Pro	Ser	Gly	Thr	Gly	Gly	Leu	Val	Lys
			100				105						110		
Asn	Ser	Phe	His	Leu	Leu	Arg	Gln	Gln	Met	Ser	Leu	Thr	Glu	Ile	Met
			115				120						125		
Asn	Ser	Ile	His	Ser	Asp	Ala	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Pro		
			130				135						140		

<210> 1845

<211> 390

<212> DNA

<213> Homo sapiens

<400> 1845

aagcttacga cgcctagctt tggagacctg aaccacttga tcagtgcac aatgagtggg
 60
 gtgacttgct gcctccgctt cccggggcag ctcaactcgg accttcggaa acttgacgtg
 120
 aacctgattc cattccctcg cctgcacttt tttatggctg gctttgcgcc actcacctcg
 180

cgtggctccc agcagtagccg tgctctcact gtccttgagc tgaccagca gatgtgggac
 240
 tccaagaaca tgatgtgtgc tgctgacccg cgtcatggcc gctacctcac agtatctgcc
 300
 atgttccgtg gaaagatgag caccaaggag gtggacgagc agatgctgaa cgtgcagaac
 360
 aagaactctt cctacttcgt ggagtggatc
 390

<210> 1846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1846

Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn His Leu Ile Ser Ala
 1 5 10 15
 Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe Pro Gly Gln Leu Asn
 20 25 30
 Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile Pro Phe Pro Arg Leu
 35 40 45
 His Phe Phe Met Val Gly Phe Ala Pro Leu Thr Ser Arg Gly Ser Gln
 50 55 60
 Gln Tyr Arg Ala Leu Thr Val Pro Glu Leu Thr Gln Gln Met Trp Asp
 65 70 75 80
 Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg His Gly Arg Tyr Leu
 85 90 95
 Thr Val Ser Ala Met Phe Arg Gly Lys Met Ser Thr Lys Glu Val Asp
 100 105 110
 Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu
 115 120 125
 Trp Ile
 130

<210> 1847

<211> 343

<212> DNA

<213> Homo sapiens

<400> 1847

cagccgtgct ttctgcgctc aactcgggaa cggctatatc gcgcagatcc aacagttcca
 60
 tggctcgaag agtagtaaaa atatcaataa ctggcagagc atcgcgctcaa gctggcgacc
 120
 ctggccgcgc ccgcgttggc cgatcacgcc atgttggagc aggccttcca gctgttccag
 180
 caaaaaagtgt gcggacaatc tcctgcccga tggtctgggtg ttgcacttca gggagcgcga
 240
 tgactgcac tacgtcgtct atgacctgga gccgctgggt caggcgggccc tggcgggcaa
 300
 gccctaacgg tggcaactgg ctgacttaca ccgcccccc cgn
 343

<210> 1848

<211> 94
 <212> PRT
 <213> Homo sapiens

<400> 1848
 Met Ala Arg Arg Val Val Lys Ile Ser Ile Thr Gly Arg Ala Ser Arg
 1 5 10 15
 Gln Ala Gly Asp Pro Gly Arg Arg Arg Val Gly Arg Ser Arg His Val
 20 25 30
 Gly Ala Gly Leu Pro Ala Val Pro Ala Lys Lys Leu Arg Thr Ile Ser
 35 40 45
 Cys Arg Met Ala Arg Cys Ser Thr Ser Gly Ser Ala Met His Cys Thr
 50 55 60
 Thr Ser Ser Met Thr Trp Ser Arg Trp Phe Arg Arg Pro Trp Arg Ala
 65 70 75 80
 Ser Pro Asn Gly Gly Asn Trp Leu Thr Tyr Thr Ala Pro Thr
 85 90

<210> 1849
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 1849
 cggaaagaac aggttcagca aagagcaata gaatgttccc gggctctcag tgcgattctt
 60
 gacattgaac atggagaccc aaaagagaat gtactaggtt cagcttttga catgaaacag
 120
 ctgaaggatg ctattgatga gactaaaata gctttgatgg gacattcttt tggaggagca
 180
 acagttcttc aagcccttag tgaggaccag agattcagat gtggagtgtc tcttgatcca
 240
 tggatgtatc cggtgaacga agagctgtac tccagaaccc tccagcctct cctctttatc
 300
 aactctgcca aattccagac tccaaaggac atcgcaaaaa tgaaaaagtt ctaccagcct
 360
 gacaaggaaa ggaaanatga ttacaatcaa
 390

<210> 1850
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 1850
 Arg Lys Glu Gln Val Gln Gln Arg Ala Ile Glu Cys Ser Arg Ala Leu
 1 5 10 15
 Ser Ala Ile Leu Asp Ile Glu His Gly Asp Pro Lys Glu Asn Val Leu
 20 25 30
 Gly Ser Ala Phe Asp Met Lys Gln Leu Lys Asp Ala Ile Asp Glu Thr
 35 40 45
 Lys Ile Ala Leu Met Gly His Ser Phe Gly Gly Ala Thr Val Leu Gln
 50 55 60
 Ala Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Val Ala Leu Asp Pro

```

65          70          75          80
Trp Met Tyr Pro Val Asn Glu Glu Leu Tyr Ser Arg Thr Leu Gln Pro
      85          90          95
Leu Leu Phe Ile Asn Ser Ala Lys Phe Gln Thr Pro Lys Asp Ile Ala
      100        105        110
Lys Met Lys Lys Phe Tyr Gln Pro Asp Lys Glu Arg Lys Xaa Asp Tyr
      115        120        125
Asn Gln
      130

```

<210> 1851

<211> 574

<212> DNA

<213> Homo sapiens

<400> 1851

```

ncgatcggag aggcctttccg cactggtgac ttggactcta agccccaccc cagccggagc
60
ttcaggccctt accgagctga agacaatgat tcctatgcct ctgagatcaa ggagctgcag
120
ctgggtgctgg ctgaggccca cgacagcctc cggggcttgc aagagcagct ctcccaggag
180
cggcagctac gaaaggagga ggccgacaat ttcaaccaga aaatggtcca gctgaaggag
240
gaccagcaga gggcgctcct gaggcgggag tttgagctgc agagtctgag cctccagcgg
300
aggctggagc agaaattctg gagccaggag aagaacatgc tgggtgcagga gtcccagcaa
360
ttcaagcaca acttctgct gctcttcag aagctcaggt ggttctctcaa gcgctggcgg
420
cagggcaagg ttttgccag cgaaggggat gacttctctg aggtgaacag catgaaggag
480
ctgtacttgc tgatggagga agacgagata aacgctcagc attctgataa caaggcctgc
540
acgggggaca gctggaccca gaacacgccc aatg
574

```

<210> 1852

<211> 191

<212> PRT

<213> Homo sapiens

<400> 1852

```

Xaa Ile Gly Glu Ala Phe Arg Thr Gly Asp Leu Asp Ser Lys Pro Asp
1      5      10      15
Pro Ser Arg Ser Phe Arg Pro Tyr Arg Ala Glu Asp Asn Asp Ser Tyr
      20      25      30
Ala Ser Glu Ile Lys Glu Leu Gln Leu Val Leu Ala Glu Ala His Asp
      35      40      45
Ser Leu Arg Gly Leu Gln Glu Gln Leu Ser Gln Arg Gln Leu Arg
      50      55      60
Lys Glu Glu Ala Asp Asn Phe Asn Gln Lys Met Val Gln Leu Lys Glu
65      70      75      80
Asp Gln Gln Arg Ala Leu Leu Arg Arg Glu Phe Glu Leu Gln Ser Leu

```

```

      85              90              95
Ser Leu Gln Arg Arg Leu Glu Gln Lys Phe Trp Ser Gln Glu Lys Asn
      100              105              110
Met Leu Val Gln Glu Ser Gln Gln Phe Lys His Asn Phe Leu Leu Leu
      115              120              125
Phe Met Lys Leu Arg Trp Phe Leu Lys Arg Trp Arg Gln Gly Lys Val
      130              135              140
Leu Pro Ser Glu Gly Asp Asp Phe Leu Glu Val Asn Ser Met Lys Asp
      145              150              155              160
Leu Tyr Leu Leu Met Glu Glu Asp Glu Ile Asn Ala Gln His Ser Asp
      165              170              175
Asn Lys Ala Cys Thr Gly Asp Ser Trp Thr Gln Asn Thr Pro Asn
      180              185              190

```

<210> 1853

<211> 338

<212> DNA

<213> Homo sapiens

<400> 1853

```

gccggcgccg accaagccac ggcgatgcccc acccacccttg gaagaggtgt cgttccgccca
60
cgctcattgag gagcgcgccg tcgaagctga ctgtttcgtc cgctcgctca atacactgca
120
gcctgcgcagc ggcattggcac ttctgcgcac ctgcgaccac atggatggca aggtcggcac
180
gacgttttct ctggatgacg atgtcatttt tgctcgccca cagaagcagc gctcagccga
240
gggcccagcga ctgaatacag agcccgtctc ttgggccgag ttgctcgagc gcgctgctgc
300
atagaatata tatacccaag ctatgatgat gccgtcgt
338

```

<210> 1854

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1854

```

Met Pro His Pro Pro Trp Lys Arg Cys Arg Ser Ala Thr Ser Leu Arg
1      5      10      15
Ser Ala Pro Ser Lys Leu Thr Cys Ser Ser Ala Arg Ser Ile His Ser
20      25      30
Ser Leu Arg Arg Ala Trp His Phe Cys Ala Ser Arg Thr Thr Trp Met
35      40      45
Ala Arg Ser Ala Arg Arg Phe Thr Trp Met Thr Met Ser Phe Leu Ser
50      55      60
Arg His Arg Ser Ser Ala Gln Pro Arg Ala Ser Asp Ser Asn Thr Ser
65      70      75      80
Pro Ser Leu Trp Pro Ser Cys Ser Ser Ala Leu Leu His Arg Ile His
85      90      95
Ile Pro Lys Leu
100

```

<210> 1855

<211> 429

<212> DNA

<213> Homo sapiens

<400> 1855

gcgtccttcg cgtacgtgga cgagggcgagg caggtgttcg tccagtgcag caccagcac
 60
 ccgagcgaaa cgcaggaaat cgtggcgacac gtcctggacc tggacaacca cgaggtcacg
 120
 gtgcagtgtc tgcgcattgg cgggtggcttt ggcggtaagg aaatgcagcc gcacgggttc
 180
 gccgcgatcg cagcactcgg cgcgaccctg accggggcgac cggttcgact gcgactgacc
 240
 cgaaaccagg acatcaccat ctccggaaa ggcaccccat acctcgcgga gtgggacgtg
 300
 gccttcgacg acgacggccg cctccaggct ctgcgcgcca ccgtcaccag cgacggcgagg
 360
 tggagcctgg acctctcgga gccggtgatg cagcggacgg tgtgtcacat cgataactcc
 420
 tattggatc
 429

<210> 1856

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1856

Ala	Ser	Phe	Ala	Tyr	Val	Asp	Glu	Gly	Gly	Gln	Val	Phe	Val	Gln	Cys
1				5					10					15	
Ser	Thr	Gln	His	Pro	Ser	Glu	Thr	Gln	Glu	Ile	Val	Ala	His	Val	Leu
			20						25					30	
Asp	Leu	Asp	Asn	His	Glu	Val	Thr	Val	Gln	Cys	Leu	Arg	Met	Gly	Gly
		35					40					45			
Gly	Phe	Gly	Gly	Lys	Glu	Met	Gln	Pro	His	Gly	Phe	Ala	Ala	Ile	Ala
	50					55					60				
Ala	Leu	Gly	Ala	Thr	Leu	Thr	Gly	Arg	Pro	Val	Arg	Leu	Arg	Leu	Thr
	65				70				75					80	
Arg	Asn	Gln	Asp	Ile	Thr	Ile	Ser	Gly	Lys	Arg	His	Pro	Tyr	Leu	Ala
			85						90					95	
Glu	Trp	Asp	Val	Ala	Phe	Asp	Asp	Gly	Arg	Leu	Gln	Ala	Leu	Arg	
			100				105					110			
Ala	Thr	Val	Thr	Ser	Asp	Gly	Gly	Trp	Ser	Leu	Asp	Leu	Ser	Glu	Pro
		115					120					125			
Val	Met	Gln	Arg	Thr	Val	Cys	His	Ile	Asp	Asn	Ser	Tyr	Trp	Ile	
		130					135					140			

<210> 1857

<211> 393

<212> DNA

<213> Homo sapiens

<400> 1857

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 60
 gataccagcc gagcacgac atgctcagca tggtcagcag cagccagaac ggaatcgcga
 120
 gcaggcgctc gaacagctca ctgccaccca gcaccagcgg gattgccccg gccacgacca
 180
 gtgcgcgcgag gagcagccac catcgcccg ctcgtctgcg gcaactcgata ccaatacgtt
 240
 gcgcttcaac caatcgatct tggtcgagcg atgcgcgcca tcttccaaca ggcgagtcac
 300
 cagactcagc cagtaacacc gcgaaaaatc gtggcgcatg tcgacagggt gcaaacccgag
 360
 acgcagcacg ggtgcctgtc ggtggcggcg gag
 393

<210> 1858

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1858

Met	Leu	Ser	Met	Val	Ser	Ser	Ser	Gln	Asn	Gly	Asn	Arg	Ser	Arg	Arg
1				5					10				15		
Ser	Asn	Ser	Ser	Leu	Pro	Pro	Ser	Thr	Ser	Gly	Ile	Ala	Pro	Ala	Thr
			20					25					30		
Thr	Ser	Ala	Pro	Arg	Ser	Ser	His	Arg	Pro	Leu	Met	Leu	Arg	His	
			35				40				45				
Ser	Ile	Pro	Ile	Arg	Cys	Ala	Ser	Thr	Asn	Arg	Ser	Trp	Ser	Arg	His
	50					55					60				
Ala	Ala	His	Leu	Pro	Thr	Gly	Glu	Ser	Pro	Asp	Ser	Ala	Ser	Asn	Thr
	65				70				75					80	
Ala	Lys	Asn	Arg	Gly	Ala	Cys	Arg	Gln	Gly	Ala	Asn	Arg	Asp	Ala	Ala
			85						90					95	
Arg	Val	Pro	Val	Gly	Gly	Gly	Arg								
			100												

<210> 1859

<211> 345

<212> DNA

<213> Homo sapiens

<400> 1859

nagatctggc gcctcgctcac caacttcttc tacttcgcga agatggattt ggattttctg
 60
 ttccacatgt tttttctcgc acgatactgc aagcttcttg aggagaactc atttagagga
 120
 agaactcgcc acttttttta catgctcttg tttgggtgcta ctgtcctaac tagcattgtt
 180
 ctgatcgagg ggatgatacc ttacatttcc gagacatttg ccagaattct gttcctgagc
 240
 aattcattga cgtttatgat ggtttatgtc tggagcaagc acaatcctat catccatag
 300
 agcaatctgg gcctgttcac ctttacggct gcatacttac catgg
 345

<210> 1860
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1860
 Xaa Ile Trp Arg Leu Val Thr Asn Phe Leu Tyr Phe Arg Lys Met Asp
 1 5 10 15
 Leu Asp Phe Leu Phe His Met Phe Phe Leu Ala Arg Tyr Cys Lys Leu
 20 25 30
 Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe Tyr Met
 35 40 45
 Leu Leu Phe Gly Ala Thr Val Leu Thr Ser Ile Val Leu Ile Gly Gly
 50 55 60
 Met Ile Pro Tyr Ile Ser Glu Thr Phe Ala Arg Ile Leu Phe Leu Ser
 65 70 75 80
 Asn Ser Leu Thr Phe Met Met Val Tyr Trp Ser Lys His Asn Pro
 85 90 95
 Ile Ile His Met Ser Asn Leu Gly Leu Phe Thr Phe Thr Ala Ala Tyr
 100 105 110
 Leu Pro Trp
 115

<210> 1861
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 1861
 gcgttgactg tagtgagtga cgaagctgat atacaaaatg cgccgggctg tagaaaagcc
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 aatagtgcgc ttcatcagct cggcttaggt gttatgaact tacatggcta tcttgctaaa
 120
 aacaaaattg gctatgagtc ggaagaagct aaagattttg ctaatatatt ctttatgatg
 180
 atgaattact attcacttga aagatcaatg caaatagcaa aagaaagaca ggaaacgttt
 240
 aaagactcttg ataagtcaga ttatgcaaat ggaaaatatt tcgaatttta tacttcgcaa
 300
 tcatttgaac cgaaatacga aaaagtacgt aaattatttg atgggtttaga aatcccaacg
 360
 cctgaagatt ggaaagcatt gcaaaaagaa gttgaaactc acgggtttatt ccatgcttat
 420
 cgtttagcga ttgca
 435

<210> 1862
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 1862
 Ala Leu Thr Val Val Ser Asp Glu Ala Asp Ile Gln Asn Ala Pro Gly

1	5	10	15
Val Arg Lys	Ala Asn Ser Glu	Leu His Ser Val Gly	Leu Gly Val Met
	20	25	30
Asn Leu His	Gly Tyr Leu Ala	Lys Asn Lys Ile Gly Tyr	Glu Ser Glu
	35	40	45
Glu Ala Lys	Asp Phe Ala Asn Ile Phe Phe	Met Met Met Asn Tyr Tyr	
	50	55	60
Ser Leu Glu	Arg Ser Met Gln Ile Ala Lys	Glu Arg Gln Glu Thr Phe	
	65	70	75
Lys Asp Phe	Asp Lys Ser Asp Tyr Ala Asn	Gly Lys Tyr Phe Glu Phe	
	85	90	95
Tyr Thr Ser	Gln Ser Phe Glu Pro Lys Tyr	Glu Lys Val Arg Lys Leu	
	100	105	110
Phe Asp Gly	Leu Glu Ile Pro Thr Pro Glu	Asp Trp Lys Ala Leu Gln	
	115	120	125
Lys Glu Val	Glu Thr His Gly Leu Phe His	Ala Tyr Arg Leu Ala Ile	
	130	135	140
Ala			
145			

<210> 1863

<211> 792

<212> DNA

<213> Homo sapiens

<400> 1863

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nggatccctca cgcgcccat catacgtggg atacgttgga gcaaatgcgt catgacgggg
60
tctccgtcgt gctcactacc cacaacatgg atgaggctca acggtcggct gatcacgtct
120
ggatcgtcga tcgcggcagg gtcgcaactc atggaactgt gccagagctc accgctgagt
180
cgagtttgga agatgtgttc ctactcaca ctagtgaccg cgcagcaggg aggaattgac
240
atgacgacac tcgatctccg ccccgcacct caggccgcac cggctgtcgc acgctgctgc
300
aaaccagctc tcaccagagt gcgtctgggt atgcgcaacg gtgagcagct gctactagct
360
ctcgtcattc ccatcgggat catcgtcgcc gggcgcttcc tgggcggccg ggtcggactg
420
acgatggacg tcttagcacc ctacgtgctg gcgctcgcca tctggtcgac atgtttcact
480
tcccaagcga tcatgaccgg ttttgaacgc cgttacgggg tgctcgaacg attgtccgca
540
accccgttag gtcggtcggg tctgctagct ggcaaggcga tggcttattc cgttatcagt
600
ctcgcctcagg tgatactgct tgtcatcacc tcttttagcgc tgggctggca ccccaacggt
660
tcgggctcgt cctggctccc aaccctgggt agcggtgtgc tcgcatgat gacattcggg
720
ctgcgagcac tggcaatggc cggcgctggc aaagctgaag tcactctcgg actggccaac
780
ttggtataca tc
792

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<210> 1864

<211> 264

<212> PRT

<213> Homo sapiens

<400> 1864

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Xaa Ile Leu Thr Pro Ala Ile Ile Arg Gly Ile Ser Leu Ser Lys Cys
 1           5           10           15
Val Met Thr Gly Ser Pro Ser Cys Ser Leu Pro Thr Thr Trp Met Arg
           20           25           30
Leu Asn Gly Trp Leu Ile Thr Ser Gly Ser Ser Ile Ala Ala Gly Ser
           35           40           45
Gln Leu Met Glu Leu Cys Gln Ser Ser Pro Leu Ser Arg Val Trp Lys
           50           55           60
Met Cys Ser Ser Leu Thr Leu Val Thr Ala Gln Gly Gly Ile Asp
65           70           75           80
Met Thr Thr Leu Asp Leu Arg Pro Ala Pro Gln Ala Ala Pro Ala Ala
           85           90           95
Ala Arg Val Arg Asn His Ala Leu Thr Glu Val Arg Leu Val Met Arg
           100          105          110
Asn Gly Glu Gln Leu Leu Leu Ala Leu Val Ile Pro Ile Gly Ile Ile
           115          120          125
Val Ala Gly Arg Phe Leu Gly Gly Arg Val Gly Leu Thr Met Asp Val
           130          135          140
Leu Ala Pro Ser Val Leu Ala Leu Ala Ile Trp Ser Thr Cys Phe Thr
145          150          155          160
Ser Gln Ala Ile Met Thr Gly Phe Glu Arg Arg Tyr Gly Val Leu Glu
           165          170          175
Arg Leu Ser Ala Thr Pro Leu Gly Arg Ser Gly Leu Leu Ala Gly Lys
           180          185          190
Ala Met Ala Tyr Ser Val Ile Ser Leu Ala Gln Val Ile Leu Leu Val
           195          200          205
Ile Ile Ser Leu Ala Leu Gly Trp His Pro His Gly Ser Gly Leu Ala
           210          215          220
Trp Leu Pro Thr Leu Val Ser Val Val Leu Ala Met Met Thr Phe Gly
225          230          235          240
Leu Ala Ala Leu Ala Met Ala Gly Ala Gly Lys Ala Glu Val Thr Leu
           245          250          255
Gly Leu Ala Asn Leu Val Tyr Ile
260

```

<210> 1865

<211> 717

<212> DNA

<213> Homo sapiens

<400> 1865

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ngccggctga tcaaacaaact cacagacatg ggcttcccgga gagagccagc tgaggaggcc
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ttgaagagta acaatatgaa tcttgatcag gccatgagcg ctctgctgga aaagaaggtg
120
gacgtggaca agcgtgggct gggagtgacc gaccataatg gaatggccgc caagcccttc
180

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ggctgcccgc cgccaatctc caaagagtct tccgtggacc gccccaccct tcttgacaag
 240
 gatggcggcc tcgtggaaga gcccacgcct tcaccgttct tgccctcccc aagcctgaag
 300
 ctcccccttt cacacagtgc actccccagt caggccctgg gtgggggtgc ctccgggctg
 360
 ggcagcaaa acttgaatto ttctagacag ataccgagtg gcaatctggg tatgtttggc
 420
 aatagtggag cagcacaagc caggaccatg cagcagccgc cacagccacc agtgcacgct
 480
 cttaactctt cccagcccag tctccgtgct caagtgcctc agttttctatc ccctcagggt
 540
 caagcacagc ttttgcagtt tgcagcaaaa aacattggtc tcaaccctgc actattaacc
 600
 tcgccaatta atcctcaaca tatgacgatg ttgaaccagc tctatcagct gcagctggga
 660
 taccacggtt tacaatatcca gcagcagatg ttacaggccc agcgtaatgt gtccgga
 717

<210> 1866

<211> 239

<212> PRT

<213> Homo sapiens

<400> 1866

Xaa Arg Leu Ile Lys Gln Leu Thr Asp Met Gly Phe Pro Arg Glu Pro
 1 5 10 15
 Ala Glu Glu Ala Leu Lys Ser Asn Asn Met Asn Leu Asp Gln Ala Met
 20 25 30
 Ser Ala Leu Leu Glu Lys Lys Val Asp Val Asp Lys Arg Gly Leu Gly
 35 40 45
 Val Thr Asp His Asn Gly Met Ala Ala Lys Pro Leu Gly Cys Arg Pro
 50 55 60
 Pro Ile Ser Lys Glu Ser Ser Val Asp Arg Pro Thr Leu Leu Asp Lys
 65 70 75 80
 Asp Gly Gly Leu Val Glu Glu Pro Thr Pro Ser Pro Phe Leu Pro Ser
 85 90 95
 Pro Ser Leu Lys Leu Pro Leu Ser His Ser Ala Leu Pro Ser Gln Ala
 100 105 110
 Leu Gly Gly Val Ala Ser Gly Leu Gly Met Gln Asn Leu Asn Ser Ser
 115 120 125
 Arg Gln Ile Pro Ser Gly Asn Leu Gly Met Phe Gly Asn Ser Gly Ala
 130 135 140
 Ala Gln Ala Arg Thr Met Gln Gln Pro Pro Gln Pro Pro Val Gln Pro
 145 150 155 160
 Leu Asn Ser Ser Gln Pro Ser Leu Arg Ala Gln Val Pro Gln Phe Leu
 165 170 175
 Ser Pro Gln Val Gln Ala Gln Leu Leu Gln Phe Ala Ala Lys Asn Ile
 180 185 190
 Gly Leu Asn Pro Ala Leu Leu Thr Ser Pro Ile Asn Pro Gln His Met
 195 200 205
 Thr Met Leu Asn Gln Leu Tyr Gln Leu Gln Leu Ala Tyr Gln Arg Leu
 210 215 220
 Gln Ile Gln Gln Gln Met Leu Gln Ala Gln Arg Asn Val Ser Gly

225

230

235

<210> 1867

<211> 518

<212> DNA

<213> Homo sapiens

<400> 1867

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 tccatgcatg ggacggcact tgggtccgcg atcaggtagc caggcatgga aggaacatgg
 120
 gaggaagga actgtctggt gcgccagtgt tgttcaagga ggatgtgaca agacaggcca
 180
 tctgggtggc tggccctggt acccaacaac gtggtaggca aggccttctg cccggagagg
 240
 ttcttggggg ccagcagggg gctacatagg acatgggtgg ggaccccgag tccgagccca
 300
 cctctctctg ctcacacctt tccaccnng cagccccgc cttctccgca gaactctccc
 360
 caagccagac gccttgacc ggctgcttaa gtcaggcttt gggacatacc ctgggaggaa
 420
 gcgaggtgct ttgcaccccc aagtgatcat gttcccgctg ccagcctgcc aaggatgatg
 480
 ggagcttggg gagcggggtc tggcagggct tttccgga
 518

<210> 1868

<211> 73

<212> PRT

<213> Homo sapiens

<400> 1868

Gln Asp Arg Pro Ser Gly Trp Leu Ala Leu Leu Pro Asn Asn Val Val
 1 5 10 15
 Ala Lys Ala Leu Cys Pro Glu Arg Phe Leu Gly Ala Ser Arg Gly Leu
 20 25 30
 His Arg Thr Trp Val Gly Thr Pro Ala Pro Ser Pro Pro Leu Leu Pro
 35 40 45
 Pro Pro Leu Pro Pro Xaa Gln Pro Pro Pro Leu Pro Gln Asn Ser Pro
 50 55 60
 Gln Ala Arg Pro Pro Gly Pro Ala Ala
 65 70

<210> 1869

<211> 436

<212> DNA

<213> Homo sapiens

<400> 1869

acgcgtcacc ttcttgctgg agctactggg agccctcgga cacctgctgt cattgcccga
 60
 ccgtgacatg ccgagcaccg aaaccacct gtggattcgc gagctgagcc gcctcgaccg
 120

cgacgtgtcg actgccaccc actttcgttg gagcgacgac ggcaccgtgc taggtcagac
 180
 gaccgacgat ggcaccgagc ctgaggttgt tgccttgcca gcggtctact gccgtcgttg
 240
 cggcgcgacg gcatggggag tccagctcgc cagcaccggc aataacctca gcgagaacaa
 300
 cgacagcacc cgacggaccc acgcggcaca cgacggctgc ttccgagcct tgccttcggc
 360
 ccctcgagag ggagccagcg cggtcgacac cggcgagcg acactgtcct tacgtcgtt
 420
 cgacaccgtc aacagg
 436

<210> 1870

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1870

Met	Pro	Ser	Thr	Glu	Thr	His	Leu	Trp	Ile	Arg	Glu	Leu	Ser	Arg	Ile
1				5					10					15	
Asp	Arg	Asp	Val	Ser	Thr	Ala	Thr	His	Phe	Arg	Trp	Ser	Asp	Asp	Gly
			20					25					30		
Thr	Val	Leu	Gly	Gln	Thr	Thr	Asp	Asp	Gly	Thr	Glu	Pro	Glu	Val	Val
			35				40					45			
Ala	Leu	Pro	Ala	Val	Tyr	Cys	Arg	Arg	Cys	Gly	Arg	Ser	Gly	Trp	Gly
			50			55					60				
Val	Gln	Leu	Ala	Ser	Thr	Gly	Asn	Asn	Leu	Ser	Glu	Asn	Asn	Asp	Ser
65					70				75					80	
Ile	Arg	Arg	Thr	His	Ala	Ala	His	Asp	Gly	Arg	Phe	Arg	Ala	Leu	Leu
			85						90				95		
Ser	Ala	Pro	Arg	Glu	Gly	Ala	Ser	Ala	Val	Asp	Thr	Gly	Glu	Ala	Thr
			100					105					110		
Leu	Ser	Leu	Arg	Trp	Phe	Asp	Thr	Val	Asn	Arg					
			115					120							

<210> 1871

<211> 474

<212> DNA

<213> Homo sapiens

<400> 1871

nntgcagcgc cccgaggtcg atgtctccaa cgtctttgcc agccttgaca tggctagcga
 60
 gcccgcaccc gtccgtaccc tgcgtaggca agcccaacaa tgaccgggga acagctcgcg
 120
 cattggatcg aggagtcgac gtcgacgggt tttttcggcg gcgcggaat gtccaccgaa
 180
 tcaggatttc cggaatttcg ctccggtggc gggttttaca ccaactcagca tgacctgcgc
 240
 ttccccgcgg agtacatgct cagtcacagc tgtttggttg agcatcccg gcgagttcttc
 300
 gacttctacc gcacctacct catccatcct caggccaggc ccaatgctgg tcacgtgctg
 360

ttggttgccct tggagcaggc tggggaactt tcgacgatca ttacccagaa tattgacggc
 420
 ctgcaccaag aagctgggtc tcgtcagggtc attgagttgc atgggtcggt gcac
 474

<210> 1872
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1872
 Met Thr Gly Glu Gln Leu Ala His Trp Ile Glu Glu Ser Thr Ser Thr
 1 5 10 15
 Val Phe Phe Gly Gly Ala Gly Met Ser Thr Glu Ser Gly Ile Pro Asp
 20 25 30
 Phe Arg Ser Ala Gly Gly Leu Tyr Thr Thr Gln His Asp Leu Pro Phe
 35 40 45
 Pro Ala Glu Tyr Met Leu Ser His Ser Cys Leu Val Glu His Pro Ala
 50 55 60
 Glu Phe Phe Asp Phe Tyr Arg Thr Tyr Leu Ile His Pro Gln Ala Arg
 65 70 75
 Pro Asn Ala Gly His Arg Ala Leu Val Ala Leu Glu Gln Ala Gly Glu
 85 90 95
 Leu Ser Thr Ile Ile Thr Gln Asn Ile Asp Gly Leu His Gln Glu Ala
 100 105 110
 Gly Ser Arg Gln Val Ile Glu Leu His Gly Ser Val His
 115 120 125

<210> 1873
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 1873
 nacgcgtaga aatgaagccc cagctggtca gagaccgaa atccggtagt gcacgggacg
 60
 gggtccctcg gggatctcgg aggggagacc cccaccggg aggactggag gcagcgcctc
 120
 tcccgcctcg gcgcgcgacg cctatttccc tctttccaag gggccaatcc ccaccgcggc
 180
 ccgcaggggg gcgcgtcaag gcaaggtccg cggcgagaa ggtgccagat gggagcgaag
 240
 ggcgaggcca gcccttggtc cttggcggc agttcgggtc ccgcctccaa attttagtat
 300
 gcataatgag caccaggaag gttttttgaa acaaattt
 338

<210> 1874
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 1874
 Ser Pro Ser Trp Ser Glu Thr Gly Asn Pro Val Val His Gly Thr Gly

```

      1             5             10             15
Ser Leu Gly Asp Leu Gly Gly Glu Thr Pro Thr Arg Glu Asp Trp Arg
      20
Gln Arg Leu Ser Arg Pro Gly Ala Arg Ser Leu Phe Pro Ser Phe Gln
      35
Gly Ala Asn Pro His Arg Gly Pro Gln Gly Ala Arg Ser Arg Gln Gly
      50
Pro Arg Arg Glu Arg Cys Pro Val Gly Ala Lys Gly Glu Ala Ser Pro
      65
Trp Ser Leu Ala Gly Ser Ser Gly Pro Ala Ser Lys Phe
      85

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<210> 1875

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1875

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aagcttggtg tacaagtggg tcgtcggttc tcaggtgggt gagccgtgta tcacgatatg
60
ggcaatatct gcttctgctt cattacagaa gatgatggcg atagcttcgg tgattttgga
120
aaattcacag aacccgtgat tgaagcactc cataaaatgg gagcaacagg ggcagagtta
180
caaggacgta acgaccttct catcgacgga aagaaattct ctggaaatgc gatgtactca
240
aacaatggcc gttaacagc gcacggaaca ttaatgttgg atttagatgt gagcattttg
300
ccacaaattt tacgtccaaa acaagagaaa atcgagtcaa aaggaatcaa gtcggttcgt
360
tcacgc
366

```

<210> 1876

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1876

```

Lys Leu Gly Val Gln Val Val Arg Arg Phe Ser Gly Gly Gly Ala Val
      1             5             10             15
Tyr His Asp Met Gly Asn Ile Cys Phe Cys Phe Ile Thr Glu Asp Asp
      20
Gly Asp Ser Phe Arg Asp Phe Gly Lys Phe Thr Glu Pro Val Ile Glu
      35
Ala Leu His Lys Met Gly Ala Thr Gly Ala Glu Leu Gln Gly Arg Asn
      50
Asp Leu Leu Ile Asp Gly Lys Lys Phe Ser Gly Asn Ala Met Tyr Ser
      65
Asn Asn Gly Arg Leu Thr Ala His Gly Thr Leu Met Leu Asp Leu Asp
      85
Val Ser Ile Leu Pro Gln Ile Leu Arg Pro Lys Gln Glu Lys Ile Glu
      100
Ser Lys Gly Ile Lys Ser Val Arg Ser Arg
      110

```


115

120

<210> 1877
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 1877
 acgcgtagt ggtcgcaaat atgacgggca agaaacgctt agaaagaaac taccatttaa
 60
 cgagggttatg caaattgcag aaatctctct atcggattgt ggctatatatta tttcatcttt
 120
 ccaagctgct ggaccaaggg ctgtagggtt gcaacgacct attatatctg aacatttttt
 180
 tcaatttgac ccatttgata aacgacattg ggttgcttca catcatttac cacacgctgc
 240
 gacagctgct ttcacttccg gatttgaaga ttgcgctgga ttagtttcag atactgccgg
 300
 atcgaacact cttgatggaa aggactatgt tgaaagctgc tgcaatgcta ttccacg
 357

<210> 1878
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 1878
 Met Gln Ile Ala Glu Ile Ser Leu Ser Asp Cys Gly Tyr Ile Ile Ser
 1 5 10 15
 Ser Phe Gln Ala Ala Gly Pro Arg Ala Val Gly Leu Gln Arg Pro Ile
 20 25 30
 Ile Ser Glu His Phe Phe Gln Phe Asp Pro Phe Asp Lys Arg His Trp
 35 40 45
 Val Val Ser His His Leu Pro His Ala Ala Thr Ala Ala Phe Thr Ser
 50 55 60
 Gly Phe Glu Asp Cys Ala Gly Leu Val Ser Asp Thr Ala Gly Ser Asn
 65 70 75 80
 Thr Leu Asp Gly Lys Asp Tyr Val Glu Ser Cys Cys Asn Ala Ile Pro
 85 90 95

<210> 1879
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<400> 1879
 nacgcgtaga tgctccttgg acggcttttt cgtggtagag ggttcccggt gcgcgcgcga
 60
 tccctgggaa gtagctgaag agaaggcaca ggaagagtcg cctccactga tggctctcct
 120
 gtccctccca caggctctga cgcctctct gcggcttcgg tggttgaaca ggccacagtc
 180
 caggagcgct tacattcagg agctccgcgt agcacctggc caaccaaact cagccctccg
 240

ttaagatcct ggttccatgc cgcagtagga cagcaggccc aagctcgcac atcccagtga
 300
 tgcaccatgc caatagtga taagttgaag gaggccctga aacccggccg caaggactcg
 360
 gctgatgatg gagaactggg gaagcttctt gcctcctctg ccaagaaggt ccttttacag
 420
 aaaatcgagt tcgagccagc cagcaagagc ttctcctacc agctggaggc cttaaagagc
 480
 aaatatgtgt tgcctcaacc caaacagag ggagctagtc gccacaagag tggagatgac
 540
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 600
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 720
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 780
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 840
 gccaacagcg gcaacgccat caagcccgtc tccttcaccc gagacctgaa aaagatcgcc
 900
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 960
 gccatgcaga aagcctgcct gaatggctgt gccaaagtgg atcgtcaaac gcaggctact
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 1062

<210> 1880

<211> 252

<212> PRT

<213> Homo sapiens

<400> 1880

Met Pro Ile Val Asp Lys Leu Lys Glu Ala Leu Lys Pro Gly Arg Lys
 1 5 10 15
 Asp Ser Ala Asp Asp Gly Glu Leu Gly Lys Leu Leu Ala Ser Ser Ala
 20 25 30
 Lys Lys Val Leu Leu Gln Lys Ile Glu Phe Glu Pro Ala Ser Lys Ser
 35 40 45
 Phe Ser Tyr Gln Leu Glu Ala Leu Lys Ser Lys Tyr Val Leu Leu Asn
 50 55 60
 Pro Lys Thr Glu Gly Ala Ser Arg His Lys Ser Gly Asp Asp Pro Pro
 65 70 75 80
 Ala Arg Arg Gln Gly Ser Glu His Thr Tyr Glu Ser Cys Gly Asp Gly
 85 90 95
 Val Pro Ala Pro Gln Lys Val Leu Phe Pro Thr Glu Arg Leu Ser Leu
 100 105 110
 Arg Trp Glu Arg Val Phe Arg Val Gly Ala Gly Leu His Asn Leu Gly
 115 120 125
 Asn Thr Cys Phe Leu Asn Ala Thr Ile Gln Cys Leu Thr Tyr Thr Pro
 130 135 140
 Pro Leu Ala Asn Tyr Leu Leu Ser Lys Glu His Ala Arg Ser Cys His

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145             150             155             160
Gln Gly Ser Phe Cys Met Leu Cys Val Met Gln Asn His Ile Val Gln
165             170             175
Ala Phe Ala Asn Ser Gly Asn Ala Ile Lys Pro Val Ser Phe Ile Arg
180             185             190
Asp Leu Lys Lys Ile Ala Arg His Phe Arg Phe Gly Asn Gln Glu Asp
195             200             205
Ala His Glu Phe Leu Arg Tyr Thr Ile Asp Ala Met Gln Lys Ala Cys
210             215             220
Leu Asn Gly Cys Ala Lys Leu Asp Arg Gln Thr Gln Ala Thr Thr Leu
225             230             235             240
Val His Gln Ile Phe Gly Gly Tyr Leu Arg Ser Arg
245             250

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<210> 1881
<211> 358
<212> DNA
<213> Homo sapiens

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<400> 1881
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120
tcaacacgaa gattaacgac gtctacaacc ctctcaacaa caatgtggac tgggtaagca
180
cgagaattga tctgctacag caagatttgg acaccactcg caagaaggat ctaaaaccag
240
ccacatcgat cgatatctgc accatcacat cgatcgatag caagtctgta gccatggaag
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atagggttaca atettataag gatatgcacg accgtttcac ctacacctatc aggcgata
358

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<210> 1882
<211> 115
<212> PRT
<213> Homo sapiens

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<400> 1882
Met Asp Ala Gly Lys Ala Thr Ser Ile Asp Val Lys Pro Gln Thr Ser
1             5             10             15
Gln Ile Pro Ala Glu Pro Gln Ser Leu Ala Glu Lys Lys Asp Glu Trp
20             25             30
Glu Ile Ala Tyr Ile Asn Thr Lys Ile Asn Asp Val Tyr Asn Pro Leu
35             40             45
Asn Asn Asn Val Asp Trp Leu Ser Thr Arg Ile Asp Leu Leu Gln Gln
50             55             60
Asp Leu Asp Thr Thr Arg Lys Lys Asp Leu Lys Pro Ala Thr Ser Ile
65             70             75             80
Asp Ile Cys Thr Ile Thr Ser Ile Asp Ser Lys Phe Val Ala Met Glu
85             90             95
Asp Arg Leu Gln Ser Tyr Lys Asp Met His Asp Arg Phe Thr Ser Pro
100            105            110
Ile Arg Arg

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115

<210> 1883
 <211> 367
 <212> DNA
 <213> Homo sapiens

<400> 1883
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 120
 tgctgaaggc gatgagtctg tatttgtcaa ctccaattca aacagctcga tgggtgcctcc
 180
 tgtcctggag aacaatgctg ttgatctcac tgatgggctg acagatttgg aatcctatat
 240
 gaggttttct atggatggcg gngcaagtga ttcaattgat agccttctga accttgatgg
 300
 atcacaggat cttggtagca atatggacct ctggaccttc gatgacatgc ccacgcgtgg
 360
 cgatttn
 367

<210> 1884
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 1884
 Met Asn Leu His Ser Asp Gln Gly Ser Asn Ser Leu Gly Cys Ser Asp
 1 5 10 15
 Leu Gly Trp Glu Asn Asp Thr Lys Thr Pro Asp Ile Thr Ser Ile Ala
 20 25 30
 Pro Ile Pro Thr Ile Ala Glu Gly Asp Glu Ser Val Phe Val Asn Ser
 35 40 45
 Asn Ser Asn Ser Ser Met Val Pro Pro Val Leu Glu Asn Asn Ala Val
 50 55 60
 Asp Leu Thr Asp Gly Leu Thr Asp Leu Glu Ser Tyr Met Arg Phe Leu
 65 70 75 80
 Met Asp Gly Gly Ala Ser Asp Ser Ile Asp Ser Leu Leu Asn Leu Asp
 85 90 95
 Gly Ser Gln Asp Leu Gly Ser Asn Met Asp Leu Trp Thr Phe Asp Asp
 100 105 110
 Met Pro Ile Ala Gly Asp Xaa
 115

<210> 1885
 <211> 392
 <212> DNA
 <213> Homo sapiens

<400> 1885
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 60

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 120
 ctgcgtagta cagctgctgt tgcgcgccgg gccgcgaccc gtaccgggtt ccaaccactg
 180
 aactggtgga tcctcgatcat tcccggtctc gctgcgctca tcctgctggt gcgcaacgcc
 240
 actggtcggg ccgcggcagg actggggat ctcttcggca tcggctctgt taccaccacc
 300
 atttcctggg taggcgtcat cggcccgccg gtggcgatac ttctcatcgc tgatcatggg
 360
 ttgtgggtgc tgctggccgg gtggacgatt cg
 392

<210> 1886

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1886

Xaa Ala Tyr Ser Gln Arg Met Ser Leu Arg His Arg Asp Ser Arg Arg
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 Pro Arg His His Val Arg Arg Ser Arg His Val Gly Asn Pro Val Ile
 20 25 30
 Ser Arg Leu Arg Arg Thr Ser Trp Leu Arg Ser Thr Ala Ala Val Ala
 35 40 45
 Ala Gly Ala Ala Thr Gly Thr Gly Phe Gln Pro Leu Asn Trp Trp Ile
 50 55 60
 Leu Val Ile Pro Gly Leu Ala Ala Leu Ile Leu Leu Val Arg Asn Ala
 65 70 75 80
 Thr Gly Arg Ala Ala Ala Gly Leu Gly Tyr Leu Phe Gly Ile Gly Leu
 85 90 95
 Phe Thr Thr Thr Ile Ser Trp Val Gly Val Ile Gly Pro Pro Val Ala
 100 105 110
 Ile Leu Leu Ile Ala Val Met Ala Leu Trp Cys Leu Leu Ala Gly Trp
 115 120 125
 Thr Ile
 130

<210> 1887

<211> 363

<212> DNA

<213> Homo sapiens

<400> 1887

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 gacttcttgg tgacgggaac ttatatatccc gatgtcgtcg agtcgtgtgg cgggtgaggc
 120
 gctgcccaata tcaagagtc ccataatggt ggtgggctcc ctgacgacct ccagttcagt
 180
 ctcggtgagc cattgcgcac cctctttaag gacgaggtgc gagccgtcgg actcgaactt
 240
 ggtctgcccc aggacatcgt ctggcgctcag cccttcccg gcccggggct ggctatccgc
 300

attattggcg aagtcaccgc ggagcgtctg gaggtgctac gcactgccga tgccatcacg
 360
 cgt
 363

<210> 1888
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1888
 Arg Glu Phe Ile Arg Thr Phe Glu Asp Val Ala Lys Arg Leu Asn Gly
 1 5 10 15
 Asp Gln Pro Ile Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val
 20 25 30
 Val Glu Ser Gly Gly Gly Glu Gly Ala Ala Asn Ile Lys Ser His His
 35 40 45
 Asn Val Gly Gly Leu Pro Asp Asp Leu Gln Phe Ser Leu Val Glu Pro
 50 55 60
 Leu Arg Thr Leu Phe Lys Asp Glu Val Arg Ala Val Gly Leu Glu Leu
 65 70 75 80
 Gly Leu Pro Glu Asp Ile Val Trp Arg Gln Pro Phe Pro Gly Pro Gly
 85 90 95
 Leu Ala Ile Arg Ile Ile Gly Glu Val Thr Ala Glu Arg Leu Glu Val
 100 105 110
 Leu Arg Thr Ala Asp Ala Ile Thr Arg
 115 120

<210> 1889
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 1889
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 ggtgggggtga tggccatgca ctacgggtcg ctgcaaatag cggaacgggtt ttcgaccctc
 120
 acagcgctct tcggtgatcg tategacatg gggctggggc gggctcccgg cggtgacatg
 180
 ctctccgcc atgccctcaa tcagggggcag gtcateccgc ctgaggccat taattccctc
 240
 atcgccgaaa cggtagggtt cgtgcgcgaa atgctaccgt cgaagcatcc gtacgcaaag
 300
 gtctctgtga ccccggcagg tcagatccag ccacagacgt ggctgctggg atcgctgggc
 360
 cagtcagcag cgtgggctgg tgagcagggt atggactacg cctacgccca gtttttcacc
 420
 gggcgccagg acaccgggat catggatcac tacgcgcgcg acctgtccga cggcttcccc
 480
 ggcaggaccc tctcagcagt gtgtgtatcg gctgctccga cgcgtccgga
 530

<210> 1890

<211> 176
 <212> PRT
 <213> Homo sapiens

<400> 1890
 Ala Pro Asp Leu Leu Met Ala Arg Ile Ala Thr Ala Thr Gln Ser Ile
 1 5 10 15
 Arg Leu Gly Ser Gly Gly Val Met Ala Met His Tyr Gly Ser Leu Gln
 20 25 30
 Ile Ala Glu Arg Phe Ser Thr Leu Thr Ala Leu Phe Gly Asp Arg Ile
 35 40 45
 Asp Met Gly Leu Gly Arg Ala Pro Gly Gly Asp Met Leu Ser Ala His
 50 55 60
 Ala Leu Asn Gln Gly Gln Val Ile Arg Pro Glu Ala Ile Asn Ser Leu
 65 70 75 80
 Ile Ala Glu Thr Val Gly Phe Val Arg Glu Met Leu Pro Ser Lys His
 85 90 95
 Pro Tyr Ala Lys Val Val Val Thr Pro Ala Gly Gln Ile Gln Pro Gln
 100 105 110
 Thr Trp Leu Leu Gly Ser Ser Gly Gln Ser Ala Ala Trp Ala Gly Glu
 115 120 125
 Gln Gly Met Asp Tyr Ala Tyr Ala Gln Phe Phe Thr Gly Arg Gln Asp
 130 135 140
 Thr Gly Ile Met Asp His Tyr Arg Ala His Leu Ser Asp Gly Phe Pro
 145 150 155 160
 Gly Arg Thr Leu Ser Ala Val Cys Val Ser Ala Ala Pro Thr Arg Pro
 165 170 175

<210> 1891
 <211> 423
 <212> DNA
 <213> Homo sapiens

<400> 1891
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 120
 cgtcaattta cagaggcagc ccagcttctt atcaactttc tggcctggct taacgggtga
 180
 atggggcagg ggcaaggcct tgaccacact catgtttctc ccccgccctc ctccactctg
 240
 ggattttgta cgggtatggg gaggcactac ggttgcagat tttagcttttc agcgtggata
 300
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 360
 gatttggctt ctgtgctcgg ttctgaccaa cagaattgct actgactgac aaatcccttg
 420
 tgc
 423

<210> 1892
 <211> 121
 <212> PRT

<213> Homo sapiens

<400> 1892

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Met Trp Ala Pro Leu Pro Gln Ser Ser Ile Cys Thr Arg Leu Pro Thr
 1           5           10           15
Leu Gln Met Ala Pro Ala Cys Arg Glu Ile Gln Arg Gln Phe Thr Glu
          20           25           30
Ala Ala Gln Leu Pro Ile Asn Phe Leu Ala Trp Leu Asn Gly Val Met
          35           40           45
Gly Arg Gly Gln Gly Leu Asp His Thr His Val Ser Pro Pro Ala Ser
          50           55           60
Ser Thr Leu Gly Phe Cys Thr Gly Met Gly Arg His Tyr Gly Cys Arg
          65           70           75           80
Phe Ser Phe Ser Ala Trp Ile Gln Ala Pro Lys Cys Pro Arg Pro Gln
          85           90           95
Gln Lys Pro Cys Cys Arg Phe Gln Pro Ala Asp Leu Val Ser Cys
          100          105          110
Cys Arg Ser Asp Gln Gln Asn Cys Tyr
          115          120

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<210> 1893

<211> 886

<212> DNA

<213> Homo sapiens

<400> 1893

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120
gtggaataca tgggtggcat ggacgacctc gtcgggatcg tcgcccagtt taagcctggg
180
ccggggcctc gccttgccgt gttggttgac cacctcgttg ccgacaccaa agagtcacgg
240
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300
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420
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660
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720
gcgagctggg tgccgctgtg accaagtatg ccggcggtat tgctcgtgggg gaggaatcag
780
ccttcgcga cccaaccatc cttgatgccg tttccgatgc tgacctggcc tgggtcatcg
840

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acccattga tggcactaag aacttcgtgc acgggtctgt tgatca
886

<210> 1894

<211> 191

<212> PRT

<213> Homo sapiens

<400> 1894

Thr	Gly	Gly	Ala	Glu	Pro	Ala	Arg	Val	Ala	Leu	Pro	Ser	Arg	Ile	Tyr
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Val	Glu	Gly	Arg	His	Asp	Ala	Glu	Leu	Val	Glu	Lys	Ile	Trp	Gly	Asp
			20					25					30		
Asp	Leu	Arg	His	Val	Gly	Val	Val	Glu	Tyr	Met	Gly	Gly	Met	Asp	
			35				40				45				
Asp	Leu	Val	Gly	Ile	Val	Ala	Glu	Phe	Lys	Pro	Gly	Pro	Gly	His	Arg
			50				55				60				
Leu	Gly	Val	Leu	Val	Asp	His	Leu	Val	Ala	Asp	Thr	Lys	Glu	Ser	Arg
					70					75					
Val	Ala	Asp	Glu	Val	Arg	Arg	Gly	Gly	Tyr	Ser	Glu	Tyr	Val	Met	Ile
					85				90					95	
Thr	Gly	His	Arg	Phe	Ile	Asp	Ile	Trp	Gln	Ala	Ile	Lys	Pro	Gln	Arg
					100			105					110		
Ile	Gly	Arg	Gln	Glu	Trp	Pro	Glu	Val	Pro	Met	Asp	Glu	Asp	Phe	Lys
					115			120				125			
Leu	Gly	Thr	Leu	Lys	Arg	Leu	Gly	Leu	Pro	His	Ser	Thr	Gln	Ala	Asp
					130			135				140			
Val	Gly	Lys	Ala	Trp	Gln	Ala	Met	Leu	Ala	Arg	Val	Arg	Asp	Trp	His
					145			150		155				160	
Asp	Leu	Asp	Pro	Arg	Phe	Asn	Thr	Glu	Met	Glu	Lys	Leu	Ile	Asp	Phe
					165			170						175	
Val	Thr	Arg	Asp	His	Val	Asp	Glu	Leu	Asp	Asn	Gly	Glu	Met	Ala	
					180			185						190	

<210> 1895

<211> 2555

<212> DNA

<213> Homo sapiens

<400> 1895

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cttccccctg tgccaaggtc taactcactg tagtctggat gtgggtgtat gttcatgtac
180
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240
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420

gatagccgctc agagattaga ctatgagaga gagattcagc ctactgctat ttgtgcctta
480
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600
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660
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720
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780
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900
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960
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1080
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1680
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2040

cttctcttctt caccctcatgc ttctcaccaa atttttgttg tcattgaggg cacttgagata
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 2220
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 2280
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 2340
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 2400
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 2555

<210> 1896

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1896

Cys	Glu	Gln	Cys	Gly	Lys	Cys	Lys	Cys	Gly	Glu	Cys	Thr	Ala	Pro	Arg
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Thr	Leu	Pro	Ser	Cys	Leu	Ala	Cys	Asn	Arg	Gln	Cys	Leu	Cys	Ser	Ala
			20					25					30		
Glu	Ser	Met	Val	Glu	Tyr	Gly	Thr	Cys	Met	Cys	Leu	Val	Lys	Gly	Ile
		35					40				45				
Phe	Tyr	His	Cys	Ser	Asn	Asp	Asp	Glu	Gly	Asp	Ser	Tyr	Ser	Asp	Asn
	50				55					60					
Pro	Cys	Ser	Cys	Ser	Gln	Ser	His	Cys	Cys	Ser	Arg	Tyr	Leu	Cys	Met
	65				70					75				80	
Gly	Ala	Met	Ser	Leu	Phe	Leu	Pro	Cys	Leu	Leu	Cys	Tyr	Pro	Pro	Ala
			85					90					95		
Lys	Gly	Cys	Leu	Lys	Leu	Cys	Arg	Arg	Cys	Tyr	Asp	Trp	Ile	His	Arg
		100						105					110		
Pro	Gly	Cys	Arg	Cys	Lys	Asn	Ser	Asn	Thr	Val	Tyr	Cys	Lys	Leu	Glu
		115				120						125			
Ser	Cys	Pro	Ser	Arg	Gly	Gln	Gly	Lys	Pro	Ser					
		130				135									

<210> 1897

<211> 938

<212> DNA

<213> Homo sapiens

<400> 1897

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 120

cagccttct ccctgagcaa acaccgggcc atccatcgtg gggagcggcc ccaccgctgt
 180
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 360
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 420
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 480
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 540
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 600
 cctgactgtg gtcgtgctt cggaggagc cggtccttgg ccaatcaccc gaccacacac
 660
 acaggtgaaa aaccccacca gtgccctagc tgtggacgtc gcttcgccta cccctccctg
 720
 ctggccagcc accggcgctg gcaactcgggc gagcggccct atgcctgcga cctttgtccc
 780
 aagcgttttg ctacgtggag ccactcggcc cagcaccagc tgctgcacac gggggagaag
 840
 cctttccctt gcctcagatg tggccgggct tccgccagag gtggtctctg gctgtccaca
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 938

<210> 1898

<211> 312

<212> PRT

<213> Homo sapiens

<400> 1898

Arg	His	Gly	Cys	Tyr	Val	Cys	Gly	Lys	Ser	Phe	Ala	Trp	Arg	Ser	Thr
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Leu	Val	Glu	His	Val	Tyr	Ser	His	Thr	Gly	Glu	Lys	Pro	Phe	His	Cys
		20					25					30			
Thr	Asp	Cys	Gly	Lys	Gly	Phe	Gly	His	Ala	Ser	Ser	Leu	Ser	Lys	His
	35					40					45				
Arg	Ala	Ile	His	Arg	Gly	Glu	Arg	Pro	His	Arg	Cys	Leu	Glu	Cys	Gly
	50				55					60					
Arg	Ala	Phe	Thr	Gln	Arg	Ser	Ala	Leu	Thr	Ser	His	Leu	Arg	Val	His
65				70				75				80			
Thr	Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Ala	Asp	Cys	Gly	Arg	Arg	Phe	Ser
			85					90			95				
Gln	Ser	Ser	Ala	Leu	Tyr	Gln	His	Arg	Arg	Val	His	Ser	Gly	Glu	Thr
			100				105				110				
Pro	Phe	Pro	Cys	Pro	Asp	Cys	Gly	Arg	Ala	Phe	Ala	Tyr	Pro	Ser	Asp
	115					120					125				
Leu	Arg	Arg	His	Val	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Pro	Cys
130					135						140				
Pro	Asp	Cys	Gly	Arg	Arg	Phe	Ser	Ser	Ser	Ser	Leu	Leu	Val	Ser	His

```

145              150              155              160
Arg Arg Ala His Ser Gly Glu Cys Pro Tyr Val Cys Asp Gln Cys Gly
165              170              175
Lys Arg Phe Ser Gln Arg Lys Asn Leu Ser Gln His Gln Val Ile His
180              185              190
Thr Gly Glu Lys Pro Tyr His Cys Pro Asp Cys Gly Arg Cys Phe Arg
195              200              205
Arg Ser Arg Ser Leu Ala Asn His Arg Thr Thr His Thr Gly Glu Lys
210              215              220
Pro His Gln Cys Pro Ser Cys Gly Arg Arg Phe Ala Tyr Pro Ser Leu
225              230              235              240
Leu Ala Ser His Arg Arg Val His Ser Gly Glu Arg Pro Tyr Ala Cys
245              250              255
Asp Leu Cys Ser Lys Arg Phe Ala Gln Trp Ser His Leu Ala Gln His
260              265              270
Gln Leu Leu His Thr Gly Glu Lys Pro Phe Pro Cys Leu Glu Cys Gly
275              280              285
Arg Ala Ser Ala Arg Gly Gly Leu Trp Leu Ser Thr Ser Val Ala Pro
290              295              300
Arg Pro Gln Thr Val Ala Leu Asp
305              310

```

<210> 1899

<211> 508

<212> DNA

<213> Homo sapiens

<400> 1899

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acacgctgga gttctctgca gggccaggac tcagccatct tcgacctcgg gcatctctat
120
gaggaaatat caggccggct gcggagggaa ctgggcaaaa gggacaggaa ccgggggcag
180
ctggaggcca ccctgctgca ggtgttgaaa aaggtggagg agtttcgaat cagggtattga
240
gatgagatct ccaagcgcac agacatggag ttacaccttg ttacagtga gaaggacctg
300
gatgcagagt gtcttcatcg gactgaactg gaaaccaagt taaaagcct ggagagcttc
360
gtggagtgtg tgaaaacat ctatgagcag gagctgaagg acctggcagc acaggtgaag
420
gatgtgtcgg tgacctcgg catggacagc cgctgccaca tcgacctgag cggcatcgtg
480
gaggaggtga aggccagta tgacgccg
508

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<210> 1900

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1900

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Lys Phe Ala Ser Leu Ile Gly Lys Val Gln Ala Leu Glu Gln Arg Asp

```

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      1           5           10           15
Gln Leu Leu Glu Thr Arg Trp Ser Phe Leu Gln Gly Gln Asp Ser Ala
      20           25           30
Ile Phe Asp Leu Gly His Leu Tyr Glu Glu Ile Ser Gly Arg Leu Arg
      35           40           45
Arg Glu Leu Gly Gln Arg Asp Arg Asn Arg Gly Gln Leu Glu Ala Thr
      50           55           60
Leu Leu Gln Val Leu Lys Lys Val Glu Glu Phe Arg Ile Arg Tyr
      65           70           75

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<210> 1901
 <211> 453
 <212> DNA
 <213> Homo sapiens

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<400> 1901
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cgggtgttcgg cgatgcgaag gcaaccgcgc cttccaagtt cgacccgttc cagccgcgcg
120
aggaattcca cgaggtcagc gcgcacctgc agttccactg gggctccttc ttccacaacg
180
cgcatccggg cgagaagtgg ccggtctacg gtttcgcgag cgacacggag cccggccgcg
240
cgaccgcgat cttcgcggcg aagtcctccg tggagtacga cccaaggcg gcgcagcgcc
300
gcgcgtggga gggctttgac atgcgcgaat ggggcatgca caggcaggac ctggtggaaa
360
cgctcaccga ttccatcgcc gacgagggca acgcttagcg acgccagcgc caccgagttt
420
agagaaatga aagaaatatt aatagagggg gga
453

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<210> 1902
 <211> 151
 <212> PRT
 <213> Homo sapiens

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<400> 1902
Thr Arg Gly Pro Arg Cys Ala Gly Ser Gly Ser Ala Pro Cys Thr Pro
1           5           10           15
Arg Thr Trp Arg Arg Cys Ser Ala Met Arg Arg Gln Pro Ala Leu Pro
      20           25           30
Ser Ser Thr Arg Ser Ser Arg Ala Arg Asn Ser Thr Arg Ser Ala Pro
      35           40           45
Pro Cys Ser Ser Thr Gly Ala Pro Ser Ser Thr Thr Arg Ile Arg Ala
      50           55           60
Arg Ser Gly Arg Ser Thr Val Ser Ala Ala Thr Arg Ser Pro Ala Ala
      65           70           75           80
Arg Pro Arg Ser Ser Arg Arg Ser Pro Pro Trp Ser Thr Thr Pro Arg
      85           90           95
Arg Arg Ser Ala Ala Arg Gly Arg Ala Leu Thr Cys Ala Asn Gly Ala
      100          105          110
Cys Thr Gly Arg Thr Trp Trp Lys Arg Ser Pro Ile Pro Ser Pro Thr

```

```

      115              120              125
Arg Ala Thr Leu Ser Asp Ala Ser Ala Thr Glu Phe Arg Glu Met Lys
      130              135              140
Glu Ile Leu Ile Glu Gly Gly
145              150

```

<210> 1903
 <211> 531
 <212> DNA
 <213> Homo sapiens

```

<400> 1903
ccggcgaggg agctgttccg ggacgccgc tccccgccg cggaactcctc gctcttctgc
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gacttgctca cgccgctggc ccagttccgc gaggacatca cgtggaggcg gccccagaga
120
atttgtgcca acccccgctt gtttccaaat gaccaacggg aagggcaggt gaagcagggg
180
ctgctggggg attgctgggt cctgtgtgcc tgcgccgcgc tgcagaagag caggcacctc
240
ctggaccagg tcattctctgc gggacagccg agctggggccg accaggagta ccggggctcc
300
ttcacctgtc gcttttgcca gtttggaagg tgggtggagg gtccatgggt cccttcgagc
360
ccctgtgggc ggggcagggt gcggatgccc tgggtggacct gaccggcggc ctggcagaaa
420
gatggaaact gaagggcgta gcaggaagcg gagccagca ggacaggcca ggccgctggg
480
agcacaggac ttgtcggcag ctgctccacc tgaaggacca gtgtctgac a
531

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<210> 1904
 <211> 133
 <212> PRT
 <213> Homo sapiens

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<400> 1904
Pro Ala Arg Glu Leu Phe Arg Asp Ala Ala Phe Pro Ala Ala Asp Ser
1          5          10          15
Ser Leu Phe Cys Asp Leu Ser Thr Pro Leu Ala Gln Phe Arg Glu Asp
20         25         30
Ile Thr Trp Arg Arg Pro Gln Arg Ile Cys Ala Asn Pro Arg Leu Phe
35         40         45
Pro Asn Asp Gln Arg Glu Gly Gln Val Lys Gln Gly Leu Leu Gly Asp
50         55         60
Cys Trp Phe Leu Cys Ala Cys Ala Ala Leu Gln Lys Ser Arg His Leu
65         70         75         80
Leu Asp Gln Val Ile Pro Ala Gly Gln Pro Ser Trp Ala Asp Gln Glu
85         90         95
Tyr Arg Gly Ser Phe Thr Cys Arg Phe Trp Gln Phe Gly Arg Trp Val
100        105        110
Glu Gly Pro Trp Val Pro Ser Ser Pro Cys Gly Arg Gly Arg Trp Arg
115        120        125
Met Pro Trp Trp Thr

```

130

<210> 1905
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 1905
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 60
 ctggccatga gccggatcct cgcgcgcttt tcggtcctgc ggggtgctgct ggccagtctc
 120
 ctccctggccg ccgtgcgctg gttgctgctg ggcgcgttgg ccgatcacct ggcgggtgctg
 180
 ttgttcgccc aggtgctgca cgcggcgacc ttgccagct ttcacgcctc tgccattcat
 240
 ttcgtgcaac gtagcttcgg cgcgcgcnc acaaggccag ggcaggcggt atactgtgca
 300
 ctggcccggt a cgggcggggc ttggggcgcg ttgtacgcg gttatagctg gaacagcctg
 360
 gggcccgacct ggactttcag catcggt
 387

<210> 1906
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1906
 Thr Arg Gly Leu Ile Gly Met Leu Trp Ala Leu Gly Val Val Ala Glu
 1 5 10 15
 Val Leu Met Phe Leu Ala Met Ser Arg Ile Leu Ala Arg Phe Ser Val
 20 25 30
 Arg Arg Val Leu Leu Ala Ser Phe Leu Leu Ala Val Arg Trp Leu
 35 40 45
 Leu Leu Gly Ala Leu Ala Asp His Leu Ala Val Leu Leu Phe Ala Gln
 50 55 60
 Val Leu His Ala Ala Thr Phe Ala Ser Phe His Ala Ser Ala Ile His
 65 70 75 80
 Phe Val Gln Arg Ser Phe Gly Ala Arg Xaa Ala Arg Pro Gly Gln Ala
 85 90 95
 Leu Tyr Ala Ala Leu Ala Gly Thr Gly Gly Ala Leu Gly Ala Leu Tyr
 100 105 110
 Ala Gly Tyr Ser Trp Asn Ser Leu Gly Pro Thr Trp Thr Phe Ser Ile
 115 120 125
 Val

<210> 1907
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 1907

acgcgttttcg accagcgcac ccgtgtcggc ggcattggcgg aaatcgctcg cttcgacaag
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 aaagtcgcgc ccgcgcgcgc gaaacgcctc gagatgtgcg tcaacgacct gttcccgagg
 120
 ggccggcgaca cgtcgaaggc cacgtttcgg acgggcctgc gcccgatgac gccggacggc
 180
 acgcccgatcg tcggccgcac gccgggtgcg aacctgttcc tgaacacggc ccacggcacg
 240
 ctccgctgga caatgggtgtg cggctcgggc caactgctcg ccgacctgat ctccggcaag
 300
 atgcccgcga tccaggccga cgacctgtct nnc
 333

<210> 1908

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1908

Thr	Arg	Phe	Asp	Gln	Arg	Ile	Arg	Val	Gly	Gly	Met	Ala	Glu	Ile	Val
1				5					10				15		
Gly	Phe	Asp	Lys	Lys	Leu	Arg	Ala	Ala	Arg	Arg	Glu	Thr	Leu	Glu	Met
			20				25					30			
Cys	Val	Asn	Asp	Leu	Phe	Pro	Gly	Gly	Gly	Asp	Thr	Ser	Lys	Ala	Thr
		35				40					45				
Phe	Trp	Thr	Gly	Leu	Arg	Pro	Met	Thr	Pro	Asp	Gly	Thr	Pro	Ile	Val
	50				55				60						
Gly	Arg	Thr	Pro	Val	Ser	Asn	Leu	Phe	Leu	Asn	Thr	Gly	His	Gly	Thr
65				70				75					80		
Leu	Gly	Trp	Thr	Met	Val	Cys	Gly	Ser	Gly	Gln	Leu	Leu	Ala	Asp	Leu
			85				90						95		
Ile	Ser	Gly	Lys	Met	Pro	Ala	Ile	Gln	Ala	Asp	Asp	Leu	Ser	Xaa	
		100					105						110		

<210> 1909

<211> 2767

<212> DNA

<213> Homo sapiens

<400> 1909

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 120
 actccggagg agctggcagc cctctttgcg ccctacggca cggatcatgag ctgcgcgcgc
 180
 atgaaacagt tcgccttcgt gcacatgcgc gagaacgcgg gcgcgcgtcg cgccatcgaa
 240
 gccctgcacg gccacgagct gcggccgggg gcgcgcgtcg tgggtggaat gtcgcgcgcc
 300
 aggcctctta atacttgga gattttcgtg ggcaatgtgt cggctgcctg cagagccag
 360
 gaactgcgca gcctcttcga gcgcgcggga cgcgtcatcg agtgtgacgt ggtgaaagac
 420

tacgcgtttg ttcacatgga gaaggaagca gatgccaaag ccgcaatcgc gcagctcaac
480
ggcaaagaag tgaaggggcaa gcgcatcaac gtggaactct ccaccaaggg tcagaagaag
540
ggggcctggcc tggctgtcca gtctggggac aagaccaaga aaccaggggc tggggatacg
600
gccttccctg gaactggttg cttctctgcc accttcgact accagcaggc ttttggaac
660
agcactgggt gctttgatgg gcaagcccg cagcccacac cacccttctt tggctcgcgac
720
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780
ccagctacct accggggccca gccgtccgtg tcaactgggag ctgcctacag ggcccagcct
840
tctgcctctt tgggtgttgg ctatcggaact cagcccatga cagccaggc agcctcttae
900
cgcgctcagc cctctgtctc ccttggggca ccatacaggg gccagctggc tagctcttagc
960
tcccagtcgt ctgcagcttc ttcactcggc ccataatggg gagccagcc ctgagcctcg
1020
gccctttctt cctatggggg tcaggcagct gcagcttctt cgctcaacte ctatggggct
1080
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1200
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1260
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1380
gcacagccag ccacagctgc tgccatagcc agccagccag cagcctacgc gcacaagcc
1440
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1560
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1620
gtcctctacc gcaactcagtc atcagcctca ttggctgctt cctatgtctg ccagcagcat
1680
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1860
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1920
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1980
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2040

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 2100
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 2160
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 2280
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 2400
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 2460
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 2520
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 2580
 agttcctgtt gggacagtca gttggtatgt atccaagtcc ctgctgacca ctaatgttct
 2640
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 2760
 tggaaaa
 2767

<210> 1910

<211> 669

<212> PRT

<213> Homo sapiens

<400> 1910

Met	Lys	Ile	Phe	Val	Gly	Asn	Val	Asp	Gly	Ala	Asp	Thr	Thr	Pro	Glu
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Glu	Leu	Ala	Ala	Leu	Phe	Ala	Pro	Tyr	Gly	Thr	Val	Met	Ser	Cys	Ala
		20						25					30		
Val	Met	Lys	Gln	Phe	Ala	Phe	Val	His	Met	Arg	Glu	Asn	Ala	Gly	Ala
		35					40					45			
Leu	Arg	Ala	Ile	Glu	Ala	Leu	His	Gly	His	Glu	Leu	Arg	Pro	Gly	Arg
	50				55					60					
Ala	Leu	Val	Val	Glu	Met	Ser	Arg	Pro	Arg	Pro	Leu	Asn	Thr	Trp	Lys
65				70					75					80	
Ile	Phe	Val	Gly	Asn	Val	Ser	Ala	Ala	Cys	Thr	Ser	Gln	Glu	Leu	Arg
			85						90					95	
Ser	Leu	Phe	Glu	Arg	Arg	Gly	Arg	Val	Ile	Glu	Cys	Asp	Val	Val	Lys
		100				105						110			
Asp	Tyr	Ala	Phe	Val	His	Met	Glu	Lys	Glu	Ala	Asp	Ala	Lys	Ala	Ala
	115					120					125				
Ile	Ala	Gln	Leu	Asn	Gly	Lys	Glu	Val	Lys	Gly	Lys	Arg	Ile	Asn	Val
	130					135					140				
Glu	Leu	Ser	Thr	Lys	Gly	Gln	Lys	Lys	Gly	Pro	Gly	Leu	Ala	Val	Gln
145				150					155					160	
Ser	Gly	Asp	Lys	Thr	Lys	Lys	Pro	Gly	Ala	Gly	Asp	Thr	Ala	Phe	Pro

[illegible]

```

      595                600                605
Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser Phe
  610                615                620
Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro Asp
  625                630                635                640
Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu
      645                650                655
Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met
      660                665

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<210> 1911

<211> 339

<212> DNA

<213> Homo sapiens

<400> 1911

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  120
cgcatcgacg atgaaagctt cctccgccca gttgagccga cccaagccgc accgtgggcg
  180
gcagcgcata gccagcaggc gtggtggaat cacctgaagt acctgcgcac cgccgcgcgt
  240
gaagcactgg tgggtcccgt cgtcattgag gtggagggga aattcgcagg gcaggtaacc
  300
ctgggaaaca ttcagcatgg cagcattcgc gattgctgg
  339

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<210> 1912

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1912

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Xaa Gly Trp Pro Glu Ser Thr Pro Ser Val Gln Leu Pro Ser Ser Ser
  1          5          10          15
Val Phe Pro Ser Gly Ala Arg Met Arg Leu Arg Pro Leu Leu Arg Ser
      20          25          30
Asp Gly His Glu Trp Arg Arg Gln Arg Ile Asp Asp Glu Ser Phe Leu
      35          40          45
Arg Pro Val Glu Pro Thr Gln Ala Ala Pro Trp Ala Ala Ala His Ser
      50          55          60
Gln Gln Ala Trp Trp Asn His Leu Lys Tyr Leu Arg Thr Ala Ala Arg
      65          70          75          80
Glu Ala Leu Val Val Pro Leu Val Ile Glu Val Glu Gly Lys Phe Ala
      85          90          95
Gly Gln Val Thr Leu Gly Asn Ile Gln His Gly Ser Ile Arg Asp Cys
      100          105          110

```

Trp

<210> 1913

<211> 767

<212> DNA

<213> Homo sapiens

<400> 1913

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 120
 gcgccagtag ctagatctcgt cctcccagcc ttgtccgaaa cctccgccaa tctcatcggc
 180
 cagaggttgc gccagggatg tcacacctcc atccccacat cgaatctacg gtgagcttcg
 240
 tcccagctgt cgggcagtag aaggcacctc ggatcaagct ttcctggcgt gaactggctc
 300
 tggtagccat caatgccacc cactgcact ccaatcccc acaagtgtgc caacacgccg
 360
 cagaattgcy tcgcagccac ccggaccttg ccatcaaggt ggcccccccc accggaccag
 420
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 480
 cccaggagct ggactcactc gtattgtctt cccctgatgg cggcgattta cgtggctcgg
 540
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 600
 ccaccaatcg tgggtgggct actgcggtcg aggaggtcgt cgcccccgct cgacaggagg
 660
 ggcgcgctca tatcgagtg ggaagcctgt ggatttcgca cgacagagaat ttccgcatc
 720
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 767

<210> 1914

<211> 190

<212> PRT

<213> Homo sapiens

<400> 1914

Met	Ser	His	Leu	His	Pro	His	Ile	Glu	Ser	Thr	Val	Ser	Phe	Val	Pro
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Ala	Val	Gly	Gln	Tyr	Lys	Ala	Pro	Arg	Ile	Lys	Leu	Ser	Trp	Arg	Glu
			20					25					30		
Leu	Val	Leu	Val	Pro	Ile	Asn	Ala	Thr	His	Leu	His	Ser	Asn	Pro	Pro
			35				40					45			
Gln	Val	Val	Gln	His	Ala	Ala	Glu	Leu	Arg	Arg	Ser	His	Pro	Asp	Leu
			50			55				60					
Ala	Ile	Lys	Val	Ala	Arg	Pro	Thr	Gly	Pro	Ala	Pro	Val	Leu	Leu	Asn
			65		70				75					80	
Leu	Val	Asp	Thr	Arg	Leu	Arg	Leu	Ala	Ala	His	Arg	Val	His	Ala	Gln
			85					90					95		
Glu	Leu	Asp	Ser	Leu	Val	Leu	Ser	Ser	Pro	Asp	Gly	Gly	Asp	Leu	Arg
			100				105						110		
Gly	Ser	Ala	Met	Leu	Ser	Arg	Leu	Thr	Arg	Leu	Trp	Ser	Gln	His	His
			115			120					125				
His	Leu	Pro	Val	Arg	Ile	Ala	Thr	Asn	Arg	Gly	Gly	Ala	Thr	Ala	Val

```

      130              135              140
Glu Glu Val Val Ala Arg Leu Arg Gln Glu Gly Arg Arg His Ile Ala
145              150              155              160
Val Gly Ser Leu Trp Ile Cys Asp Asp Glu Asn Phe Arg Ile His Thr
      165              170              175
Arg Gln Ala Leu His Ala Gly Ala Glu Val Val Ala Ala Pro
      180              185              190

```

<210> 1915
 <211> 571
 <212> DNA
 <213> Homo sapiens

```

<400> 1915
acgcgtccca ggccccacag gccccctctg gctctcaggc ccccgcccca gtggccagga
60
agggtgtgagc gcacgatggg cagtcacgcc gcacacacgc tctgtctatg tccctcccca
120
ggaccctctg accgggcaca agggcagctg tgaggacaag gccacagcca caaaccaacc
180
tggcacacac ggctcagggc gaggcactgc cccatggggc tgcctgatcc acgctcacag
240
gtgtcattgt ctatgctcag gggggcttgg caccatggga aaccacacca gaacacatgg
300
agaagccaca gcacaacctc agcgcccgcc atgcaggacc ctgggtctca cccattgcac
360
ccaccgtgcg ggacccctgc gcctcaccgc gaacatccac agtgtgggac tgctgcgtct
420
caccactgc acctgccgtg caggatccct gagtctcacc cgccgcaccc gccgtgcggg
480
atccctgagt ctacccgcc gcaccgcgc tacctgccgc atccgccatg cgggaccctt
540
gcgtctcacc caccgcaccc gccgtgcggg a
571

```

<210> 1916
 <211> 119
 <212> PRT
 <213> Homo sapiens

```

<400> 1916
Met Gly Leu His Asp Pro Arg Ser Gln Val Ser Leu Ser Met Leu Arg
1      5      10      15
Gly Ala Trp His His Gly Lys Pro Thr Gln Asn Thr Trp Arg Ser His
      20      25      30
Ser Thr Thr Ser Ala Pro Ala Met Gln Asp Pro Gly Ser His Pro Leu
      35      40      45
His Pro Pro Cys Gly Thr Pro Ala Pro His Pro Glu His Pro Gln Cys
      50      55      60
Gly Thr Ala Ala Ser His Pro Leu His Leu Pro Cys Arg Ile Pro Glu
      65      70      75      80
Ser His Pro Pro His Pro Pro Cys Gly Ile Pro Glu Ser His Pro Pro
      85      90      95
His Pro Pro Tyr Leu Pro His Pro Pro Cys Gly Thr Pro Ala Ser His

```

100 105 110
 Pro Pro His Pro Pro Cys Gly
 115
 <210> 1917
 <211> 360
 <212> DNA
 <213> Homo sapiens
 <400> 1917
 nnacgcgtga cggcggaaga tctccgcacc ctatctgccg ggtacacgcc ggggtgattcc
 60
 gatattgtctt gggctgccat cactttgtgg cgcggtgtcg ttgcctccgc cttggaccgt
 120
 catccctatg gcccggtgaa gtcggtaaag gtagcaggtc cggccggcca cccagccccc
 180
 gatttcgcgc cgggatgggt gtcgaccgc ttggcagttc ccgtacatcg cacagtggcc
 240
 gactcccaaa ggagacactt cccggtgact catttgcaat tcaatcgga gacaacccac
 300
 gtgacgtcgc atgtcattga cgagcgcacg gtcgtgtat gtgttccggg ttcgcccggaa
 360
 <210> 1918
 <211> 120
 <212> PRT
 <213> Homo sapiens
 <400> 1918
 Xaa Arg Val Thr Gly Glu Asp Leu Arg Thr Leu Ser Ala Gly Tyr Thr
 1 5 10 15
 Pro Gly Asp Ser Asp Met Ser Trp Ala Ala Ile Thr Leu Trp Arg Gly
 20 25 30
 Val Val Ala Ser Ala Leu Asp Arg His Pro Tyr Gly Pro Val Lys Ser
 35 40 45
 Val Lys Val Ala Gly Pro Ala Gly His Pro Ala Pro Asp Phe Ala Ala
 50 55 60
 Gly Trp Leu Leu Asp Arg Leu Ala Val Pro Val His Arg Thr Val Ala
 65 70 75 80
 Asp Ser Pro Arg Arg His Phe Pro Val Thr His Leu Gln Phe Asn Arg
 85 90 95
 Glu Thr Thr His Val Asp Val Asp Val Ile Asp Glu Arg Thr Val Arg
 100 105 110
 Val Cys Val Pro Gly Ser Pro Glu
 115 120
 <210> 1919
 <211> 354
 <212> DNA
 <213> Homo sapiens
 <400> 1919
 nncggccgca gctgtgtcca ctgcgctgtc cctgccacct cggccatctg cctctctctt
 60

ccaggctgca gccatccctc ctgcactgct gaggcctggc cagcgcctc ncggccacgc
 120
 ccacetcctat cctctttgcc cttactataa cactggggagc ccgccccccc gcgacaggcc
 180
 aggcagcggg gaaggtgtag acgaacagcc caaaggattc agcagtgtaa gtacccccac
 240
 tacgcactta caaagtgcag gccaccgccc agccccacct ccagacacag gcggaggcca
 300
 agctcggggg caccgtatca tcccggtgcc tctccacct acccctgcca attg
 354

<210> 1920

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1920

Xaa	Gly	Arg	Ser	Cys	Val	His	Cys	Ala	Val	Pro	Ala	Thr	Ser	Ala	Ile
1				5					10					15	
Cys	Leu	Ser	Leu	Pro	Gly	Cys	Ser	His	Pro	Ser	Cys	Thr	Ala	Glu	Ala
			20					25					30		
Trp	Pro	Arg	Ala	Ser	Arg	Pro	Arg	Pro	Pro	Ser	Ser	Leu	Pro	Leu	
		35				40					45				
Thr	Lys	His	Trp	Glu	Pro	Ala	Arg	Pro	Arg	Gln	Ala	Arg	Pro	Ala	Gly
		50				55				60					
Arg	Cys	Arg	Arg	Thr	Ala	Gln	Arg	Ile	Gln	Gln	Cys	Lys	Tyr	Pro	Thr
65				70					75					80	
Tyr	Ala	Leu	Thr	Lys	Cys	Arg	Pro	Pro	Pro	Ser	Pro	Thr	Ser	Arg	His
			85					90						95	
Arg	Arg	Arg	Pro	Ser	Ser	Arg	Ala	Pro	Tyr	His	Pro	Val	Pro	Ser	Pro
			100					105					110		
Pro	Tyr	Pro	Cys	Gln	Leu										
			115												

<210> 1921

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1921

gaattcatct ggaggcagag agatggggaa gcgggtggga gaagagcaag aacggaaact
 60
 atttttaata caaatccagt catggtattg tatacacagc agcctctgtc ttccagaaac
 120
 ctacacggcc gccacaccaa agttaatgcc accaggcgct atcacacaga tgtgagggtgc
 180
 aggtgccact ccacagccgt gggcagacct gggagccccag ctctctctgg ttccacctc
 240
 cacactgccc accccatcct tctctcccag tctccactcc atcgaagcct cccagatgac
 300
 ttcatgtggg gacaggagaa ctacagatca tggctgagaa gggcgcnctg tngtcca
 357

<210> 1922

<211> 92
 <212> PRT
 <213> Homo sapiens

<400> 1922
 Met Val Leu Tyr Thr Gln Gln Pro Leu Ser Ser Arg Asn Leu His Gly
 1 5 10 15
 Arg His Thr Lys Val Asn Ala Thr Arg Arg His His Thr Asp Val Arg
 20 25 30
 Cys Arg Cys His Ser Thr Ala Val Gly Arg Pro Gly Ser Pro Ala Pro
 35 40 45
 Pro Gly Phe Thr Leu His Thr Ala His Pro Ile Leu Leu Ser Gln Ser
 50 55 60
 Pro Leu His Arg Ser Leu Pro Asp Asp Phe Met Trp Gly Gln Glu Asn
 65 70 75 80
 Tyr Arg Ser Trp Leu Arg Arg Ala Xaa Cys Xaa Pro
 85 90

<210> 1923
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 1923
 nattnaatta tgggtgagaaa aggccttatgc gttgcattgc tcgtgcttgc cacactgtca
 60
 ggtagtgcac agaagaaaga atgggttcagc aacattaaac tctcaggcta tggaaatgacc
 120
 cagtatcaat atactgatca agaggggaagc aaaggccatt catttaactc gcgattgttc
 180
 ccgttgccctt taaacggacg tatcttaaat gacttttatt ggaaggcaca ggcccaattc
 240
 aatggaaaca catcgacatt gggaagcagt ccacgtcttg tagacctatt tgtagagtgg
 300
 cagaaatatg attatttcaa ggtgaagtta ggccagttta agcgaccatt cacgtttgaa
 360
 aatcccag
 368

<210> 1924
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 1924
 Met Val Arg Lys Gly Leu Cys Val Ala Leu Leu Val Leu Val Thr Leu
 1 5 10 15
 Ser Gly Ser Ala Gln Lys Lys Glu Trp Phe Ser Asn Ile Lys Leu Ser
 20 25 30
 Gly Tyr Gly Met Thr Gln Tyr Gln Tyr Thr Asp Gln Glu Gly Ser Lys
 35 40 45
 Gly His Ser Phe Asn Leu Arg Leu Phe Pro Leu Pro Leu Asn Gly Arg
 50 55 60
 Ile Leu Asn Asp Phe Tyr Trp Lys Ala Gln Ala Gln Phe Asn Gly Asn

```

65              70              75              80
Thr Ser Thr Leu Gly Ser Ser Pro Arg Leu Val Asp Leu Phe Val Glu
              85              90              95
Trp Gln Lys Tyr Asp Tyr Phe Lys Val Lys Leu Gly Gln Phe Lys Arg
              100              105              110
Pro Phe Thr Phe Glu Asn Pro
              115

```

<210> 1925

<211> 427

<212> DNA

<213> Homo sapiens

<400> 1925

```

actagtgttt ccagcaggga gcgatttaat tgttcttgca ttgaaaccca gtgtggcaag
60
ccccctgtg atttgaggct aatccctccc caccctgttc tggcacatgt gcggtgcccc
120
gggctcccc caggctgtga gcagataaag ccttcgctgg cttcacaaca gtgactgggt
180
ctgagaaaca ggtccttgta caagcgacag ggagtgtcga caccagatgt ggcagccctt
240
ccacgccagg ctgtgtgggt cagccgcctg gtatatgtgt ccacgtctga tgaaacacagc
300
gttggtgtgt gcatgactgt tgtctgtttt ctctatggaa acaaggaaac ctaagcatta
360
aaacaacacc atccacgtct ggttccttag agcaaattgga agcaccaggc tctgggtgcac
420
ggcgcgcg
427

```

<210> 1926

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1926

```

Met His His Thr Thr Leu Phe Ser Ser Ala Met Asp Thr Tyr Thr Arg
1              5              10              15
Arg Leu His His Thr Ala Trp Arg Gly Gly Ala Ala Thr Ser Gly Val
              20              25              30
Ser Thr Pro Cys Arg Leu Tyr Lys Asp Leu Phe Leu Arg Thr Ser His
              35              40              45
Cys Cys Glu Ala Thr Gln Gly Phe Ile Cys Ser Gln Pro Gly Gly Ser
              50              55              60
Pro Gly His Arg Thr Cys Ala Arg Thr Gly Trp Gly Gly Ile Ser Leu
65              70              75              80
Lys Ser Gln Gly Gly Leu Pro His Trp Val Ser Met Gln Glu Gln Leu
              85              90              95
Asn Arg Cys Leu Leu Glu Thr Leu
              100

```

<210> 1927

<211> 516

<212> DNA

<213> Homo sapiens

<400> 1929

```

nnccgcgag actcagggtc tgggggtccct cttccccaag aggcctgact gcctgggtgt
60
ttctccaggta catgtccttc aaggagaaat acacttctctg gctctggcct gggccagggt
120
ctttctgggc cttgtctgga gtgccacag cagaggctgg cttctctgga ctatctgtgc
180
cagaggagccc agggccccgt gcagccctgc ctctgggctg ggtctgaacc tgctccacgc
240
ccacgggccc ctgagtccca caggagtcag gctcgtctga gctggggatg cagttttctg
300
aagaacggcg gctttgggct gccttctcta actctggcct cgcacacctg cttggattcc
360
tcattctttt ttttcttctt gggcccaact tctctcttga gggctctctg agggcccgagc
420
tccatggcgt cacagatgta tgtcagcaag ccattgctctc cgtcctctcc attctcggtg
480
gcagcctccc cgttgggtgt cacttctcca gaagcaaaact gttgatcagg cccaaacctg
540
agtgctgagc agtctcagtc tctccctcct gccaaagcgc cagggtccca ccctcaggct
600
ccctggtagg gaccgagggg cccggcgctt gagccccgct caatcgccgc ttctcgtagg
660
agcggtcggg gctgagcttg cgcagagtgt cgacctcccc aggcaccgac ttctcgtgct
720
tccagctctg ctgatctcg cgcagctttg ccgcagcctt gcgcttcaac ttggcgaacc
780
agcgtctggt gatcttgtag tcatgcatgg tgcccacctc ccaggacctt gagcaggaca
840
caa
843

```

<210> 1930

<211> 120

<212> PRT

<213> Homo sapiens

<400> 1930

```

Leu Pro Gly Cys Ser Pro Gly Thr Cys Pro Ser Arg Arg Asn Thr Leu
1      5      10
Pro Gly Leu Gly Leu Gly Gln Gly Pro Ser Gly Pro Cys Leu Glu Cys
20     25     30
Pro Gln Gln Arg Leu Ala Ser Trp Tyr Tyr Leu Cys Gln Arg Thr Gln
35     40     45
Ala Pro Val Gln Pro Cys Leu Trp Ala Gly Ser Glu Pro Ala Pro Arg
50     55     60
Pro Arg Ala Pro Glu Ser His Arg Ser Gln Ala Arg Leu Ser Trp Gly
65     70     75
Cys Ser Phe Leu Lys Asn Gly Gly Phe Gly Leu Pro Ser Leu Thr Leu
85     90     95
Ala Ser Ala Pro Cys Leu Asp Ser Ser Ser Phe Phe Phe Phe Leu Ala

```

100 105 110
 Pro Leu Ser Ser Leu Arg Ala Leu
 115 120

<210> 1931
 <211> 719
 <212> DNA
 <213> Homo sapiens

<400> 1931
 acgcgtaggc ctgagccgct ccacagccct ggggagggca gaaaaggagg aaagtaggca
 60
 gtgcaagaaa caggaggaaa cccccagag cgcagcctcc tggaagcggga agggagcact
 120
 gaagaggagg tggtagtggt tgcagaagc tgctgagaag ccagtaggat aaagcggaga
 180
 agcttcctac taggacagct tcctcccagc ccagtgtaggc cacgtggtgt tcctcgggtga
 240
 ccagacacgt ggccatgaat ttctcagtggt gctttattgt tgattaaatg cagtgcggctc
 300
 acgaggctga ctttggaac aggaggtccg tgggtcgtgg aataagaaag ggcatcatgg
 360
 ttgcagagga agggaaggaa gccacgggct gccttgggga gctttctgaa aggcaggctc
 420
 gatcatgcct ctctgggcta cgggtctcctc acgggtggctc ctggttgga ctgaagtgggt
 480
 ccccttgggc cctctctccc atctcagcat tagccaggac ttttggcttg gcggcccccag
 540
 caggggctgcc cccttgcaac acttcttttc ccacatgata gtgccttcca aacctacttc
 600
 cagcgctgcc ctcttcagggt agcctttcat aaccacctct ccttccact ggctaaagat
 660
 gaggttgagc aactgcagga cttgggacct tgttcctgcc cctgtggctg cctggatcc
 719

<210> 1932
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 1932
 Met Pro Leu Trp Ala Thr Val Ser Ser Arg Trp Leu Leu Val Gly Thr
 1 5 10 15
 Glu Val Val Pro Leu Val Pro Leu Ser His Leu Ser Ile Ser Gln Asp
 20 25 30
 Phe Trp Leu Gly Gly Pro Ser Arg Ala Ala Pro Leu Gln His Phe Phe
 35 40 45
 Ser His Met Ile Val Pro Ser Lys Pro Thr Ser Ser Val Ala Leu Phe
 50 55 60
 Arg Glu Pro Phe Ile Thr Thr Ser Pro Phe His Trp Leu Lys Met Arg
 65 70 75 80
 Leu Ser Asn Cys Arg Thr Trp Asp Leu Val Pro Ala Pro Val Ala Ala
 85 90 95
 Trp Ile

<210> 1933
 <211> 295
 <212> DNA
 <213> Homo sapiens .

<400> 1933
 ggccgagcgtgtgtggcgc catggagcgc atgcctgccg acctgattat cctcgacctg
 60
 atgctgccgg gggataacgg cctcttgctg tgccagcgcc tgcgccagca atacgcaaca
 120
 ccagtgatca tgctgaccgc catgggcgaa ctgagtgate gcgtgggggg cctggaaatg
 180
 ggccgcatg actacctgaa caaaccttgc gatgcccggtg aattactctg ccgggtgcgc
 240
 gctgtactgc gtccggcgtg tgaaccgca cgcagcttgg gcgacgtgtc gcgcc
 295

<210> 1934
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 1934
 Gly Ala Glu Leu Trp Ala Ala Met Glu Arg Met Pro Ala Asp Leu Ile
 1 5 10 15
 Ile Leu Asp Leu Met Leu Pro Gly Asp Asn Gly Leu Leu Leu Cys Gln
 20 25 30
 Arg Leu Arg Gln Gln Tyr Ala Thr Pro Val Ile Met Leu Thr Ala Met
 35 40 45
 Gly Glu Leu Ser Asp Arg Val Gly Gly Leu Glu Met Gly Ala Asp Asp
 50 55 60
 Tyr Leu Asn Lys Pro Phe Asp Ala Arg Glu Leu Ala Arg Val Arg
 65 70 75 80
 Ala Val Leu Arg Pro Ala Cys Glu Asn Arg Pro Thr Leu Gly Asp Val
 85 90 95
 Ser Arg

<210> 1935
 <211> 298
 <212> DNA
 <213> Homo sapiens

<400> 1935
 accggtgtgg cgggcgcgcg cttcaccacc atcggtcca cggggccgac ggccgggttcg
 60
 caatacatcg tcgatacctt cctggtagtgt gtgttcgggg gggcccaag cctgttcggc
 120
 cccatcgctt cggcgttcgt gattgcccg acccaatcgc tgcggagttt ttctctcagt
 180
 ggctcgatgg ccaaggtgct gacctgtctg tcggtgatc tgatcctgat gctgcgccg
 240

caagggtgtg tctccatcaa agtgcgcaag taaaggcgag cagataaggg ttttaagca
298

<210> 1936

<211> 90

<212> PRT

<213> Homo sapiens

<400> 1936

```

Thr Gly Val  Ala Gly  Ala Ala  Phe Thr  Thr  Ile  Gly  Ser  Thr  Gly  Pro
 1              5              10              15
Thr Ala Gly  Ser  Gln  Tyr  Ile  Val  Asp  Thr  Phe  Leu  Val  Val  Val  Phe
              20              25              30
Gly Gly Ala  Gln  Ser  Leu  Phe  Gly  Pro  Ile  Ala  Ser  Ala  Phe  Val  Ile
              35              40              45
Ala  Gln  Thr  Gln  Ser  Leu  Ser  Glu  Phe  Phe  Leu  Ser  Gly  Ser  Met  Ala
              50              55              60
Lys  Val  Leu  Thr  Leu  Ser  Ser  Val  Ile  Leu  Ile  Leu  Met  Leu  Arg  Pro
65              70              75              80
Gln  Gly  Leu  Phe  Ser  Ile  Lys  Val  Arg  Lys
              85              90

```

<210> 1937

<211> 513

<212> DNA

<213> Homo sapiens

<400> 1937

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gcacggcgca cagtaacacc aactcgaaag agaccttatg aatgcaaggt gtgcgggaaa
60
gcctttaatt ctccaattt atttcaaatt catcaaagaa ctcacactgg aaagaggtcc
120
tataaatgta gggaaatagt gagagccttc acagttttcca gtttctttcg aaaacatgga
180
aaaatgcata ctggagaaaa acgctatgaa tgtaataact ttggaaaacc tatcgattat
240
cccagtttat ttcaaattca tgtagaact cactctggag aaaaacccta caaatgtaaa
300
caatgtggta aagccttcat ttccgcaggt tacgttcgga cacatgaaat cagatctcac
360
gcgctggaga aatcccacca atgtcaggaa tgtgggaaga aactcagttg ttccagttcc
420
cttcacagac atgaagaac tcatagtgga ggaaaactct acgaatgtca aaaatgtgac
480
caagtcttta gatgtccac gtccttcac gcg
513

```

<210> 1938

<211> 171

<212> PRT

<213> Homo sapiens

<400> 1938

```

Ala Arg Arg Thr Val Thr Pro Thr Arg Lys Arg Pro Tyr Glu Cys Lys

```


1	5	10	15
Val Cys Gly Lys Ala Phe Asn Ser Pro Asn Leu Phe Gln Ile His Gln	20	25	30
Arg Thr His Thr Gly Lys Arg Ser Tyr Lys Cys Arg Glu Ile Val Arg	35	40	45
Ala Phe Thr Val Ser Ser Phe Phe Arg Lys His Gly Lys Met His Thr	50	55	60
Gly Glu Lys Arg Tyr Glu Cys Lys Tyr Cys Gly Lys Pro Ile Asp Tyr	65	70	75
Pro Ser Leu Phe Gln Ile His Val Arg Thr His Ser Gly Glu Lys Pro	85	90	95
Tyr Lys Cys Lys Gln Cys Gly Lys Ala Phe Ile Ser Ala Gly Tyr Val	100	105	110
Arg Thr His Glu Ile Arg Ser His Ala Leu Glu Lys Ser His Gln Cys	115	120	125
Gln Glu Cys Gly Lys Lys Leu Ser Cys Ser Ser Ser Leu His Arg His	130	135	140
Glu Arg Thr His Ser Gly Gly Lys Leu Tyr Glu Cys Gln Lys Cys Asp	145	150	155
Gln Val Phe Arg Cys Pro Thr Ser Leu His Ala	165	170	

<210> 1939

<211> 1233

<212> DNA

<213> Homo sapiens

<400> 1939

gccggcagcg ccgctcccca gggaggagggt ccgcagcctg aggtcttctc caagaaaaaa
 60
 aaagaaaaaa aaacaacatg gctgc aaagg agaaactgga ggcagtgta aatgtggccc
 120
 tgagggtgcc aagcatcatg ctgttgatg tcctgtacag atgggatgac agctctcttt
 180
 tccagcagat ccaaagaagt agccttagta ataaccctct tttccagtat aagtatttgg
 240
 ctcttaatat gcattatgta ggttatatct taagtgtggt gctgctaaca ttgccacaggc
 300
 agcatctggt tcagctttat ctatatcttt tgactgctct getcctctat gctggacatc
 360
 aaatttccag ggactatggt cggagtgaac tgggggttgc ctatgagggga ccaatgtatt
 420
 tagaacctct ctctatgaat cgggtttacca cagccttaat aggtcagttg gtggtgtgta
 480
 ctttatgctc ctgtgtcatg aaaacaaagc agatttggct gttttcagct cacatgcttc
 540
 ctctgctagc acgactctgc ctgttctctt tggagacaat tgctatcatc aataaatttg
 600
 ctatgatttt tactggattg gaagtctctc atttctcttg gtctaactct ttggtaacctt
 660
 ataaccttgc taaatctgca tacagagaat tggttcaggt agtgagggta tatggccttc
 720
 tcgccttggg aatgtccctg tggaaatcaac tggtagtccc tgttctcttc atggtttctc
 780

ggctcgtctt atttgcctt cagatttact cctatttcag tactcgagat cagcctgcat
 840
 cacgtgagag gcttcttttc ctttttctga caaggtaatt aataagagcc tatgatacta
 900
 tatataacct tagaaagaga aaactttgat ctggaatag taagttttgc agattacttt
 960
 tatcgttcat gttacacaac ttcgtatttt gttaagatag gattttcatt cactggatac
 1020
 ctagggttgg caatgcagag aggtgctaac ataataatgt ggtttatttg gctgcactat
 1080
 ggaccagagt gtagcaaatg atttgtggaa aggtacatag cacatcgtaa aagtattttt
 1140
 tcaatttcaa gttaaaatta ttgggtcaat cagaaaaaag tatattataa aaataacatt
 1200
 tattgagtat tttaaatgta ccataccatt naa
 1233

<210> 1940

<211> 266

<212> PRT

<213> Homo sapiens

<400> 1940

Met	Ala	Ala	Lys	Glu	Lys	Leu	Glu	Ala	Val	Leu	Asn	Val	Ala	Leu	Arg
1			5						10					15	
Val	Pro	Ser	Ile	Met	Leu	Leu	Asp	Val	Leu	Tyr	Arg	Trp	Asp	Val	Ser
			20				25						30		
Ser	Phe	Phe	Gln	Gln	Ile	Gln	Arg	Ser	Ser	Leu	Ser	Asn	Asn	Pro	Leu
		35				40						45			
Phe	Gln	Tyr	Lys	Tyr	Leu	Ala	Leu	Asn	Met	His	Tyr	Val	Gly	Tyr	Ile
		50				55				60					
Leu	Ser	Val	Val	Leu	Leu	Thr	Leu	Pro	Arg	Gln	His	Leu	Val	Gln	Leu
					70				75					80	
Tyr	Leu	Tyr	Phe	Leu	Thr	Ala	Leu	Leu	Tyr	Ala	Gly	His	Gln	Ile	
			85					90					95		
Ser	Arg	Asp	Tyr	Val	Arg	Ser	Glu	Leu	Gly	Phe	Ala	Tyr	Glu	Gly	Pro
		100						105					110		
Met	Tyr	Leu	Glu	Pro	Leu	Ser	Met	Asn	Arg	Phe	Thr	Thr	Ala	Leu	Ile
		115				120						125			
Gly	Gln	Leu	Val	Val	Cys	Thr	Leu	Cys	Ser	Cys	Val	Met	Lys	Thr	Lys
		130				135					140				
Gln	Ile	Trp	Leu	Phe	Ser	Ala	His	Met	Leu	Pro	Leu	Leu	Ala	Arg	Leu
				150					155					160	
Cys	Leu	Val	Pro	Leu	Glu	Thr	Ile	Ala	Ile	Asn	Lys	Phe	Ala	Met	
			165					170					175		
Ile	Phe	Thr	Gly	Leu	Glu	Val	Leu	Tyr	Phe	Leu	Gly	Ser	Asn	Leu	Leu
		180					185					190			
Val	Pro	Tyr	Asn	Leu	Ala	Lys	Ser	Ala	Tyr	Arg	Glu	Leu	Val	Gln	Val
		195				200					205				
Val	Glu	Val	Tyr	Gly	Leu	Leu	Ala	Leu	Gly	Met	Ser	Leu	Trp	Asn	Gln
		210				215				220					
Leu	Val	Val	Pro	Val	Leu	Phe	Met	Val	Phe	Trp	Leu	Val	Leu	Phe	Ala
					225					235				240	
Leu	Gln	Ile	Tyr	Ser	Tyr	Phe	Ser	Thr	Arg	Asp	Gln	Pro	Ala	Ser	Arg

245 250 255
 Glu Arg Leu Leu Phe Leu Phe Leu Thr Arg
 260 265

<210> 1941
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 1941
 ctggggccct gccccacagc atcatgatgg ggaaactccc cctgggggtc gtctccctt
 60
 atgtgaagat gagttcgggg ggctacacgg accccctgaa attctacgcc accagctact
 120
 gcacagccta cggtcgggag gatttcaagc cccgtgtggg cagtcacgta ggcaccggct
 180
 acaaatcaaa tttccagccc gtgggtctcat gccaaagccag tctggaggcc ttagacaacc
 240
 cggccagggg ggaacaagcc caggaccatt tccagtctgt ggccagccag agctaccggc
 300
 ccctggagggt gcctgacggc aagcatcccc tgccctggag catgcgccag accagctcag
 360
 gctatgggag ggagaagccc agtgcgggtc cccccaccaa ggagggtccg a
 411

<210> 1942
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1942
 Met Met Gly Lys Leu Pro Leu Gly Val Val Ser Pro Tyr Val Lys Met
 1 5 10 15
 Ser Ser Gly Gly Tyr Thr Asp Pro Leu Lys Phe Tyr Ala Thr Ser Tyr
 20 25 30
 Cys Thr Ala Tyr Gly Arg Glu Asp Phe Lys Pro Arg Val Gly Ser His
 35 40 45
 Val Gly Thr Gly Tyr Lys Ser Asn Phe Gln Pro Val Val Ser Cys Gln
 50 55 60
 Ala Ser Leu Glu Ala Leu Asp Asn Pro Ala Arg Gly Glu Gln Ala Gln
 65 70 75 80
 Asp His Phe Gln Ser Val Ala Ser Gln Ser Tyr Arg Pro Leu Glu Val
 85 90 95
 Pro Asp Gly Lys His Pro Leu Pro Trp Ser Met Arg Gln Thr Ser Ser
 100 105 110
 Gly Tyr Gly Arg Glu Lys Pro Ser Ala Gly Pro Pro Thr Lys Glu Val
 115 120 125
 Arg

<210> 1943
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 1943

nagaacatt cagggctcca acaggggtgga aaacatgagg ctgcaggatg tttaacagga
 60
 gtctttctgt cagctcctct tggagccttt aacgagatac tatcatgcct atgaactgcc
 120
 acacagatgt acatggcata gcactgcccc aaagtatcag cccaaggaac cctactttcc
 180
 ccagcaacat ctaactcaga aatgctgac tttggcctca atctgggtccc aaaatacctc
 240
 cagggtatatt tgggcttcgg tgtgttcaca cacttgggtca tgtaaatctg aacacagact
 300
 ctctctgcct tggcaagaac cccccacacc cccatagata attacaccct ttggttctcc
 360
 ctctgcaatc tcacctgcta gagacg
 386

<210> 1944

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1944

Met	Gly	Val	Trp	Gly	Val	Leu	Ala	Lys	Ala	Glu	Arg	Val	Cys	Val	Gln
1				5					10				15		
Ile	Tyr	Met	Thr	Lys	Cys	Val	Asn	Thr	Pro	Lys	Pro	Lys	Ile	Pro	Trp
			20					25					30		
Arg	Tyr	Phe	Gly	Thr	Arg	Leu	Arg	Pro	Lys	Ile	Ser	Ile	Ser	Glu	Leu
			35				40					45			
Asp	Val	Ala	Gly	Glu	Ser	Arg	Val	Pro	Trp	Ala	Asp	Thr	Phe	Gly	Gln
	50					55					60				
Cys	Tyr	Ala	Met	Tyr	Ile	Cys	Val	Ala	Val	His	Arg	His	Asp	Ser	Ile
	65				70					75				80	
Ser	Leu	Lys	Ala	Pro	Arg	Gly	Ala	Ala	Lys	Thr	Pro	Val	Lys	His	
				85				90					95		
Pro	Ala	Ala	Ser	Cys	Phe	Pro	Pro	Cys	Trp	Ser	Pro	Glu	Cys	Phe	
			100					105					110		

<210> 1945

<211> 443

<212> DNA

<213> Homo sapiens

<400> 1945

nacgcgtcac gaagcgcgct cggcccacgt ggctccaagg gcgtccacgc gccctcctc
 60
 gaccgattgg tgtcgaacat ggcacgggtgg catgcgcacgc gcaccaagat ccagctcaag
 120
 ctccgcgatcc agcgantcgg catgctacag gagaaaaaag ccgcactgca taaaaaagtg
 180
 cgactggaaa ttgcggacnn tcgtagacgc caaaagcttg aactcgcgcg cgctcaaaacc
 240
 gaatcgctga tcatggacga tatacatctg gagttgcttg aactgcttga gctctactgt
 300

gagacactct atgccagatt cggattacta gaaggacgcg acaatgagcc tgaatgatgcg
 360
 atccgcgagc cgatgatgcg cattattcat gcggctcctc gcacagaggt gaaggaacta
 420
 catgtgctcc aaaacatgct gaa
 443

<210> 1946

<211> 147

<212> PRT

<213> Homo sapiens

<400> 1946

Xaa	Ala	Ser	Arg	Ser	Ala	Leu	Gly	Pro	Arg	Gly	Ser	Lys	Gly	Val	His
1				5					10					15	
Ala	Pro	Leu	Leu	Asp	Arg	Leu	Val	Ser	Asn	Met	Ala	Arg	Trp	His	Ala
		20						25					30		
Thr	Arg	Thr	Lys	Ile	Gln	Leu	Lys	Leu	Ala	Ile	Gln	Arg	Xaa	Gly	Met
		35				40					45				
Leu	Gln	Glu	Lys	Lys	Ala	Ala	Leu	His	Lys	Lys	Val	Arg	Leu	Glu	Ile
	50				55						60				
Ala	Asp	Xaa	Arg	Arg	Arg	Gln	Lys	Leu	Glu	Ser	Ala	Arg	Val	Lys	Thr
	65				70				75					80	
Glu	Ser	Leu	Ile	Met	Asp	Asp	Ile	His	Leu	Glu	Leu	Leu	Glu	Leu	Leu
		85							90					95	
Glu	Leu	Tyr	Cys	Glu	Thr	Leu	Tyr	Ala	Arg	Phe	Gly	Leu	Leu	Glu	Gly
		100						105					110		
Arg	Asp	Asn	Glu	Pro	Asp	Asp	Ala	Ile	Arg	Glu	Pro	Met	Ile	Ala	Ile
		115					120					125			
Ile	His	Ala	Ala	His	Arg	Thr	Glu	Val	Lys	Glu	Leu	His	Val	Leu	Gln
		130				135						140			
Asn	Met	Leu													

145

<210> 1947

<211> 472

<212> DNA

<213> Homo sapiens

<400> 1947

cgcccggtgta ggccgtgacg gtgaccaaca gagccacagc gggcccgctg taggcggggag
 60
 gactgtgccc caggtgcagg agggtcagat ggaacaaaaa ggccagggcg gcctccacaa
 120
 gcgccccgtg gggcacggat gtgcgcaggg ccgagctgca gctctgggcc atgaggctct
 180
 gcagcagggt caggtcactg agctcccagg cccagcagag gcgcgtcagg gtgcaggcgg
 240
 cctgcatgcc cagccccctgt gccgccagct tcagcagcgt gccaggcaga gactcctcgg
 300
 ccatgaggaa ctctgcagg gacacggtgg ggttggccga ggccccgtcc aaggtgaccc
 360
 cgtgcgccag gaagagcagg aagagcaggg tgagcagcag gtcaggccca aagtccccag
 420

cccaggggccc gagctcgaac agcgtcctca tctccaggaa gcaggccccg ag
472

<210> 1948

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1948

Met	Arg	Thr	Leu	Phe	Glu	Leu	Gly	Pro	Trp	Ala	Gly	Asp	Phe	Gly	Pro
1			5					10					15		
Asp	Leu	Leu	Leu	Thr	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Ala	His	Gly	Val
	20						25						30		
Thr	Leu	Asp	Gly	Ala	Ser	Ala	Asn	Pro	Thr	Val	Ser	Leu	Gln	Glu	Phe
	35						40					45			
Leu	Met	Ala	Glu	Glu	Ser	Leu	Pro	Gly	Thr	Leu	Leu	Lys	Leu	Ala	Ala
	50					55					60				
Gln	Gly	Leu	Gly	Met	Gln	Ala	Ala	Cys	Thr	Leu	Thr	Arg	Leu	Cys	Trp
65					70				75					80	
Ala	Trp	Glu	Leu	Ser	Asp	Leu	His	Leu	Leu	Gln	Ser	Leu	Met	Ala	Gln
				85					90				95		
Ser	Cys	Ser	Ser	Ala	Leu	Arg	Thr	Ser	Val	Pro	His	Gly	Ala	Leu	Val
			100				105						110		
Glu	Ala	Ala	Cys	Ala	Phe	Cys	Phe	His	Leu	Thr	Leu	Leu	His	Leu	Arg
	115						120					125			
His	Ser	Pro	Pro	Ala	Tyr	Ser	Gly	Pro	Ala	Val	Ala	Leu	Leu	Val	Thr
	130					135					140				
Val	Thr	Ala	Tyr	Thr	Ala										
145					150										

<210> 1949

<211> 395

<212> DNA

<213> Homo sapiens

<400> 1949

acgcgttgag ggaggcgaca tgcttcatga gcgcttgccg ccaactgctca agcgacatct
60
gccccttgct gatgttgcaa ggcggacagg acggcatgta attcgactcg acgtcacgct
120
ccggatgcct cgacgggacg etcacaagct tccattggcc attcgcggtt cgcttggtct
180
cgacgcgcgc tacaaccggg tctacatggt cgccatgccca ccgatcgggc aatggcattc
240
cacagtaacg gcacgggccg tcgtatttgc gccggagccg atcgcgctgt gctttcgtca
300
gccggctcac gctttatgct ccacggcagg tgtggcagca tcctggcagg cgactccaag
360
atccgcgcct gcgtcacgct tgacggcgcc ggggtt
395

<210> 1950

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1950

```

Met Leu His Glu Arg Leu Ala Pro Leu Leu Lys Arg His Leu Pro Leu
 1             5             10             15
Ala Asp Val Ala Arg Arg Thr Gly Arg His Val Ile Arg Leu Asp Val
      20             25             30
Thr Leu Arg Met Pro Arg Arg Asp Ala His Lys Leu Pro Leu Ala Ile
      35             40             45
Arg Gly Ser Leu Gly Leu Asp Arg Ala Tyr Asn Arg Val Tyr Met Val
      50             55             60
Ala Met Pro Pro Ile Gly Gln Trp His Ser Thr Val Arg Ala Ala Ala
      65             70             75             80
Val Val Phe Ala Pro Glu Pro Ile Ala Leu Cys Phe Arg Gln Pro Ala
      85             90             95
His Ala Leu Cys Ser Thr Ala Gly Val Ala Ala Ser Trp Gln Ala Thr
      100            105            110
Pro Arg Ser Ala Pro Ala Ser Ser Leu Thr Ala Pro Gly
      115            120            125

```

<210> 1951

<211> 363

<212> DNA

<213> Homo sapiens

<400> 1951

```

cggcgcgcgc ctctccgctc ccggggccccc gccgccaccg cggccccgcg gggagatgga
60
acagcggaaac cggctcgggtg ccctcgggata cctgccgcct ctgctgctgc atgccctgct
120
gctcttcctg ggcgacgctg cattcacaga agtccccaaa gatgtgacag tacgggaggg
180
agacgacatc gaaatgccct gcgcgttccg ggccagcggga gccacctcgt attcgtcgga
240
gattcagtgt tggtaacctca aggagccacc ccgggagctg ctgcacgagc tggcgctcag
300
cgtgccgggc gcccgaggca aggtaacaaa taaggatgca actaaaatca gcaccgtacg
360
cgt
363

```

<210> 1952

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1952

```

Arg Pro Pro Pro Leu Arg Ser Arg Ala Pro Ala Ala Thr Ala Pro Pro
 1             5             10             15
Ala Gly Asp Gly Thr Ala Glu Pro Ala Arg Cys Pro Arg Ile Pro Ala
      20             25             30
Ala Ser Ala Ala Ala Cys Pro Ala Ala Leu Arg Gly Arg Arg Cys Ile
      35             40             45
His Arg Ser Pro Gln Arg Cys Asp Ser Thr Gly Gly Arg Arg His Arg

```

```

      50              55              60
Asn Ala Leu Arg Val Pro Gly Gln Arg Ser His Leu Val Phe Ala Gly
65
Asp Ser Val Val Val Pro Gln Gly Ala Thr Pro Gly Ala Ala Ala Arg
      70              75              80
      85              90              95
Ala Gly Ala Gln Arg Ala Gly Arg Pro Glu Gln Gly Asn Lys
      100              105              110

```

<210> 1953
 <211> 329
 <212> DNA
 <213> Homo sapiens

```

<400> 1953
acgcgtcagc ctgagcccaa taactataaa agagtcgcaa ccatgactgt gctattgagt
60
gagcgcagcc agattttccg ggggtccgat gcctacgcgg tgtcggacta cgtaaccag
120
catgtgggca gccactgcat tcgcctgcct cccaagggcc ggccacgggc gagtatcagc
180
catcgcacct ttgccagcct ggacctgtgc cgcacatgct acggcgctcc ggtaagggtc
240
acatcggtgg cgctggagac catctatcac ctgcagatcc tgttgagcgg gcattgccgc
300
tccagctccc gtggtgagga tgacgtggn
329

```

<210> 1954
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 1954
Thr Arg Gln Pro Glu Pro Asn Asn Tyr Lys Arg Val Ala Thr Met Thr
1      5      10      15
Val Leu Leu Ser Glu Arg Ser Gln Ile Phe Arg Gly Ala Asp Ala Tyr
20      25      30
Ala Val Ser Asp Tyr Val Asn Gln His Val Gly Ser His Cys Ile Arg
35      40      45
Leu Pro Pro Lys Gly Arg Pro Arg Ala Ser Ile Ser His Arg Thr Phe
50      55      60
Ala Ser Leu Asp Leu Cys Arg Ile Ser Tyr Gly Ala Pro Val Arg Val
65      70      75      80
Thr Ser Val Ala Leu Glu Thr Ile Tyr His Leu Gln Ile Leu Leu Ser
85      90      95
Gly His Cys Arg Ser Ser Ser Arg Gly Glu Asp Asp Val
100      105

```

<210> 1955
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 1955

acgcgtggct cgacgaaac caagtacgag acatgccga caaggtacta tcacacatgg
 60
 tgggaatactg ctggggggcgc ttcacagaca acatcaaata cgctgtagct gcccaatatt
 120
 ggaaagggcc acacaagccc gatagtggacc atcaacggat cattgtaggc tatttcaaaa
 180
 ccgccaaaca agccatgaac gcagcaaaac aattccactg gaacaccogg ctacaacaac
 240
 aatggaaaaa atggatactc ccagtcacca acggcaccgt gtccgagttt ttcacccaac
 300
 aaaaaacttt gctagacgag caagacgata gcaatagcga gctgccggag catctacaaa
 360
 acgtcatgtg cggcaaaaaca ctccaccacc aagacgacac catatcgtgg tgcac
 415

<210> 1956

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1956

Met	Pro	Asp	Lys	Val	Leu	Ser	His	Met	Val	Glu	Tyr	Cys	Trp	Gly	Arg
1				5					10					15	
Phe	Thr	Asp	Asn	Ile	Lys	Tyr	Ala	Val	Ala	Ala	Gln	Tyr	Trp	Lys	Gly
			20					25					30		
Pro	His	Lys	Pro	Asp	Ser	Asp	His	Gln	Arg	Ile	Ile	Val	Gly	Tyr	Phe
		35					40					45			
Lys	Thr	Ala	Lys	Gln	Ala	Met	Asn	Ala	Ala	Lys	Gln	Phe	His	Trp	Asn
	50					55					60				
Thr	Arg	Leu	Gln	Gln	Gln	Trp	Lys	Thr	Trp	Ile	Leu	Pro	Val	His	Asn
	65				70				75					80	
Gly	Thr	Val	Ser	Glu	Phe	Phe	Thr	Gln	Gln	Lys	Thr	Leu	Leu	Asp	Glu
			85						90					95	
Gln	Asp	Asp	Ser	Asn	Ser	Glu	Leu	Pro	Glu	His	Leu	Gln	Asn	Val	Met
			100					105					110		
Cys	Gly	Lys	Thr	Leu	His	His	Gln	Asp	Asp	Thr	Ile	Ser	Trp	Cys	
		115					120						125		

<210> 1957

<211> 526

<212> DNA

<213> Homo sapiens

<400> 1957

acgcgttccg gagagatttt cctaacctct ctccgagctg ctgagccgat cggtgaccac
 60
 caggagctcc tccctgtgag gacaaagttc cagagtcggg gtcacggggc ttacttattg
 120
 gggaggaggc ccgccggggc cgcagtgggc gagggggcct tggcgcgctc ctgggaggtc
 180
 agacctggca cagtgtggcg aaggtttcca gtgcgatccc gaggcagggg cgcatttcgc
 240
 ggtgactgcc agcatgaacc gcagccgacc gaggttctgcg atcgggcttc tccgcagagt
 300

ggggaccctg gggaaggcgc caacttctct cctctgccca cctcactccc cgcggggctc
 360
 cctggggcgc ctgcccgggc cgcactgggc ggcctccatc gtcccttccc tctacctgca
 420
 ctgccccagg cgaggagagag gccttggccc nncaggagac cagctgcagc gggcagcggg
 480
 gtctctctcc cccaaccccc gcccatggc acggggctga accggg
 526

<210> 1958

<211> 175

<212> PRT

<213> Homo sapiens

<400> 1958

Thr	Arg	Ser	Gly	Glu	Ile	Phe	Leu	Thr	Ser	Leu	Arg	Ala	Ala	Glu	Pro
1				5					10					15	
Ile	Gly	Asp	His	Gln	Glu	Leu	Leu	Pro	Val	Arg	Thr	Lys	Phe	Gln	Ser
			20					25					30		
Arg	Gly	His	Gly	Pro	Tyr	Leu	Leu	Gly	Arg	Arg	Pro	Ala	Gly	Ala	Ala
		35					40					45			
Val	Gly	Glu	Gly	Pro	Leu	Ala	Arg	Ser	Trp	Glu	Val	Arg	Pro	Gly	Thr
	50					55				60					
Val	Trp	Arg	Arg	Phe	Pro	Val	Arg	Ser	Arg	Val	Glu	Gly	Ala	Phe	Arg
65					70				75					80	
Gly	Asp	Cys	Gln	His	Glu	Pro	Gln	Pro	Thr	Glu	Phe	Cys	Asp	Arg	Ala
			85					90					95		
Ser	Pro	Gln	Ser	Gly	Asp	Pro	Gly	Glu	Gly	Ala	Asn	Phe	Ser	Pro	Leu
			100				105						110		
Pro	Thr	Ser	Leu	Pro	Ala	Gly	Val	Pro	Gly	Pro	Pro	Ala	Arg	Ala	Ala
			115				120					125			
Leu	Gly	Gly	Leu	His	Arg	Pro	Phe	Pro	Leu	Pro	Ala	Leu	Pro	Gln	Ala
	130					135					140				
Gly	Glu	Arg	Pro	Trp	Pro	Xaa	Glu	Gly	Pro	Ala	Ala	Ala	Gly	Ser	Gly
145					150				155					160	
Val	Leu	Leu	Pro	Gln	Pro	Pro	Pro	His	Gly	Thr	Gly	Leu	Asn	Arg	
			165					170					175		

<210> 1959

<211> 378

<212> DNA

<213> Homo sapiens

<400> 1959

gtgcaccgga cggctcctcc aacggatcat ggcacggccc agcgggaaggc tcaccgcagtg
 60
 cgtcagaagg atcagggcgc ttgtcgtcgt cagacttcag gacatccac gacatgggtga
 120
 acggctggga ggagaccttg tcccgcgcg tcttggcgcc gacaacaaca ccgctcatgg
 180
 tgtatttttc ggcgatgagt aagaaccagt gggcatgctg atgaccttg atcggcagtg
 240
 aggtccttt gaccacctga tatgtgtcat cagcgaggaa ggtgccgagt ttggcgttct
 300

cgctgccttc ggggtgaattg ccgaggaggt acatcttgcc tggaccgcta atcgcggtga
 360
 agtcgacgcg caacgcgt
 378

<210> 1960
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 1960
 Met Tyr Leu Leu Gly Asn Ser Pro Glu Ala Asp Glu Asn Ala Lys Leu
 1 5 10 15
 Gly Thr Phe Leu Ala Asp Asp Thr Tyr Gln Val Val Lys Gly Ala Ser
 20 25 30
 Leu Pro Ile Lys Gly His Gln His Ala His Trp Phe Phe Thr His Ala
 35 40 45
 Gly Lys Tyr Thr Met Ser Gly Val Val Val Gly Ala Lys Thr Asp Gly
 50 55 60
 Asp Lys Val Ser Ser Gln Pro Phe Thr Met Ser Trp Asp Val Leu Lys
 65 70 75 80
 Ser Asp Asp Asp Lys Arg Pro Asp Pro Ser Asp Asp Ser Gly Glu Pro
 85 90 95
 Ser Ala Gly Pro Ser His Asp Pro Leu Glu Glu Pro Ser Gly Ala
 100 105 110

<210> 1961
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 1961
 ggatccacc cggaaaccgg caggatgaag ggggcaagtg aggagaagct ggcattctgtg
 60
 tccaacctgg tcaactgtgtt tgagaatagc aggacccag aagcagcacc cagaggccag
 120
 aggctagagg acgtgcatca ccgccctgag tgcaggcctc ccgagtcccc aggaccacgg
 180
 gagaagacga atgtcgggga ggcctgtggg tctgagccca ggacagtcag caggaggtac
 240
 ctgaactccc tgaagaacaa gctgtccagc gaagcctgga ggaatatcttg ccagcctgtg
 300
 accctctcag gatcggggac gcaggagcca gagaagaaga tcgtccagga gctgctggag
 360
 acagagcagg cctatgtggc gcgc
 384

<210> 1962
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1962
 Gly Ser Thr Pro Glu Thr Gly Arg Met Lys Gly Ala Ser Glu Glu Lys

```

      1           5           10           15
Leu Ala Ser Val Ser Asn Leu Val Thr Val Phe Glu Asn Ser Arg Thr
      20           25           30
Pro Glu Ala Ala Pro Arg Gly Gln Arg Leu Glu Asp Val His His Arg
      35           40           45
Pro Glu Cys Arg Pro Pro Glu Ser Pro Gly Pro Arg Glu Lys Thr Asn
      50           55           60
Val Gly Glu Ala Val Gly Ser Glu Pro Arg Thr Val Ser Arg Arg Tyr
      65           70           75           80
Leu Asn Ser Leu Lys Asn Lys Leu Ser Ser Glu Ala Trp Arg Lys Ser
      85           90           95
Cys Gln Pro Val Thr Leu Ser Gly Ser Gly Thr Gln Glu Pro Glu Lys
      100          105          110
Lys Ile Val Gln Glu Leu Leu Glu Thr Glu Gln Ala Tyr Val Ala Arg
      115          120          125

```

<210> 1963

<211> 323

<212> DNA

<213> Homo sapiens

<400> 1963

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nnncccttcc taccctccca tactcccccac cccctcttcc cccctgtgc tgagcttgca
60
ggcatgaaac acccacctgg cctctctccc tctgttttgc cccctctgtc gtctctctcc
120
cacagctgcc tggctcttcg gcgtcagtc accaccttct gcagctctcc ctcaccctgg
180
cgaccactca ggcatgcata tcgcggggccc ccttcagacc tctcggggtc atcttccccct
240
tccctggcca ttatttttct tcactctgggc tggggcccgga gggcgcttcc ccccttctct
300
cttcttttct tttttttctc ttt
323

```

<210> 1964

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1964

```

Xaa Pro Phe Leu Pro Ser His Thr Pro His Pro Ser Ser Ser Pro Cys
      1           5           10           15
Ala Glu Leu Ala Gly Met Lys His Pro Pro Gly Leu Ser Pro Ser Val
      20           25           30
Leu Pro Leu Leu Ser Ser Leu Ser His Ser Cys Leu Ala Leu Arg Arg
      35           40           45
Gln Ser Thr Thr Phe Cys Ser Ser Pro Ser Pro Trp Arg Pro Leu Arg
      50           55           60
His Ala Ser Arg Gly Pro Pro Ser Asp Leu Ser Gly Ser Ser Ser Pro
      65           70           75           80
Ser Leu Ala Ile Ile Phe Leu His Leu Gly Trp Ala Arg Arg Gly Val
      85           90           95
Pro Pro Leu Pro Leu Leu Ser Phe Phe Phe Ser

```

100

105

<210> 1965

<211> 1416

<212> DNA

<213> Homo sapiens

<400> 1965

cggctggggc aggagctgga cgacgccacc atggacctgg agcagcagcg gcagcttggtg
 60
 agcacccctgg agaagaagca gcgcaagttt gaccagcttc tggcagagga gaaggcagct
 120
 gtacttcggg cagtggagga acgtgagcgg gccgaggcag agggccggga gcgtgaggct
 180
 cgggcccctgt cactgacacg ggcaactggag gaggagcagg agggcacgtga ggagctggag
 240
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1416

<210> 1966

<211> 472

<212> PRT

<213> Homo sapiens

<400> 1966

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			20					25					30		
Leu	Leu	Ala	Glu	Glu	Lys	Ala	Ala	Val	Leu	Arg	Ala	Val	Glu	Glu	Arg
			35				40					45			
Glu	Arg	Ala	Glu	Ala	Glu	Gly	Arg	Glu	Arg	Glu	Ala	Arg	Ala	Leu	Ser
			50			55					60				
Leu	Thr	Arg	Ala	Leu	Glu	Glu	Gln	Glu	Ala	Arg	Glu	Glu	Leu	Glu	
65					70				75					80	
Arg	Gln	Asn	Arg	Ala	Leu	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Leu	Ser	Ser
				85					90					95	
Lys	Asp	Asp	Val	Gly	Lys	Ser	Val	His	Glu	Leu	Glu	Arg	Ala	Cys	Arg
			100					105					110		
Val	Ala	Glu	Gln	Ala	Ala	Asn	Asp	Leu	Arg	Ala	Gln	Val	Thr	Glu	Leu
			115				120					125			
Glu	Asp	Glu	Leu	Thr	Ala	Ala	Glu	Asp	Ala	Lys	Leu	Arg	Leu	Glu	Val
			130			135					140				
Thr	Val	Gln	Ala	Leu	Lys	Thr	Gln	His	Glu	Arg	Asp	Leu	Gln	Gly	Arg
145					150					155					160
Asp	Glu	Ala	Gly	Glu	Glu	Arg	Arg	Arg	Gln	Leu	Ala	Lys	Gln	Leu	Arg
			165						170					175	
Asp	Ala	Glu	Val	Glu	Arg	Asp	Glu	Glu	Arg	Lys	Gln	Arg	Thr	Leu	Ala
			180					185					190		
Val	Ala	Ala	Arg	Lys	Lys	Leu	Glu	Gly	Glu	Leu	Glu	Glu	Leu	Lys	Ala
			195				200					205			
Gln	Met	Ala	Ser	Ala	Gly	Gln	Gly	Lys	Glu	Glu	Ala	Val	Lys	Gln	Leu
			210			215						220			
Arg	Lys	Met	Gln	Ala	Gln	Met	Lys	Glu	Leu	Trp	Arg	Glu	Val	Glu	Glu
				230					235					240	
Thr	Arg	Thr	Ser	Arg	Glu	Glu	Ile	Phe	Ser	Gln	Asn	Arg	Glu	Ser	Glu
			245						250					255	
Lys	Arg	Leu	Lys	Gly	Leu	Glu	Ala	Glu	Val	Leu	Arg	Leu	Gln	Glu	Glu
			260				265						270		
Leu	Ala	Ala	Ser	Asp	Arg	Ala	Arg	Gln	Ala	Gln	Gln	Asp	Arg	Asp	
			275				280					285			
Glu	Met	Ala	Asp	Glu	Val	Ala	Asn	Gly	Asn	Leu	Ser	Lys	Ala	Ala	Ile
			290			295					300				
Leu	Glu	Glu	Lys	Arg	Gln	Leu	Glu	Gly	Arg	Leu	Gly	Gln	Leu	Glu	Glu
				310					315					320	
Glu	Leu	Glu	Glu	Glu	Gln	Thr	Xaa	Ser	Glu	Leu	Leu	Asn	Asp	Arg	Tyr
			325					330					335		
Arg	Lys	Leu	Leu	Leu	Gln	Val	Glu	Ser	Leu	Thr	Thr	Glu	Leu	Ser	Ala
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Glu	Arg	Ser	Phe	Ser	Ala	Lys	Ala	Glu	Ser	Gly	Arg	Gln	Gln	Leu	Glu

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          355              360              365
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Ala  Arg  Ala  Arg  His  Lys  Met  Thr  Ile  Ala  Ala  Leu  Glu  Ser  Lys  Leu
385              390              395              400
Ala  Gln  Ala  Glu  Glu  Gln  Leu  Glu  Gln  Glu  Thr  Arg  Glu  Arg  Ile  Leu
          405              410              415
Ser  Gly  Lys  Leu  Val  Pro  Lys  Ser  Lys  Lys  Arg  Phe  Lys  Glu  Val  Val
          420              425              430
Leu  Gln  Val  Glu  Glu  Glu  Arg  Arg  Val  Ala  Asp  Gln  Leu  Arg  Asp  Gln
          435              440              445
Leu  Glu  Lys  Gly  Asn  Leu  Arg  Val  Lys  Gln  Leu  Lys  Arg  Gln  Leu  Glu
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<210> 1967

<211> 401

<212> DNA

<213> Homo sapiens

<400> 1967

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240
tagtggaactg tacgggatct catttggtcg accggaccgc cttagatagg gcgcttcgca
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401

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<210> 1968

<211> 94

<212> PRT

<213> Homo sapiens

<400> 1968

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          20              25              30
Trp  Ala  Phe  Gln  Ser  Ala  Ala  Trp  Leu  Val  Asp  Cys  Thr  Gly  Ser  His
          35              40              45
Leu  Ala  Asp  Arg  Thr  Ala  Leu  Asp  Arg  Ala  Leu  Arg  Ser  Tyr  His  Arg
          50              55              60
Tyr  His  Arg  His  Ser  Leu  Gly  Trp  His  Glu  Arg  Leu  Ile  Ser  Arg  Tyr
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Ala  Asn  Gly  Arg  Gly  Phe  His  Ala  Leu  Glu  Lys  Leu  Met  Leu

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85

90

<210> 1969
 <211> 464
 <212> DNA
 <213> Homo sapiens

<400> 1969
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 180
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 240
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 464

<210> 1970
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 1970
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 20 25 30
 Leu Leu Gly His Val Ala Asn Thr Gln Val Met Ala Thr Gln Arg Asp
 35 40 45
 Leu Lys Pro Ser Val Phe Val Asn Leu Ser Ser Ser Glu Gly Leu Pro
 50 55 60
 Val Ser Met Met Glu Val Ala Ser Leu Gly Ile Pro Ile Ile Ala Thr
 65 70 75 80
 Gly Val Gly Gly Val Gly Glu Ile Val Ser Ser Asp Asn Gly His Leu
 85 90 95
 Leu Pro Ala Glu Phe Thr Asp Thr Gln Ala Ser Asp Ala Leu Val Gln
 100 105 110
 Leu Ala Arg Leu Ser Glu Asp Glu Tyr Gln Gln Val Cys Gln Ala Ser
 115 120 125
 Arg Gln Val Trp Glu Glu Lys Phe Arg Ala Ser Val Val Tyr Pro Glu
 130 135 140
 Phe Cys Arg Glu Cys Trp Gly Asp Ala Asp
 145 150

<210> 1971
 <211> 520

<212> DNA

<213> Homo sapiens

<400> 1971

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 180
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 240
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 300
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<210> 1972

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1972

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Glu	Ile	Ser	Gly	Lys	Met	Asn	Thr	Tyr	Met	Asn	Ser	Thr	Thr	Ser	Lys
			20					25					30		
Lys	Asp	Thr	Gly	Val	Gln	Thr	Asp	Asp	Leu	Asn	Ile	Gly	Ile	Phe	Thr
			35				40					45			
Asn	Ala	Glu	Ser	His	Cys	Gly	Ser	Leu	Met	Glu	Arg	Asp	Ile	Thr	Asn
			50			55					60				
Cys	Ser	Ser	Pro	Glu	Ile	Ser	Ala	Glu	Leu	Ile	Gly	Gln	Phe	Ser	Thr
			65			70				75			80		
Lys	Lys	Asn	Lys	Gln	Glu	Leu	Thr	Gln	Asp	Lys	Gly	Ala	Ser	Leu	Glu
			85					90					95		
Lys	Glu	Asn	Asn	Arg	Cys	Asn	Asp	Gln	Cys	Asn	Gln	Phe	Thr	Arg	Ile
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Glu	Lys	Gln	Thr	Lys	Gln										
			115												

<210> 1973

<211> 331

<212> DNA

<213> Homo sapiens

<400> 1973

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 180
 ccgcctcgat ctttctccgc ttggggcgctg cgcggaacga cttttctgc gccgtcgatg
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 331

<210> 1974
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1974
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 35 40 45
 Gly Ile Asp Leu Ser Pro Ala Arg Ser Phe Ser Ala Trp Ala Leu Arg
 50 55 60
 Gly Thr Thr Phe Ser Ala Pro Ser Met Thr Lys Ala Ser Arg Ser Ser
 65 70 75 80
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 85 90 95
 Pro Pro Val Lys Ser Cys Ala
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<210> 1975
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 1975
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 180
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 240
 ctcgactggt gcaggccgct tcggaggcgc caaaggctgc tgccgaagtg gttgccgagc
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 370

<210> 1976

<211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1976
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 20 25 30
 Arg Leu Arg Gly Gly Leu His Gln Ser Arg Asn Leu Gly Asp Arg Val
 35 40 45
 Val Gly Val Gly Leu Cys Leu Arg Arg Asp Val Ala Arg Ser Leu Arg
 50 55 60
 Gln Arg Ile Ala Asn Leu Leu Thr Ala Arg Arg Val Gly Thr Arg
 65 70 75 80
 Leu Leu Pro Arg Leu Ala Gln Leu Gly Ala His Cys Thr Gln Arg Ile
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 100 105 110
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<210> 1977
 <211> 551
 <212> DNA
 <213> Homo sapiens

<400> 1977
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 180
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 240
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<210> 1978
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 1978

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          20          25          30
Pro Leu Pro Ala Val Ser Pro Thr Ser Phe Ile Pro Pro Val Thr Arg
          35          40          45
Glu Val Gln Ile Phe Gln Pro Gly His Cys Leu Pro Ser Arg Leu Ala
          50          55          60
Pro Pro Val His Leu Leu Cys Ser Ser Leu Cys Asn Ser Leu Ala Ala
65          70          75          80
Cys Leu Leu Ser Pro Leu Thr Gln Leu Leu Thr Cys Pro Thr Pro Ala
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Gln Pro Thr Ser Ser
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<210> 1979

<211> 5530

<212> DNA

<213> Homo sapiens

<400> 1979

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120
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240
gccgcccagc ccgcgcgcgc gcagggggag gaggtgcagg agcgagccga gcctcccgcc
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960

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<210> 1980

<211> 929

<212> PRT

<213> Homo sapiens

<400> 1980

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Gln Pro Pro Thr Ala Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly			
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Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu			
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Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu			
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Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg			
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Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly			
	100	105	110
Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser			
	115	120	125
His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala			
	130	135	140
Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His			
	145	150	155
Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu			
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Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val			
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Tyr Thr Arg Arg Ala Ser Ala Ser Arg Pro Cys Arg Arg Ala Pro Ala			
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Ala Lys Pro Pro Arg Pro His Arg Arg Pro Thr Ser Met Leu Arg Arg			
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Thr Ala Thr Arg Ala Asp Ala Gln His Ala Ser Gln Leu Leu Asp Gln			
	225	230	235
Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp Arg			
	245	250	255
Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Leu			
	260	265	270
Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln His			
	275	280	285
Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His Ala			
	290	295	300
Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val Leu			
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Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr Thr			
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	370	375	380
Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp Gly			
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Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu Gly			
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Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser Thr			
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Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala Ser			

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 595 600 605
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 Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val Gln
 820 825 830
 Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser Phe
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 Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser His
 850 855 860
 Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val Thr

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Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His Thr
                        885                      890                      895
Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly Cys
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Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys Lys
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<210> 1981

<211> 327

<212> DNA

<213> Homo sapiens

<400> 1981

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<210> 1982

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1982

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20      25      30
Gly Val Asn Pro Arg Gly Val Asp Asn Arg Thr Ser Met Ala Val Phe
35      40      45
Ser Pro Pro Lys Ala Ala Gly Gly Arg Cys Pro Gly Pro Cys Arg
50      55      60
Ile Met Ala Trp Pro Gly Gln Arg Ala Ser Ser Ser Gly Arg Gly Arg
65      70      75      80
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<210> 1983

<211> 383

<212> DNA

<213> Homo sapiens

<400> 1983

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 240
 gaagttaatc gtgcagggtg agtcgttaat aaattcgccg gcgatgcagt actagccatt
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<210> 1984

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1984

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			20					25					30		
Ala	Gln	Pro	Glu	Glu	Arg	Asn	Val	Pro	Lys	Arg	Asp	Ala	Ser	Val	Phe
		35					40					45			
Phe	Ile	Asp	Ile	Ile	Gly	Ser	Thr	Lys	Leu	Ser	Leu	Glu	Tyr	Asp	Ser
	50					55				60					
Tyr	Thr	Val	Val	Asp	Leu	Leu	Asn	Arg	Phe	Tyr	Thr	Ile	Val	Val	Glu
	65				70				75				80		
Glu	Val	Asn	Arg	Ala	Gly	Gly	Val	Val	Asn	Lys	Phe	Ala	Gly	Asp	Ala
			85					90					95		
Val	Leu	Ala	Ile	Phe	Asn	Val	Pro	His	Asp	His	Pro	Asp	Pro	Ala	Gly
			100				105						110		
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<210> 1985

<211> 381

<212> DNA

<213> Homo sapiens

<400> 1985

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 240

cagaaccgaa gaaatatttt gcatgcgaaa ctcaattgag ccttcagtac ggccaaccaa
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 381

<210> 1986

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1986

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			20				25						30		
Ile	Glu	Phe	Arg	Met	Gln	Asn	Ile	Ser	Ser	Val	Leu	Val	Gln	Met	Gly
		35				40						45			
Leu	Asp	Arg	Ile	Lys	Gly	Tyr	Lys	Ala	Cys	Glu	Pro	Met	Trp	Gly	Pro
	50				55				60						
Gly	Gly	Arg	Pro	Thr	Thr	Phe	Ala	Arg	Pro	Phe	Ala	Asp	Thr	Arg	Val
	65			70					75					80	
Phe	Glu	Ser	Asp	Glu	Thr	Ala	Gln	Thr	Ala	Asp	Glu	Gln	Thr	Leu	Ile
			85				90						95		
Arg	Arg	Ala	Asn	Lys	Leu	Gln	Leu	Lys	Arg	Phe	Asp	Gln	Val	Pro	Asp
			100				105						110		
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<210> 1987

<211> 419

<212> DNA

<213> Homo sapiens

<400> 1987

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 300
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 419

<210> 1988

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1988

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 20           25           30
Ile Gly Phe Met Gly Val Arg Thr Met Ile Asn Arg Tyr Leu Leu Arg
 35           40           45
Thr Pro Asp Lys Gln Ala Leu Glu Val Pro Gln Tyr Phe Trp Met Arg
 50           55           60
Val Ala Met Gly Leu Ser Leu Thr Glu Asp Asp Pro Thr Ser Ser Ala
 65           70           75           80
Xaa Cys Leu Tyr Asp Ser Met Ser Asn Leu Arg His Leu Ala Ala Gly
 85           90           95
Ser Thr Leu Val Asn Ala Gly Thr His Xaa Ala Gln Leu Ser Asn Cys
100           105           110
Phe Val Met Arg Thr Glu Asp Asn Leu Glu His Ile Ala Gln Thr Ile
115           120           125
Arg Asp Val Met Trp Ile Thr Lys Gly Thr Val
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<210> 1989

<211> 10795

<212> DNA

<213> Homo sapiens

<400> 1989

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780

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<212> PRT

<213> Homo sapiens

<400> 1992

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 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 1994
 Xaa Lys Thr Tyr Gly Met Thr Arg Ala Leu Asp His Ile Asp Ile Ala
 1 5 10 15
 Ile Pro Ala Gly Gln Ser Val Ala Val Met Gly Pro Ser Gly Ser Gly

[illegible]

<210> 1995

<211> 285

<212> DNA

<213> Homo sapiens

<400> 1995

catcaccacc	attatcaaca	ccatcatcac	caccattatc	acctttatca	ccaccatcat
60					
caccatcacc	accatcatca	ctaccaccat	cacgcccac	atcatgtgat	gactctcaat
120					
actgtctctca	tcatgtgtga	cttggaactgt	ggaccagccc	ctcgggctct	gctctgtgga
180					
ccatattctt	ttgtctcttg	ttcctgagaa	gctggggagt	gagacccgat	aagggtgtgt
240					
acagacactt	gtgaccccaa	attccatgag	acagaggacc	tcccn	
285					

<210> 1996

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1996

His	His	His	His	Tyr	Gln	His	His	His	His	His	His	Tyr	His	Leu	Tyr
1				5					10					15	
His	His	His	His	His	His	His	His	His	His	His	Tyr	His	His	His	Ala
				20					25					30	
His	His	His	His	Val	Met	Thr	Leu	Asn	Thr	Val	Leu	Ile	Met	Cys	Asp

35
40
 Asp Cys Gly Pro Ala Pro Arg Ala Leu Leu Cys
50
55

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<210> 1997
<211> 313
<212> DNA
<213> Homo sapiens
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400> 1997
ccgctggtgg tgggtgctgct gattggcatg gccatctata ccttcgcaa gaaagacctg
60
ggcaagctgc acaagccggc cagcatcggc cggcgcgaga tgctggtggg gctggccatc
120
ggtggcgcca tcggttttta cgacggcgctg ttcggggcgg gtaccggcag ttctctgatg
180
ttctctgttc tgcggttttt gcgttttgat ttcttgcatt cttctgccgc ggccaagggt
240
gtcaacctgg ccaccaatgt ggcggcactg tgctttttca ttccacggcg caatgtgctg
300
tatggctacg cgt
313

```

```
<210> 1998
<211> 104
<212> PRT
<213> Homo sapiens
```

```

400> 1998
Pro Leu Val Val Val Leu Leu Ile Gly Met Ala Ile Tyr Thr Phe Arg
1      5      10
Lys Lys Asp Leu Gly Lys Leu His Lys Pro Val Ser Ile Gly Arg Arg
20     25     30
Glu Met Leu Val Gly Leu Ala Ile Gly Gly Gly Ile Gly Phe Tyr Asp
35     40     45
Gly Leu Phe Gly Pro Gly Thr Gly Ser Phe Leu Met Phe Leu Phe Val
50     55     60
Arg Phe Leu Arg Phe Asp Phe Leu His Ala Ser Ala Ala Lys Val
65     70     75     80
Val Asn Leu Ala Thr Asn Val Ala Ala Leu Cys Phe Phe Ile Pro Ser
85     90     95
Gly Asn Val Leu Tyr Gly Tyr Ala
100

```

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<210> 1999
<211> 399
<212> DNA
<213> Homo sapiens
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c400> 1999
cccgccggcgca agttggaatg gcaaaacatt ttcatgcccg gcgagcaagg tagcttgagt
60
tccactgcgc agagggcgaga tgtgaagtac tccggtagctg ttcatattac cgggtgtggc
120

```

ggaagaatgg atcttactct cgctgaccct gagattgtcg ttaacaatgg cgatgatcat
 180
 gtgattatgt ctgtgaagtc caagactatg gtcgggcagt tggttgacta tggccgtata
 240
 actttcgttg atatgaccgg ctctattacg cagggtcaaa acgatgcagc tcaggttgtg
 300
 gggaccaatg tcaagctgaa tagccaagcc gtcgatgcat tcgctggcct ctatcaagct
 360
 ggaaagccca tggatgacat cgattcgtcc ttaaagctt
 399

<210> 2000

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2000

Met	Asp	Leu	Thr	Leu	Ala	Asp	Pro	Glu	Ile	Val	Val	Asn	Asn	Gly	Asp
1				5					10					15	
Asp	His	Val	Ile	Met	Ser	Val	Lys	Ser	Lys	Thr	Met	Val	Gly	Gln	Leu
				20				25					30		
Val	Asp	Tyr	Gly	Arg	Ile	Thr	Phe	Val	Asp	Met	Thr	Gly	Ser	Ile	Thr
				35			40					45			
Gln	Gly	Gln	Asn	Asp	Ala	Ala	Gln	Val	Val	Gly	Thr	Asn	Val	Lys	Leu
				50		55					60				
Asn	Ser	Gln	Ala	Val	Asp	Ala	Phe	Ala	Gly	Phe	Tyr	Gln	Ala	Gly	Lys
65				70					75					80	
Pro	Met	Asp	Asp	Ile	Asp	Ser	Ser	Leu	Lys	Leu					
				85					90						

<210> 2001

<211> 1434

<212> DNA

<213> Homo sapiens

<400> 2001

nngaataag gacgtcataa ttgtctgac agcagtgacg ctgactggag gagggacaaa
 60
 ttggcgagga cccactgca ctatgcagct gctaacggta gctaccagtg tgcagtaaca
 120
 ttggtgactg ctggggcagg tgctcaacgag gccgactgta aaggctgctc tccctccac
 180
 tacgctgcgc cttctgacac ttacaggnag agcgggaaccc catacacctt ccagccatga
 240
 tgccgaagag ganncgagcc actgaaggag tcccgagga aggaggcctt cttctgtctg
 300
 gagttcttac tggataacgg tgcagacccc tccctgcggg acaggcaggg ctacacagct
 360
 gtgcactatg cagccgccta tggcaacaga cagaacctcg aactgtctct agaaatgtcc
 420
 ttttaactgcc tggaggatgt ggagagcacc attccagtca gcccttgca cttagctgcc
 480
 tacaacgggc actgtgaagc cttgaagacg ctggcggaga cgctggtgaa tctggacgta
 540

agggaccaca agggccggac cgcactcttc ctggccacgg agcgcgggctc tactgagtgt
 600
 gtggaggtgc ttacagccca cggcgccctct gccctcatca aggagcgcaa gcgcaagtgg
 660
 acacccccgc acgccgctgc tgccctctggc cacactgact ccctgcactt gctgatcgac
 720
 agtggggaac gagctgacat cacagatgtc atggatgcct atggacagac cccactgatg
 780
 ctggccatca tgaatggcca tgtggactgt gtacatctgc tgctagagaa aggatccaca
 840
 gctgatgtgc ctgacctccg gggccgcact gccctccacc gcggggcagt gactggctgt
 900
 gaggactgcc tggctgccct gctggaccac gacgcatttg tgctgtgccg agactttaag
 960
 ggccgcacgc ccattcacct ggcctcagcc tgtggccaca ctgcagtact gcggaccctg
 1020
 ctgcaggctg ccctttccac agatccccct gatgccgggg tggattacag cggatactcg
 1080
 cccatgcact gggcctccta cactggacat gaagattgtc tggagtgtt acttgaacac
 1140
 agccccgtttt cgtacctgga aggaaccccc ttcactcctt tgcactgtgc agtgattaat
 1200
 aaccaagaca gcaccacaga gatgctactg ggagctctgg gtgccaagat tgtgaacagc
 1260
 cgagatgccca aaggacggac cccccctcac gccgtgcct tcgcggaaca tgtctctggg
 1320
 ctccggatgc tgctgcagca tcaagctgag gtgaacgcca ctgaccacac tggccgcact
 1380
 gcgctcatga cggcggctga gaaaggcgac accgctgtgt tggaaatttct gctg
 1434

<210> 2002

<211> 79

<212> PRT

<213> Homo sapiens

<400> 2002

Xaa	Asn	Glu	Gly	Arg	His	Asn	Leu	Leu	Ile	Ser	Ser	Ala	Ala	Asp	Trp
1				5					10					15	
Arg	Arg	Asp	Lys	Phe	Gly	Arg	Thr	Pro	Leu	His	Tyr	Ala	Ala	Ala	Asn
			20					25					30		
Gly	Ser	Tyr	Gln	Cys	Ala	Val	Thr	Leu	Val	Thr	Ala	Gly	Ala	Gly	Val
			35					40				45			
Asn	Glu	Ala	Asp	Cys	Lys	Gly	Cys	Ser	Pro	Leu	His	Tyr	Ala	Ala	Ala
	50					55					60				
Ser	Asp	Thr	Tyr	Arg	Xaa	Ser	Gly	Thr	Pro	Tyr	Thr	Phe	Gln	Pro	
65					70					75					

<210> 2003

<211> 688

<212> DNA

<213> Homo sapiens

<400> 2003

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ntcatgacta cggagacact gaagaaaatt cagattgata ggcagttttt cagcgatgtg
60
attgcagata ccattaagga gttgcaagat tcggccactt acaacagtct cctgcaagct
120
ttgagcaaaag agaggggaaaa caaaatgcat ttctatgaca tcatttccag ggaggaaaaa
180
ggaagaaaaac agataatatc acttcaaaaa cagctaatta atttcaaaaa ggaatggcaa
240
tttgaagtcc agagtcagaa tgagtatatt gctaacctca aggaccaact gcaagagatg
300
aaggcaaaat ccaacttgga gaatcgctac atgaaaaacca ataccgagct gcagattgcc
360
cagacccaga aaaagtgtaa cagaacagag gaactcttgg tggaagagat tgagaaactc
420
aggatgaaaa ccgaagaaga ggcccggact catcacagaa ttgaaatgtt ccttagaaaa
480
gagcagcagg tgggtcccca cagcttttct atgctttgac ttttttttgg tactctgctt
540
atactgagga aacaaaaaga atattttgaa ggaaaaccaa ccatcattct ttcagcctaa
600
tgaactttag ctcatgtttt ctttcagggt tatgcacttg aatagatatc ttatatagct
660
gtaatttgag agagtgcagg taaaattg
688

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<210> 2004

<211> 172

<212> PRT

<213> Homo sapiens

<400> 2004

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Xaa Met Thr Thr Glu Thr Leu Lys Lys Ile Gln Ile Asp Arg Gln Phe
1 5 10 15
Phe Ser Asp Val Ile Ala Asp Thr Ile Lys Glu Leu Gln Asp Ser Ala
20 25 30
Thr Tyr Asn Ser Leu Leu Gln Ala Leu Ser Lys Glu Arg Glu Asn Lys
35 40 45
Met His Phe Tyr Asp Ile Ile Ser Arg Glu Glu Lys Gly Arg Lys Gln
50 55 60
Ile Ile Ser Leu Gln Lys Gln Leu Ile Asn Phe Lys Lys Glu Trp Gln
65 70 75 80
Phe Glu Val Gln Ser Gln Asn Glu Tyr Ile Ala Asn Leu Lys Asp Gln
85 90 95
Leu Gln Glu Met Lys Ala Lys Ser Asn Leu Glu Asn Arg Tyr Met Lys
100 105 110
Thr Asn Thr Glu Leu Gln Ile Ala Gln Thr Gln Lys Lys Cys Asn Arg
115 120 125
Thr Glu Glu Leu Leu Val Glu Glu Ile Glu Lys Leu Arg Met Lys Thr
130 135 140
Glu Glu Glu Ala Arg Thr His Thr Glu Ile Glu Met Phe Leu Arg Lys
145 150 155 160
Glu Gln Gln Val Gly Pro His Ser Phe Ser Met Leu
165 170

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<210> 2005
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 2005
 gctagcacca agccaagggt atgtttcctt gcttgcatgt ggggtttctg gccagtcagc
 60
 caagtgaact gattgacccc cagccctgtg gggaatttca ggggggtatt gtcttggtca
 120
 tcggagtcag ggggtggcctt tnagccaagg ctgcattaac ttttgggaaa agaaatggga
 180
 agcccgccgt gtcacagggt ctctgacgg gctgggtagg gtttgccctt atcttacagc
 240
 cagtgtctgtg tttgctcaga tggacgcaca tggaaaccag gctaggatca tcttcccaat
 300
 gtctactccc tgctttgggtc tgtcctgaaa acaattgcaa agacattgtg gctg
 354

<210> 2006
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 2006
 Met Phe Pro Cys Leu His Val Gly Phe Leu Ala Ser Gln Pro Ser Glu
 1 5 10 15
 Leu Ile Asp Pro Gln Pro Cys Gly Glu Phe Gln Gly Gly Ile Val Leu
 20 25 30
 Val Ile Gly Val Arg Gly Gly Leu Xaa Ala Lys Ala Ala Leu Thr Phe
 35 40 45
 Gly Lys Arg Asn Gly Lys Pro Ala Val Ser Gln Gly Leu Leu Thr Gly
 50 55 60
 Trp Val Gly Phe Gly Leu Ile Leu Gln Pro Val Leu Cys Leu Leu Arg
 65 70 75 80
 Trp Thr His Met Glu Thr Arg Leu Gly Ser Ser Ser Gln Cys Leu Leu
 85 90 95
 Pro Ala Leu Val Cys Pro Glu Asn Asn Cys Lys Asp Ile Val Ala
 100 105 110

<210> 2007
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 2007
 nnaacgctgc catgtgcatg tgtatatgca tgtatgtgcg tatgtgtgtg catgtgtgtg
 60
 tgtatatgca tgtgtgtatg tgcattgtacg tgttngtgca tatgcgtgtg catgcatgcg
 120
 tgtgcgtatg tgtgcatann catgtgcaca catgtacaca cgtgtacatg ttcattgcatg
 180
 tgcacgtgca tatgtgtaca cgtgtatgcg tgtacatgta tgagcatatg tacacgtgtg
 240

gatgtgtgtg tatgcatgtg tgtgtgcaca gatatgcctt ttcctttcat acaggctggg
 300
 ttgagtattg ctggtaggca gggacaactt tccgt
 335

<210> 2008
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 2008
 Xaa Arg Val Pro Cys Ala Cys Val Tyr Ala Cys Met Cys Val Cys Val
 1 5 10 15
 Cys Met Cys Val Cys Ile Cys Met Cys Val Cys Ala Cys Thr Cys Xaa
 20 25 30
 Cys Ile Cys Val Cys Met His Ala Cys Ala Tyr Val Cys Ile Xaa Met
 35 40 45
 Cys Thr His Val His Thr Cys Thr Cys Ser Cys Met Cys Thr Cys Ile
 50 55 60
 Cys Val His Val Tyr Ala Cys Thr Cys Met Ser Ile Cys Thr Arg Val
 65 70 75 80
 Asp Val Cys Val Cys Met Cys Val Cys Thr Asp Met Pro Phe Pro Phe
 85 90 95
 Ile Gln Ala Gly Leu Ser Ile Ala Gly Arg Gln Gly Gln Leu Ser
 100 105 110

<210> 2009
 <211> 288
 <212> DNA
 <213> Homo sapiens

<400> 2009
 gacatcaccc cgctgtctggc caaccccaac gggtttctccg cagcgatcga ggaactgggtg
 60
 ctgcgttccc caccgcacat cgacgtgtgc gtcggcatgg aggcctcggg cttcctcttc
 120
 gcagctccgg tcgccctggc catcggggca ggattcgtgc cggtcgcaaa gccgggggaa
 180
 ctccccggcc aggtgtattc cgagaccttt gccatggagt acggggaggga gaccctcacc
 240
 gtccaccagt acgccatcaa gccgggggtcg cgcgtcatca tcgtcgac
 288

<210> 2010
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 2010
 Asp Ile Thr Pro Leu Leu Ala Asn Pro Asn Gly Phe Ser Ala Ala Ile
 1 5 10 15
 Glu Glu Leu Val Leu Arg Ser Pro Arg Asp Ile Asp Val Val Val Gly
 20 25 30
 Met Glu Ala Arg Gly Phe Leu Phe Ala Ala Pro Val Ala Leu Ala Ile

```

          35              40              45
Gly Ala Gly Phe Val Pro Val Arg Lys Pro Gly Lys Leu Pro Gly Gln
 50              55              60
Val Tyr Ser Glu Thr Phe Ala Met Glu Tyr Gly Glu Glu Thr Leu Thr
 65              70              75              80
Val His Gln Tyr Ala Ile Lys Pro Gly Ser Arg Val Ile Ile Val Asp
          85              90              95

```

<210> 2011

<211> 384

<212> DNA

<213> Homo sapiens

<400> 2011

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ctcgagcagt ctctgcatgt taacaccccc gtacggcccg taaagcataa ccgtctccga
60
cttgccgcgcg cctgcgtgct tcgctaggcg gccggtgaac ccacctgagg gccggatgta
120
gaagtcaacg gtggacgacg ggttgaggagg tttgttgatt ggcgagtgagg gaagcgagca
180
gattgtaaat tggtagaacg gggaacagag attagtccaa atgacgagaa cgacaacaga
240
atgttgattg ttatagccat ctctggagga gagggaaaaa gccaggatgc tagacagcga
300
aagcaaatgt gagccgaggg gacagtgcgc tccttcgttc ctcggaact cccacgaggg
360
accttcatt ctgtggcgag aatt
384

```

<210> 2012

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2012

```

Met Glu Gly Ala Ser Trp Glu Leu Pro Arg Asn Glu Gly Arg His Cys
 1              5              10              15
Pro Leu Gly Ser His Leu Leu Ser Leu Ser Arg Tyr Leu Ala Phe Ser
          20              25              30
Leu Ser Ser Arg Asp Gly Tyr Asn Asn Gln His Ser Val Val Val Leu
          35              40              45
Val Ile Val Thr Asn Leu Cys Ser Pro Phe Tyr Gln Phe Thr Ile Cys
          50              55              60
Ser Leu Pro His Ser Pro Ile Asn Lys Pro Ser Asn Pro Ser Ser Thr
          65              70              75              80
Val Asp Phe Tyr Ile Arg Pro Ser Gly Gly Phe Thr Gly Arg Leu Ala
          85              90              95
Lys His Ala Gly Gly Gly Lys Ser Glu Thr Val Met Leu Tyr Gly Pro
          100              105              110
Tyr Gly Gly Val Asn Met Gln Arg Leu Leu Glu
          115              120

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<210> 2013

<211> 309

<212> DNA
<213> Homo sapiens

<400> 2013
gcgtatcccc acggctacgg catgaccgag cttatcggcc cggacctgtc caccgtcgaa
60
gccttgctcg cccaggtcca cagcacacaa accccgggtgt acctggccaa tatcaatgcc
120
gataaccaga cggttatcgc gggcagcgac ggggcaatga aagcagtcgc caatctggtc
180
cgcggaacg gcgtcgccaa acgcttgccc gtcagcgtgc cgtccattg tgcgtgctg
240
gaaaaacctg ccgaaacact ggcccaagcc ttcgctgaag tgacgtgaa aacgccgncn
300
nnnccnncn
309

<210> 2014
<211> 103
<212> PRT
<213> Homo sapiens

<400> 2014
Ala Tyr Pro His Gly Tyr Gly Met Thr Ala Leu Ile Gly Pro Asp Leu
1 5 10 15
Ser Thr Val Glu Ala Leu Leu Ala Gln Val His Ser Thr Gln Thr Pro
20 25 30
Val Tyr Leu Ala Asn Ile Asn Ala Asp Asn Gln Thr Val Ile Ala Gly
35 40 45
Ser Asp Gly Ala Met Lys Ala Val Ala Asn Leu Val Arg Gly Asn Gly
50 55 60
Val Ala Lys Arg Leu Ala Val Ser Val Pro Ser His Cys Ala Leu Leu
65 70 75 80
Glu Lys Pro Ala Glu Thr Leu Ala Gln Ala Phe Ala Glu Val Thr Leu
85 90 95
Lys Thr Pro Xaa Xaa Pro Xaa
100

<210> 2015
<211> 329
<212> DNA
<213> Homo sapiens

<400> 2015
acgcgtgcca tgctcggtat ccgccgccac caccctgtct ttgggaccgg cgagttcacc
60
gatctaggcg ggcgggacat ggcagtgatg tccttctact gtcacaacga gcacgaaacg
120
gtcctgtgccc tggctaactc ctccgatact gagcggacgg ttgcccttca ccttcacaaa
180
ttcgcggggc tggcggggctc ttctctctac catggtcagg acgcgcaacc agtaaaagct
240
gacggaacac tgtccgtacc gttgtggcca tatggctatc gatggctgca gatgtccggg
300

gaggagaggt catgaccgct tgggaagac
329

<210> 2016

<211> 104

<212> PRT

<213> Homo sapiens

<400> 2016

```

Thr Arg Ala Met Leu Gly Ile Arg Arg His His Pro Val Phe Gly Thr
 1           5           10           15
Gly Glu Phe Thr Asp Leu Gly Gly Pro Asp Met Ala Val Met Ser Phe
          20           25           30
Leu Arg His Asn Glu His Glu Thr Val Leu Cys Leu Ala Asn Leu Ser
          35           40           45
Asp Thr Glu Arg Thr Val Ala Leu His Leu Pro Gln Phe Ala Gly Val
          50           55           60
Ala Gly Ser Ser Leu Ile His Gly Gln Asp Ala Gln Pro Val Lys Ala
          65           70           75           80
Asp Gly Thr Leu Ser Val Pro Leu Trp Pro Tyr Gly Tyr Arg Trp Leu
          85           90           95
Gln Met Ser Gly Glu Glu Arg Ser
          100

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<210> 2017

<211> 457

<212> DNA

<213> Homo sapiens

<400> 2017

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accaaggtca gattcatggc ctcttttcct ccagcggcca gcaggaaacg cggggagccc
 60
ttgatcatct ccgacatcaa gaaaggcagc gtggcacaca ggacggggac cctggagcca
120
ggcgacaagc tactggccat tgacaatatc cgctctggaca actgccccat ggaggacgcc
180
gtgcaaatcc tgcggcagtg cgaggacctg gtgaagctga agatccggaa ggacgaggac
240
aactctgatg agctggagac cacagggtgc gtcagttaca cagtggagct gaagcgctac
300
gggggtcccc tgggcatcac catttcgggc acggaggaac cttttgacct cattttcatc
360
tcaggcctcc ccaaacgtgg cctggctgag aggactggtg ccatccagtg ggggaaccgc
420
ttcggaccat aacaacgtta ttctcagggc cggacca
457

```

<210> 2018

<211> 143

<212> PRT

<213> Homo sapiens

<400> 2018

```

Thr Lys Val Arg Phe Met Ala Ser Phe Pro Pro Ala Ala Ser Arg Lys

```

1				5						10					15
Arg	Gly	Glu	Pro	Leu	Ile	Ile	Ser	Asp	Ile	Lys	Lys	Gly	Ser	Val	Ala
			20					25					30		
His	Arg	Thr	Gly	Thr	Leu	Glu	Pro	Gly	Asp	Lys	Leu	Leu	Ala	Ile	Asp
		35					40					45			
Asn	Ile	Arg	Leu	Asp	Asn	Cys	Pro	Met	Glu	Asp	Ala	Val	Gln	Ile	Leu
	50					55					60				
Arg	Gln	Cys	Glu	Asp	Leu	Val	Lys	Leu	Lys	Ile	Arg	Lys	Asp	Glu	Asp
65					70					75				80	
Asn	Ser	Asp	Glu	Leu	Glu	Thr	Thr	Gly	Ala	Val	Ser	Tyr	Thr	Val	Glu
			85					90					95		
Leu	Lys	Arg	Tyr	Gly	Gly	Pro	Leu	Gly	Ile	Thr	Ile	Ser	Gly	Thr	Glu
			100					105					110		
Glu	Pro	Phe	Asp	Pro	Ile	Phe	Ile	Ser	Gly	Leu	Pro	Lys	Arg	Gly	Leu
		115					120					125			
Ala	Glu	Arg	Thr	Gly	Ala	Ile	Gln	Trp	Gly	Asn	Arg	Phe	Gly	Pro	
	130						135					140			

<210> 2019

<211> 483

<212> DNA

<213> Homo sapiens

<400> 2019

cgcgtcggcg acgattttat cctcgggggtt cggtataccg ccgatgaatg tctcgagaac
60
ggcaccggca aggcggaagg catcgaaatc tccagacggc tgaaggagag cggcctgatc
120
gactatetca acgtcatcag gggacatcgc gacaccgatc ccggcctgac cgacgtcatc
180
cccattcagg gcatggcgag cgcgcggcat cttgatttcg caggcgaaat ccgcgcggcg
240
accagcttcc cgtcttccca tgccgccaaa attcaggatg tcgccaccgc ccggcatgcg
300
attgccgccc gcaagggtcga catgatcgcc atgaccgcgc cccacatgac cgatccgcat
360
atcgctccga agatcatgga aaaacaggag gaggacatcc gccctgcgt cggcgccaat
420
tattgtcttg atcgcattta tcaaggcgcc ctcgccttct gcattcaca tgcggcaacc
480
ggc
483

<210> 2020

<211> 161

<212> PRT

<213> Homo sapiens

<400> 2020

Arg	Val	Gly	Asp	Asp	Phe	Ile	Leu	Gly	Val	Arg	Tyr	Thr	Ala	Asp	Glu
1				5					10					15	
Cys	Leu	Glu	Asn	Gly	Thr	Gly	Lys	Ala	Glu	Gly	Ile	Glu	Ile	Ser	Arg
			20					25					30		
Arg	Leu	Lys	Glu	Ser	Gly	Leu	Ile	Asp	Tyr	Leu	Asn	Val	Ile	Arg	Gly

[illegible]

<210> 2021

<211> 797

<212> DNA

<213> Homo sapiens

<400> 2021

60	ngaattcggg	cactggccta	actcggagca	cagcttcacc	acgaccatg	acaaggaagg
120	gtttctcctg	agaagggccca	gcaagtgtgt	ttaaggacat	cctccctcct	gtccctgcag
180	ccctctctccc	tcagtactcg	cgagactacg	aaaacacgtg	ctgaaatgga	caccgcgtcc
240	gggagccagt	gttcgcgtac	cccagaagcg	atactcaata	atgaaaagct	ggtcttgcgc
300	ccccgcatac	ccagagtga	cggtcggctg	ttaccctcgc	actacttcca	gggtggtgac
360	tgggctgtct	tcgtgggcct	ttcctcgccc	accttcggga	tcttcattcc	cttctcgctt
420	cacgcctgga	aatacatcgc	ctatgtggta	tccttttcat	cgtggcatgg	tctaagcggg
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<210> 2022

<211> 135

<212> PRT

<213> Homo sapiens

<400> 2022

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Leu Asn Asn Glu Lys Leu Val Leu Pro Pro Arg Ile Ser Arg Val Asn
      20              25              30
Gly Trp Ser Leu Pro Leu His Tyr Phe Gln Val Val Thr Trp Ala Val
 35              40              45
Phe Val Gly Leu Ser Ser Ala Thr Phe Gly Ile Phe Ile Pro Phe Leu
 50              55              60
Pro His Ala Trp Lys Tyr Ile Ala Tyr Val Val Ser Phe Ser Ser Trp
 65              70              75              80
His Gly Leu Ser Gly Arg Gly Ser Trp Arg Thr Leu Arg Trp Thr Trp
      85              90              95
Leu Trp Gly Leu Gly His Gly Cys Pro Val Ala Pro Val Thr Cys Pro
      100              105              110
Gly Pro Asp Tyr Val Pro Arg Ala Cys Arg Trp Ala Gln Trp Pro Leu
      115              120              125
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<210> 2023

<211> 462

<212> DNA

<213> Homo sapiens

<400> 2023

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<211> 154

<212> PRT

<213> Homo sapiens

<400> 2024

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Asp Ser Pro	Asp Glu Met	Ala Pro Thr	Ala Pro Arg
35	40	45	
His Ile Pro	Val Asp Lys	Ile Gly Glu	Val Ile Gly
50	55	60	
Met Ile Asn	Gln Ile Gln	Asp Thr Gly	Ala Asn
65	70	75	
Asp Asp Gly	Thr Ile Phe	Ile Gly Ala	Asp Asn
85	90	95	
Ser Ala Arg	Ser Met Ile	Asn Ala Ile	Ala Asn
100	105	110	
Val Gly Glu	Arg Tyr Leu	Gly Thr Val	Val Lys Thr
115	120	125	
Ala Phe Val	Ser Leu Leu	Pro Gly Lys	Asp Gly Leu
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<211> 872

<212> DNA

<213> Homo sapiens

<400> 2025

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<211> 157

<212> PRT

<213> Homo sapiens

<400> 2026

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          20          25          30
Ala Ile Asp Val Asp Met Ala Phe Phe Glu Pro Lys Met Arg Glu Ile
          35          40          45
Leu Glu Gln Asn Cys Thr Gly Asp Glu Asp Cys Asn Phe Phe Asp Cys
          50          55          60
Phe Ser Arg Cys Asp Leu Arg Val Asn Lys Cys Gly Ala Gln Arg Val
          65          70          75          80
Asn Asn Asn Leu Gln Val Ile Cys Asp Lys Ile Phe Arg His Trp Phe
          85          90          95
Ser Ala Pro Leu Lys Ser Ser Ala Val Ser Phe Gln Leu Gln Leu Gln
          100          105          110
Leu Gln Glu Ala Val Gln Glu Cys Ala Asp Pro Gly Val Pro Ser Gly
          115          120          125
Asn Thr Arg Arg Ala Ala Ser Ser Val Phe Trp Lys Leu Arg Gln Leu
          130          135          140
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<210> 2027

<211> 721

<212> DNA

<213> Homo sapiens

<400> 2027

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<210> 2028

<211> 114

<212> PRT

<213> Homo sapiens

<400> 2028

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			20					25					30		
Lys	Leu	Phe	Phe	Cys	Gln	Leu	Cys	Ile	Thr	Ser	Asp	Asp	Ile	Gly	Tyr
		35					40					45			
Ser	Cys	Arg	Leu	Lys	Phe	Lys	Ile	Gln	Val	Ala	Pro	Tyr	Ser	Ile	Phe
		50				55					60				
Leu	His	Lys	Glu	Arg	Leu	His	Val	Leu	Ile	Leu	Cys	Gly	Leu	Cys	Tyr
65				70					75					80	
Leu	Arg	Ser	Asn	Gln	Glu	Ser	Leu	Ile	Leu	Ser	Gln	Lys	Cys	Leu	Leu
			85						90				95		
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Ser Gly

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<211> 8028

<212> DNA

<213> Homo sapiens

<400> 2029

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<210> 2030

<211> 794

<212> PRT

<213> Homo sapiens

<400> 2030

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala Val Leu Leu
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 Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 20 25 30
 Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 35 40 45
 Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
 50 55 60
 Glu Ser Glu Leu Glu Ser Ser Ile Gln Glu Glu Asp Ser Leu Lys
 65 70 75 80
 Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser

85										90										95									
Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu	Glu	Pro	Lys	Lys	Val	Arg	Lys														
100										105										110									
Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly	Thr	Ala	His	Gly	Glu	Pro	Cys	His														
115										120										125									
Phe	Pro	Phe	Leu	Phe	Leu	Asp	Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp														
130										135										140									
Gly	Arg	Glu	Asp	Gly	Arg	Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys														
145										150										155									
Ala	Asp	Glu	Lys	Trp	Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys														
160										165										170									
Arg	Arg	Gln	Met	Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys														
175										180										185									
Ile	Leu	Asn	Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg														
190										195										200									
Tyr	Leu	Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg														
205										210										215									
Val	Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln														
220										225										230									
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro	Lys														
235										240										245									
Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly	Val	Asn														
250										255										260									
Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly	Ala	Leu	Gly														
265										270										275									
Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Gly	Tyr	Arg	Tyr	Trp	Ala	Gly														
280										285										290									
Ile	Gly	Val	Leu	Gln	Ser	Cys	Gly	Ser	Ala	Leu	Thr	His	Tyr	Arg	Leu														
295										300										305									
Val	Ala	Asn	His	Val	Ala	Ser	Asp	Ile	Ser	Ser	Leu	Thr	Gly	Gly	Ser	Val													
310										315										320									
Val	Gln	Arg	Ile	Arg	Leu	Pro	Asp	Glu	Val	Glu	Asn	Pro	Gly	Met	Asn														
325										330										335									
Ser	Gly	Met	Leu	Glu	Glu	Asp	Leu	Ile	Gln	Tyr	Tyr	Gln	Phe	Leu	Ala														
340										345										350									
Glu	Lys	Gly	Asp	Val	Gln	Ala	Gln	Val	Gly	Leu	Gly	Gln	Leu	His	Leu														
355										360										365									
His	Gly	Gly	Arg	Gly	Val	Glu	Gln	Asn	His	Gln	Arg	Ala	Phe	Asp	Tyr														
370										375										380									
Phe	Asn	Leu	Ala	Ala	Asn	Ala	Gly	Asn	Ser	His	Ala	Met	Ala	Phe	Leu														
385										390										395									
Gly	Lys	Met	Tyr	Ser	Glu	Gly	Ser	Asp	Ile	Val	Pro	Gln	Ser	Asn	Glu														
400										405										410									
Thr	Ala	Leu	His	Tyr	Phe	Lys	Lys	Ala	Ala	Asp	Met	Gly	Asn	Pro	Val														
415										420										425									
Gly	Gln	Ser	Gly	Leu	Gly	Met	Ala	Tyr	Leu	Tyr	Gly	Arg	Gly	Val	Gln														
430										435										440									
Val	Asn	Tyr	Asp	Leu	Ala	Leu	Lys	Tyr	Phe	Gln	Lys	Ala	Ala	Glu	Gln														
445										450										455									
Gly	Trp	Val	Asp	Gly	Gln	Leu	Gln	Leu	Gly	Ser	Met	Tyr	Tyr	Asn	Gly														
460										465										470									
Ile	Gly	Val	Lys	Arg	Asp</																								

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      515                      520                      525
His  Ala Ser Gly Thr Gly Val Met Arg Ser Cys His Thr Ala Val Glu
530                      535                      540
Leu  Phe Lys Asn Val Cys Glu Arg Gly Arg Trp Ser Glu Arg Leu Met
545                      550                      555
Thr  Ala Tyr Asn Ser Tyr Lys Asp Gly Asp Tyr Asn Ala Ala Val Ile
565                      570                      575
Gln  Tyr Leu Leu Leu Ala Glu Gln Gly Tyr Glu Val Ala Gln Ser Asn
580                      585                      590
Ala  Ala Phe Ile Leu Asp Gln Arg Glu Ala Ser Ile Val Gly Glu Asn
595                      600                      605
Glu  Thr Tyr Pro Arg Ala Leu Leu His Trp Asn Arg Ala Ala Ser Gln
610                      615                      620
Gly  Tyr Thr Val Ala Arg Ile Lys Leu Gly Asp Tyr His Phe Tyr Gly
625                      630                      635
Phe  Gly Thr Asp Val Asp Tyr Glu Thr Ala Phe Ile His Tyr Arg Leu
645                      650                      655
Ala  Ser Glu Gln Gln His Ser Ala Gln Ala Met Phe Asn Leu Gly Tyr
660                      665                      670
Met  His Glu Lys Gly Leu Gly Ile Lys Gln Asp Ile His Leu Ala Lys
675                      680                      685
Arg  Phe Tyr Asp Met Ala Ala Glu Ala Ser Pro Asp Ala Gln Val Pro
690                      695                      700
Val  Phe Leu Ala Leu Cys Lys Leu Gly Val Val Tyr Phe Leu Gln Tyr
705                      710                      715
Ile  Arg Glu Thr Asn Ile Arg Asp Met Phe Thr Gln Leu Asp Met Asp
725                      730                      735
Gln  Leu Leu Gly Pro Glu Trp Asp Leu Tyr Leu Met Thr Ile Ile Ala
740                      745                      750
Leu  Leu Leu Gly Thr Val Ile Ala Tyr Arg Gln Arg Gln His Gln Asp
755                      760                      765
Met  Pro Ala Pro Arg Pro Pro Gly Pro Arg Pro Ala Pro Pro Gln Gln
770                      775                      780
Glu  Gly Pro Pro Glu Gln Gln Pro Pro Gln
785                      790

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<210> 2031

<211> 662

<212> DNA

<213> Homo sapiens

<400> 2031

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atcatcgaaa gcagcgcccg ccagcaggat tcgatttctc gccaaactgac ccagcagttc
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atcagccaat ggcagcgcg caccgcggcg gatcagatca ccgtgcgtga cgtggcgctg
120
aaccccgctgc cgcacctgga cagcatctg ctcgggcggt ggatgaacac tgccgaacag
180
cgcagcgcgca tcgaacaggc ttccctggac cgctccaatc aattgaccga cgaattgtct
240
gccgcccagc tgctgggtgat ggctgcaccg atgtacaact tcgctatccc cagcaccctc
300
aaagcctggc tggaccacgt gttgcgtgcc ggtgtgacct tcaagtacac cgccaccggc
360

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cccaggggat tgctgcacgg caagcgcgcg attgtgctga cgcctcgcg cggcattcat
 420
 accggcgcca gctccgatca ccaggaaccg tacctgcgcc aggtcatggc ctttatcggg
 480
 attcatgacg tcacgttcat tcatgccgaa ggggtgaact tgagcgggtga cttccaggaa
 540
 aaaggcctta accacgcaa ggcgttgctg gcgcaacttg tggcatgaac cgagtcaacg
 600
 gttaatcgct acataatcgc cgggtgttta tatogettca cgcaaaccct tcaagtacgc
 660
 gt
 662

<210> 2032

<211> 195

<212> PRT

<213> Homo sapiens

<400> 2032

Ile	Ile	Glu	Ser	Ser	Ala	Arg	Gln	Gln	Asp	Ser	Ile	Ser	Arg	Gln	Leu
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Thr	Gln	Gln	Phe	Ile	Ser	Gln	Trp	Gln	Ala	Ala	His	Pro	Ala	Asp	Gln
		20					25						30		
Ile	Thr	Val	Arg	Asp	Val	Ala	Leu	Asn	Pro	Val	Pro	His	Leu	Asp	Thr
		35				40						45			
His	Leu	Leu	Gly	Gly	Trp	Met	Lys	Pro	Ala	Glu	Gln	Arg	Ser	Ala	Ile
	50				55					60					
Glu	Gln	Ala	Ser	Leu	Asp	Arg	Ser	Asn	Gln	Leu	Thr	Asp	Glu	Leu	Leu
65				70					75					80	
Ala	Ala	Asp	Val	Leu	Val	Met	Ala	Ala	Pro	Met	Tyr	Asn	Phe	Ala	Ile
		85						90					95		
Pro	Ser	Thr	Leu	Lys	Ala	Trp	Leu	Asp	His	Val	Leu	Arg	Ala	Gly	Val
		100					105						110		
Thr	Phe	Lys	Tyr	Thr	Ala	Thr	Gly	Pro	Gln	Gly	Leu	Leu	His	Gly	Lys
	115					120					125				
Arg	Ala	Ile	Val	Leu	Thr	Ala	Arg	Gly	Gly	Ile	His	Thr	Gly	Ala	Ser
	130				135					140					
Ser	Asp	His	Gln	Glu	Pro	Tyr	Leu	Arg	Gln	Val	Met	Ala	Phe	Ile	Gly
145				150					155					160	
Ile	His	Asp	Val	Thr	Phe	Ile	His	Ala	Glu	Gly	Val	Asn	Leu	Ser	Gly
		165						170					175		
Asp	Phe	Gln	Glu	Lys	Gly	Leu	Asn	His	Ala	Lys	Ala	Leu	Leu	Ala	Gln
	180						185						190		
Leu	Val	Ala													
		195													

<210> 2033

<211> 380

<212> DNA

<213> Homo sapiens

<400> 2033

aaatttttaa acggtcatca ttttaacaggc gaagctgtaa aacgcagtct tgaagaggga
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atgaaaaaaa gtgatttggt aaaaggatca cttcctatca aatcaatcaa cgctcatgga
 120
 caaaaaagtc caatcaatac taaagaacct tatccagaat taaagtctga actcgcaagc
 180
 ccatttgctg ctatatacga cacaaaaagct aaaaacaaag taactgatca acctgttggt
 240
 acgggtcctt atcaaattga cagttataaa cgttcgcaaa aaatcgtatt aaaacaattc
 300
 aaagactact ggcaaggtag gccaaaatta aaaagaatta atgtcactta tcatgaagat
 360
 ggtaatantc gtgttgatca
 380

<210> 2034

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2034

Met	Lys	Lys	Ser	Asp	Leu	Leu	Lys	Gly	Ser	Leu	Pro	Ile	Lys	Ser	Ile
1			5					10					15		
Asn	Ala	His	Gly	Gln	Lys	Val	Thr	Ile	Asn	Thr	Lys	Glu	Pro	Tyr	Pro
		20						25				30			
Glu	Leu	Lys	Ser	Glu	Leu	Ala	Ser	Pro	Phe	Ala	Ala	Ile	Tyr	Asp	Thr
		35					40				45				
Lys	Ala	Lys	Asn	Lys	Val	Thr	Asp	Gln	Pro	Val	Gly	Thr	Gly	Pro	Tyr
		50				55				60					
Gln	Ile	Asp	Ser	Tyr	Lys	Arg	Ser	Gln	Lys	Ile	Val	Leu	Lys	Gln	Phe
		65			70				75					80	
Lys	Asp	Tyr	Trp	Gln	Gly	Thr	Pro	Lys	Leu	Lys	Arg	Ile	Asn	Val	Thr
		85						90					95		
Tyr	His	Glu	Asp	Gly	Asn	Xaa	Arg	Val	Asp						
		100						105							

<210> 2035

<211> 495

<212> DNA

<213> Homo sapiens

<400> 2035

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 120
 tatgctntaa tgttccccct tcatctcgca tgtctccact tctgctgcta ttgctgttac
 180
 ttgtgtgttg gtgcacctaa tgggtgtccca tatttctctg atgctgtgtt catttttctt
 240
 gattctttct actgtctggt cttcagtttg cataatccat attgttctct ctactagtcc
 300
 actggtgctt ttgcttgcca gctctaattt actgttatcc cctttagtga aattttttct
 360
 ttttttctct tctcattcca gttattatac agaactatcc aacttcaaga tttgtggggg
 420

tttgttttgt tttgttttga gaccccatct caaaaaaaaa aaaaaccagc tttctcctca
 480
 acttggggga acctt
 495

<210> 2036
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 2036
 Xaa Ile Pro Leu Leu Leu Ala Thr Gln Ala Gln Ala Thr Arg Ser His
 1 5 10 15
 Asp Thr Ser Cys Leu His Phe Phe His Val Cys Met Tyr Val Cys Met
 20 25 30
 Tyr Val Cys Met Tyr Val Cys Met Tyr Ala Xaa Met Phe Pro Phe His
 35 40 45
 Leu Ala Cys Leu His Phe Cys Cys Tyr Cys Cys Tyr Leu Cys Val Gly
 50 55 60
 Ala Pro Asn Gly Val Pro Tyr Phe Ser Asp Ala Val Phe Ile Phe Leu
 65 70 75 80
 Asp Ser Phe Tyr Cys Leu Val Phe Ser Leu His Asn Pro Tyr Cys Ser
 85 90 95
 Leu Tyr

<210> 2037
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 2037
 acgctgaag ggaaggggga gaccccgga gaaatggaga aatgggggag cacacagagc
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 ggaagagatga ggttgagtg cctttccgc getcatcttc cgtecccaact ccaagccagc
 120
 caaatccaaa caccgcgcc tctggtggcc cgggcttcca tttcccttg aggggcaagg
 180
 gcgtttcttc ttccgcccaa cggggcgct gagcggcggg aacagcggg ggggctttgt
 240
 ggtcccgggg ggtccgagtg tgtgtcagg gctggggcgg gggatgggag cggcccttg
 300
 gtatccctca cggctctggt tcatgag
 327

<210> 2038
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 2038
 Met Glu Lys Trp Gly Arg Thr Gln Thr Gly Arg Val Arg Leu Glu Cys
 1 5 10 15
 Leu Ser Arg Ala His Leu Pro Ser Pro Leu His Ala Gln Gln Ile Gln

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                20                25                30
Thr Pro Arg Pro Leu Val Ala Arg Ala Ser Ile Ser Pro Gly Gly Ala
      35                40                45
Arg Ala Phe Pro Leu Pro Pro Asn Arg Gly Ala Glu Arg Arg Glu Gln
      50                55                60
Arg Arg Gly Leu Cys Gly Pro Gly Gly Ser Glu Cys Val Ser Gly Ala
      65                70                75                80
Gly Ala Gly Asp Gly Arg Gly Pro Trp Val Ser Leu Thr Val Leu Val
      85                90                95
His Glu

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<210> 2039

<211> 307

<212> DNA

<213> Homo sapiens

<400> 2039

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accggtgac cactctgcga aagcggccgc gagcgaagcg ttcttggtct tcttcgagat
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cgcgatgtat tgccccgaaa acagcggcct gatgccgtca ttgagagget ctgggcccaac
120
accggtacgg gcatatgcct gggcggcatt cttttggatg ttgcaagaa aggacgcatt
180
cgcggtgcgg aaagccaggg atccttcacc gtagaccttg gaccgatgga gggccccggc
240
aatcgagtcc ttcgaaattc ccccttgcca tacatgtcgg ccatcgtcgt cagccagagt
300
aacgcgt
307

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<210> 2040

<211> 94

<212> PRT

<213> Homo sapiens

<400> 2040

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Met Ala Asp Met Tyr Ala Lys Gly Glu Phe Arg Arg Thr Arg Leu Pro
  1                5                10                15
Gly Ala Ser Ile Gly Pro Arg Ser Thr Val Lys Asp Pro Trp Leu Ser
      20                25                30
Ala Arg Arg Met Arg Pro Phe Phe Ala Thr Ser Lys Arg Met Pro Pro
      35                40                45
Arg His Met Pro Val Pro Val Leu Ala Gln Ser Leu Ser Met Thr Ala
      50                55                60
Ser Ser Arg Cys Phe Pro Gly Asn Thr Ser Arg Ser Arg Arg Arg Pro
      65                70                75                80
Arg Thr Leu Arg Ser Arg Pro Leu Ser Gln Ser Gly Ser Pro
      85                90

```

<210> 2041

<211> 348

<212> DNA

<213> Homo sapiens

<400> 2041
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 60
 gccagcttcc tgccgttcgc cagacgcacg gccgaggcgg ggggtgcgcaa ttcgctcgcc
 120
 cagctggtcg ccaagctgac cctgcccggc atgccccaca tctaccaggg ctgcgagatg
 180
 tgggacctca gcctgggtcga cggggacaat cggcgccccg tcgactacga gacacgcgac
 240
 gcggccctgg ccggctgggt cgcgaccccc cggagggaac gcgcccggcg gctgcgcacc
 300
 ctgctgacgg attggcgag cggcgcggtc aagctggcgg tgacgcgt
 348

<210> 2042
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 2042
 Xaa Arg Arg Cys Arg Asp Ser Pro Ala Met Arg Ser Asn Pro Ala Arg
 1 5 10 15
 Gly Ala Phe Leu Ala Ser Phe Leu Pro Phe Ala Arg Arg Ile Ala Glu
 20 25 30
 Ala Gly Val Arg Asn Ser Leu Ala Gln Leu Val Ala Lys Leu Thr Leu
 35 40 45
 Pro Gly Met Pro Asp Ile Tyr Gln Gly Cys Glu Met Trp Asp Leu Ser
 50 55 60
 Leu Val Asp Arg Asp Asn Arg Arg Pro Val Asp Tyr Glu Thr Arg Asp
 65 70 75 80
 Ala Ala Leu Ala Gly Trp Val Ala Thr Pro Pro Glu Glu Arg Ala Ala
 85 90 95
 Ala Leu Arg Thr Leu Leu Thr Asp Trp Arg Ser Gly Ala Val Lys Leu
 100 105 110
 Ala Val Thr Arg
 115

<210> 2043
 <211> 712
 <212> DNA
 <213> Homo sapiens

<400> 2043
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 gaagattcgg tgccgagagc cctgtctcga atgcgctccc gggatgccgt ccacggcgag
 120
 gaacgtgccg ataccgggga tggacccccg cgggtggatca ttgatccgat cgacggcact
 180
 gcgaattttc tgctgtgggt ccagtggtgg gccaccctca ttgcctcag cgtcgaggac
 240
 cagattgtcg catctgtggt ctctgtctct gccctcaagc gacgctgggt ggcagcccg
 300

ggctcaggag catggtcggg caaatccctg gcctcagcga caccgatcca cgtctcgaat
 360
 gtgcgcaatc ttgccgacgc attcttgtcc tactcttcgc tgcacggatg ggtcgagagc
 420
 ggacgagggc acgggttcgg tgaactcatg cggtcgggtg ggcggaccgg agccttcggc
 480
 gattttcggg cttacatgat ggtggcagaa ggtgtcgtcg atgtggcatg cgagccggaa
 540
 ctcagcctgc acgacatggc cgccctcgac gctatcgtca ccgagcgagg cggtaaagttc
 600
 accggtctcg atggcaaaga cggcccgtagg tctgggaatg ctctggcgctc gaatggtttc
 660
 cttcatgacc aggccttagc catggtccag cctcaggagt gagcaccgat cg
 712

<210> 2044

<211> 233

<212> PRT

<213> Homo sapiens

<400> 2044

Asp	Leu	Thr	Val	Ser	Thr	Lys	Pro	Asp	His	Ser	Glu	Val	Thr	Asp	Ala
1			5					10						15	
Asp	Leu	Ala	Val	Glu	Asp	Ser	Val	Arg	Arg	Ala	Leu	Ser	Arg	Met	Arg
			20					25					30		
Ser	Arg	Asp	Ala	Val	His	Gly	Glu	Glu	Arg	Ala	Asp	Thr	Gly	Asp	Gly
			35				40					45			
Pro	Arg	Arg	Trp	Ile	Ile	Asp	Pro	Ile	Asp	Gly	Thr	Ala	Asn	Phe	Leu
	50					55				60					
Arg	Gly	Val	Pro	Val	Trp	Ala	Thr	Leu	Ile	Ala	Leu	Ser	Val	Glu	Asp
	65				70				75					80	
Gln	Ile	Val	Ala	Ser	Val	Val	Ser	Ala	Pro	Ala	Leu	Lys	Arg	Arg	Trp
			85						90					95	
Trp	Ala	Ala	Arg	Gly	Ser	Gly	Ala	Trp	Ser	Gly	Lys	Ser	Leu	Ala	Ser
			100				105						110		
Ala	Thr	Pro	Ile	His	Val	Ser	Asn	Val	Arg	Asn	Leu	Ala	Asp	Ala	Phe
		115					120				125				
Leu	Ser	Tyr	Ser	Ser	Leu	His	Gly	Trp	Val	Glu	Ser	Gly	Arg	Gly	His
	130					135					140				
Gly	Phe	Gly	Glu	Leu	Met	Arg	Ser	Val	Trp	Arg	Thr	Arg	Ala	Phe	Gly
	145				150					155				160	
Asp	Phe	Trp	Ser	Tyr	Met	Met	Val	Ala	Glu	Gly	Val	Val	Asp	Val	Ala
			165						170					175	.
Cys	Glu	Pro	Glu	Leu	Ser	Leu	His	Asp	Met	Ala	Ala	Leu	Asp	Ala	Ile
		180					185						190		
Val	Thr	Glu	Ala	Gly	Gly	Lys	Phe	Thr	Gly	Leu	Asp	Gly	Lys	Asp	Gly
		195					200					205			
Pro	Trp	Ser	Gly	Asn	Ala	Leu	Ala	Ser	Asn	Gly	Phe	Leu	His	Asp	Gln
	210					215					220				
Ala	Leu	Ala	Met	Val	Gln	Pro	Gln	Glu							
	225					230									

<210> 2045

<211> 406

<212> DNA

<213> Homo sapiens

<400> 2045

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 atgcgcgcga tggcgacg tgatggaccg ggcgctggac ctggcggtgc gcttcgacga
 120
 cantacaggc ttggccgag cggggttgga agaaaccggt caaccggtgg ttggccccg
 180
 catcaatgcc cagaaccaga agccttgccg attcgtccca ggccgttcaa ggccgatggc
 240
 gagatcgctg cgatgactgg cgacggtgtc aacgacgcc cctcgctcaa ggcgcccat
 300
 atcgggtgtg ccatggacaa acgcggcacc gacgtcgcgc gcgaggcttc cgccatggtc
 360
 ctgctcgagg atgattttgg atcgatcgtg cagtcggtcc ggctcg
 406

<210> 2046

<211> 135

<212> PRT

<213> Homo sapiens

<400> 2046

Xaa	Trp	Thr	Pro	Ala	Thr	Met	Pro	Pro	Pro	His	Gly	Ser	Ile	Ala	Asp
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Pro	Gly	Gln	Gly	Met	Arg	Arg	Met	Gly	Asp	Gly	Asp	Gly	Pro	Gly	Ala
		20					25						30		
Gly	Pro	Gly	Arg	Ser	Leu	Arg	Arg	Xaa	Tyr	Arg	Leu	Trp	Pro	Arg	Arg
		35				40					45				
Val	Gly	Arg	Asn	Arg	Ser	Thr	Gly	Gly	Leu	Ala	Pro	His	Gln	Cys	Pro
	50				55						60				
Glu	Pro	Glu	Ala	Leu	Arg	Ile	Arg	Pro	Arg	Pro	Phe	Lys	Ala	Asp	Gly
	65			70					75					80	
Glu	Ile	Val	Ala	Met	Thr	Gly	Asp	Gly	Val	Asn	Asp	Ala	Pro	Ser	Leu
		85						90					95		
Lys	Ala	Ala	His	Ile	Gly	Val	Ala	Met	Asp	Lys	Arg	Gly	Thr	Asp	Val
		100					105						110		
Ala	Arg	Glu	Ala	Ser	Ala	Met	Val	Leu	Leu	Glu	Asp	Asp	Phe	Gly	Ser
		115				120						125			
Ile	Val	Gln	Ser	Val	Arg	Leu									
	130					135									

<210> 2047

<211> 796

<212> DNA

<213> Homo sapiens

<400> 2047

aagctttgga acgagacccc tgagctctgg gttcagcccc gaggaagccc agcaacagga
 60
 tgaggaattt gagaagaaga ttccaagtgt ggaagacagc cttggagagg gcagcagggg
 120

tgcctggccgg ccaggagaga gaggatccgg gggcttgttc agtcctagca ctgcccacgt
 180
 gccggatggg gcaactcgggc agagagacca gagcagctgg caaacacgtg atgctagcca
 240
 ggaggtggga gggcatcagg agagacagca ggcaggggct cagggccctg gcagtgtga
 300
 cctggaagat ggggagatgg gaaagcgagg ctgggtcggg gagtttagcc tcagtgttg
 360
 cccccagca gaggcagcat ttagcccagg gcagcaggac tggagccggg acttctgc
 420
 cgaggccagt gagaggagct atcagtttgg catcattggc aacgacagag tgagtgtg
 480
 tggcttttag ccttctagca agatggaagg tggtcacttt gtgcctcctg ggaagaccac
 540
 agctggctcg gtggactgga ctgaccagct gggctcagg aacttggaag tgtccagctg
 600
 tgtgggttct gggggctcga gcgagggcag ggagagtgcc gtgggacaga tgggctggtc
 660
 aggtggcctg agcttgagag acatgaacct gaccggctgt ttggaagtg gagggctcga
 720
 agagccgggg ggaatcggaa ttggggagaa ggactggact tctgatgta atgtgaagag
 780
 caaagatttg gctgag
 796

<210> 2048

<211> 160

<212> PRT

<213> Homo sapiens

<400> 2048

Met	Gly	Lys	Arg	Gly	Trp	Val	Gly	Glu	Phe	Ser	Leu	Ser	Val	Gly	Pro
1				5					10					15	
Gln	Arg	Glu	Ala	Ala	Phe	Ser	Pro	Gly	Gln	Gln	Asp	Trp	Ser	Arg	Asp
			20					25					30		
Phe	Cys	Ile	Glu	Ala	Ser	Glu	Arg	Ser	Tyr	Gln	Phe	Gly	Ile	Ile	Gly
		35				40						45			
Asn	Asp	Arg	Val	Ser	Gly	Ala	Gly	Phe	Ser	Pro	Ser	Ser	Lys	Met	Glu
	50					55				60					
Gly	Gly	His	Phe	Val	Pro	Pro	Gly	Lys	Thr	Thr	Ala	Gly	Ser	Val	Asp
65					70					75				80	
Trp	Thr	Asp	Gln	Leu	Gly	Leu	Arg	Asn	Leu	Glu	Val	Ser	Ser	Cys	Val
				85				90						95	
Gly	Ser	Gly	Gly	Ser	Ser	Glu	Ala	Arg	Glu	Ser	Ala	Val	Gly	Gln	Met
			100					105					110		
Gly	Trp	Ser	Gly	Gly	Leu	Ser	Leu	Arg	Asp	Met	Asn	Leu	Thr	Gly	Cys
		115				120					125				
Leu	Glu	Ser	Gly	Gly	Ser	Glu	Glu	Pro	Gly	Gly	Ile	Gly	Ile	Gly	Glu
		130				135					140				
Lys	Asp	Trp	Thr	Ser	Asp	Val	Asn	Val	Lys	Ser	Lys	Asp	Leu	Ala	Glu
145					150					155					160

<210> 2049

<211> 516

<212> DNA

<213> Homo sapiens

<400> 2049

cgcgctcgctt acggtgcgct gaataccagc ctgctggcgc tggcggtcag cttcgcgctg
 60
 ctgttctctg ggatagtgtt cgggctgatg ccacgtctga tgtcggggtt gattgaactg
 120
 gccaacgcctc ccccaccaat cgccctgggc ctgttagtag tcgcatttag cgcccttca
 180
 gcctacgggtg ccgctgtgc ggtgatgttg gtcagttggg ctccgctggc cgccattgt
 240
 gcttcgttgt tggcggaagc ccgcacgcag cctatatcc gcattgttgc ggtattggg
 300
 gtgcggcgat ggcgcacgct gacccaactac ctgctgccgg cgctctctgc tccctgctg
 360
 cgccacgccca tgttcgtctt gccgggcatt gcgctggcgc tggcggcctt gggttttttt
 420
 ggtcttgggc cgcagccacc cagtgcagaa tgggggctgg tgctggcgga aggcattgct
 480
 tatctcgaac gggcgccctg gggagtcctg gcaccg
 516

<210> 2050

<211> 172

<212> PRT

<213> Homo sapiens

<400> 2050

Arg	Val	Ala	Tyr	Gly	Ala	Leu	Asn	Thr	Ser	Leu	Leu	Ala	Leu	Ala	Val
1				5				10					15		
Ser	Phe	Ala	Ser	Leu	Phe	Leu	Gly	Ile	Val	Phe	Gly	Leu	Met	Pro	Arg
			20				25					30			
Leu	Met	Cys	Gly	Val	Ile	Glu	Leu	Ala	Asn	Ala	Pro	Pro	Pro	Ile	Ala
		35				40					45				
Leu	Gly	Leu	Leu	Val	Val	Ala	Ile	Ser	Gly	Pro	Ser	Ala	Tyr	Gly	Ala
	50				55					60					
Ala	Cys	Ala	Val	Met	Leu	Val	Ser	Trp	Ala	Pro	Leu	Ala	Ala	His	Cys
65				70					75					80	
Ala	Ser	Leu	Leu	Ala	Glu	Ala	Arg	Thr	Gln	Pro	Tyr	Ile	Arg	Met	Leu
			85					90					95		
Pro	Val	Leu	Gly	Val	Gly	Arg	Trp	Arg	Thr	Leu	Thr	His	Tyr	Leu	Leu
		100					105						110		
Pro	Ala	Leu	Ser	Ala	Pro	Leu	Leu	Arg	His	Ala	Met	Leu	Arg	Leu	Pro
	115					120					125				
Gly	Ile	Ala	Leu	Ala	Leu	Ala	Ala	Leu	Gly	Phe	Phe	Gly	Leu	Gly	Pro
	130				135					140					
Gln	Pro	Pro	Ser	Ala	Glu	Trp	Gly	Leu	Val	Leu	Ala	Glu	Gly	Met	Pro
145			150					155						160	
Tyr	Leu	Glu	Arg	Ala	Pro	Trp	Gly	Val	Leu	Ala	Pro				
			165					170							

<210> 2051

<211> 411

<212> DNA

<213> Homo sapiens

<400> 2051

gagcaaaact atcgctctac cggcaatatt ctgaaaagtg ccaaccaact tatttcgaat
 60
 aatagtgatc gtctcggtaa gaattttatgg accgacgggtg aaatggggga gccagtaggt
 120
 attttatcgc catttaatga attagatgag gcaaaaatttg tggcgtctca aatccaaaat
 180
 tgggtagatg atgggtgggga attagatgat tgtgctgttt tatatcgtag taatagccaa
 240
 tctcgtgtta ttgaagaagc cttgattcgt tgccaaattc cttatcgaat ttatggcggg
 300
 atgcgatctt tcgaacgccca agaaattaaa gatgcgttgg catattttacg ttttaattaat
 360
 aatcgtcaag atgatgccgc atttgagcgt gtgattaata cgcctacgcg t
 411

<210> 2052

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2052

Glu	Gln	Asn	Tyr	Arg	Ser	Thr	Gly	Asn	Ile	Leu	Lys	Ser	Ala	Asn	Gln
1			5					10						15	
Leu	Ile	Ser	Asn	Asn	Ser	Asp	Arg	Leu	Gly	Lys	Asn	Leu	Trp	Thr	Asp
			20					25					30		
Gly	Glu	Met	Gly	Glu	Pro	Val	Gly	Ile	Tyr	Ala	Ala	Phe	Asn	Glu	Leu
		35					40					45			
Asp	Glu	Ala	Lys	Phe	Val	Ala	Ser	Gln	Ile	Gln	Asn	Trp	Val	Asp	Asp
		50				55				60					
Gly	Gly	Glu	Leu	Asp	Asp	Cys	Ala	Val	Leu	Tyr	Arg	Ser	Asn	Ser	Gln
65				70					75					80	
Ser	Arg	Val	Ile	Glu	Glu	Ala	Leu	Ile	Arg	Cys	Gln	Ile	Pro	Tyr	Arg
			85					90					95		
Ile	Tyr	Gly	Gly	Met	Arg	Phe	Phe	Glu	Arg	Gln	Glu	Ile	Lys	Asp	Ala
		100					105						110		
Leu	Ala	Tyr	Leu	Arg	Leu	Ile	Asn	Asn	Arg	Gln	Asp	Asp	Ala	Ala	Phe
		115					120					125			
Glu	Arg	Val	Ile	Asn	Thr	Pro	Thr	Arg							
		130					135								

<210> 2053

<211> 287

<212> DNA

<213> Homo sapiens

<400> 2053

nccatggaag ccttcaatct tgtaagagaa agtgaacagc tgttttccat atgccaaatc
 60
 ccgctcctct gctggatcct gtgtaccagt ctgaagcaag agatgcagaa aggaaaagac
 120

ctggccctga cctgccagag cactacctct gtgtactcct ctttcgtctt taacctgttc
 180
 acacctgagg gtgccgaggg ccgactccg caaaccacgc accagctgaa ggcctgtgc
 240
 tccctggctg cagaggggtat gtggacagac acatttgagt tttgtga
 287

<210> 2054

<211> 79

<212> PRT

<213> Homo sapiens

<400> 2054

Ile	Cys	Gln	Ile	Pro	Leu	Leu	Cys	Trp	Ile	Leu	Cys	Thr	Ser	Leu	Lys
1				5					10					15	
Gln	Glu	Met	Gln	Lys	Gly	Lys	Asp	Leu	Ala	Leu	Thr	Cys	Gln	Ser	Thr
			20					25					30		
Thr	Ser	Val	Tyr	Ser	Ser	Phe	Val	Phe	Asn	Leu	Phe	Thr	Pro	Glu	Gly
			35				40					45			
Ala	Glu	Gly	Pro	Thr	Pro	Gln	Thr	Gln	His	Gln	Leu	Lys	Ala	Leu	Cys
	50					55				60					
Ser	Leu	Ala	Ala	Glu	Gly	Met	Trp	Thr	Asp	Thr	Phe	Glu	Phe	Cys	
65					70					75					

<210> 2055

<211> 298

<212> DNA

<213> Homo sapiens

<400> 2055

nnacgcgttg ttatgaacaa tgacgggtgc ctctaccccg atacctgcgt ggggtactgat
 60
 tccccacacca ccattgaaaaa tggctcttggc attctgggct ggggcgtcgg tggtattgaa
 120
 gccgaggctg ctatgcttgg ccagcccatc tccatgctta tccccctgtg tgttggcttt
 180
 aaacttactg gccaaacaca gccgggtgtc accgctacag atgttgttct taccattact
 240
 gatatgcttc gccagcatgg tgtgggtgga aaattcgggg aattctatgg gggaagcg
 298

<210> 2056

<211> 99

<212> PRT

<213> Homo sapiens

<400> 2056

Xaa	Arg	Val	Val	Met	Asn	Asn	Asp	Gly	Val	Leu	Tyr	Pro	Asp	Thr	Cys
1				5					10					15	
Val	Gly	Thr	Asp	Ser	His	Thr	Thr	Met	Glu	Asn	Gly	Leu	Gly	Ile	Leu
				20				25					30		
Gly	Trp	Gly	Val	Gly	Gly	Ile	Glu	Ala	Glu	Ala	Ala	Met	Leu	Gly	Gln
			35				40					45			
Pro	Ile	Ser	Met	Leu	Ile	Pro	Arg	Val	Val	Gly	Phe	Lys	Leu	Thr	Gly

50		55		60	
Gln Thr Gln Pro Gly Val Thr Ala Thr Asp Val Val Leu Thr Ile Thr					
65		70		75	80
Asp Met Leu Arg Gln His Gly Val Gly Gly Lys Phe Gly Glu Phe Tyr					
	85		90		95

Gly Gly Ser

<210> 2057
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 2057
 acgcggtcccg acagtaccga ctataacgga ggaaactatc aggaacggta taaaatttta
 60
 gcagaaattc gtaaggctct tgaagacgga gatcgccaaa aagccaaacg attagctgaa
 120
 caaaatctag ttggaccaa caacgccag tatggtcggt atctagcctt tgggtatatt
 180
 ttcatggtct tcaataacca gaaaaagggg ctggatacag ttacagacta tcaccgtggt
 240
 ttggatatca cagaagccac tactacaact ttttacacc aagatggaac gacctttaaa
 300
 agagaaacct tctcaagtt cctgatgat gttactgtta ctacttgac ccaaaaggg
 360
 gacaaaaaac ttgattttac agtttgaat agcttaacag aagatttact tgctaacgga
 420
 gactactcag cggaatattc taactacaag agtggccatg ttacgacaga cccaaatggt
 480
 atcctactaa aaggtacagt caaagataat ggcctccagt tcgcatccta tctaggaatt
 540
 aaaaacggac gaaaagttac tgttcatga
 569

<210> 2058
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 2058
 Met Val Phe Asn Asn Gln Lys Lys Gly Leu Asp Thr Val Thr Asp Tyr
 1 5 10 15
 His Arg Gly Leu Asp Ile Thr Glu Ala Thr Thr Thr Thr Tyr Tyr Thr
 20 25 30
 Gln Asp Gly Thr Thr Phe Lys Arg Glu Thr Phe Ser Ser Tyr Pro Asp
 35 40 45
 Asp Val Thr Val Thr His Leu Thr Gln Lys Gly Asp Lys Lys Leu Asp
 50 55 60
 Phe Thr Val Trp Asn Ser Leu Thr Glu Asp Leu Leu Ala Asn Gly Asp
 65 70 75 80
 Tyr Ser Ala Glu Tyr Ser Asn Tyr Lys Ser Gly His Val Thr Thr Asp
 85 90 95
 Pro Asn Gly Ile Leu Leu Lys Gly Thr Val Lys Asp Asn Gly Leu Gln

1555

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115              120              125
Glu Phe
130

<210> 2061
<211> 481
<212> DNA
<213> Homo sapiens

<400> 2061
gttaacctgg taaggagagc gacacaggaa ggtgcagggg ttgccatggt gtgccccag
60
atgctgtgat tacgcgccag ccccgtcaca ccgtacgggt ggtaggactg ggcaaagaag
120
acgccgccac ctggatgcac tgagggtgtgc acagccacgt ggagatgatg ctggggggctc
180
acgggtgactc tcaggaggcc ctggcctggc ctatctggag ccttctctgt gaaatgaggc
240
tggtaacgcc cactagcagg gttgtagggg acatggatct gtggccacct cctcaagggt
300
tgccacacgc accaggtcct gactggggagt ccggccccc gggcctgtgg atggctggcc
360
tgggcccagc ctccgcccc aagggtgctg gcacctggca tgtgcccagc agttgggggc
420
ggctggtggg aaggtgtgtg tcagggtggcg gagcctcggt gccaggatct cactcacgcg
480
t
481

<210> 2062
<211> 133
<212> PRT
<213> Homo sapiens

<400> 2062
Met Pro Gly Ala Ser Thr Leu Gly Gly Gly Trp Ala Gln Ala Ser
1          5          10          15
His Pro Gln Ala Leu Gly Ala Gly Leu Pro Val Arg Thr Trp Cys Val
20          25          30
Trp Gln Pro Leu Arg Arg Trp Pro Gln Ile His Val Pro Tyr Asn Pro
35          40          45
Ala Ser Gly Arg Tyr Gln Pro His Phe Thr Glu Lys Ala Pro Asp Arg
50          55          60
Pro Gly Gln Gly Leu Leu Arg Val Thr Val Ser Pro Gln His His Leu
65          70          75          80
His Val Ala Val His Thr Ser Val His Pro Gly Gly Gly Val Phe Phe
85          90          95
Ala Gln Ser Tyr His Pro Tyr Gly Val Thr Gly Leu Ala Arg Asn His
100         105         110
Ser Ile Trp Gly His Thr Met Ala Thr Pro Ala Pro Ser Cys Val Ala
115         120         125
Leu Leu Thr Arg Leu
130

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<210> 2063
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 2063
 gccggcgccg tcgagcgcggt gccctttcaat atcgaggccc aagacatggt gctgctcctc
 60
 ggggacacca atgccccgca catgctttcc gaaggccaat acgcctcccg cgggggcacat
 120
 atcgacgccc tccaatctgc cgcgggttgc tccatccgag agatctcgaa tgcggtggac
 180
 ttgcccgcga ccgtcaatcc cgcgaggcg gaactctatc gccgcgcggt gcaccacgtg
 240
 gtggaagaaa ccaaccggac cctagatgcc gctaccgcgc tggcatcttc cgatctagat
 300
 acattccggc ggcttatgag cgagagccac atctccctgc gcgaccttta tgaggtcacc
 360
 actccggagc tcgactccgt ttttaccgag gccggcgagc tgggcgctcg catgannnn
 419

<210> 2064
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 2064
 Ala Gly Ala Val Glu Arg Val Pro Phe Asn Ile Glu Ala Gln Asp Met
 1 5 10 15
 Val Leu Leu Ile Ala Asp Thr Asn Ala Pro His Met Leu Ser Asp Gly
 20 25 30
 Gln Tyr Ala Ser Arg Arg Gly Ile Ile Asp Ala Val Gln Ser Ala Ala
 35 40 45
 Gly Cys Ser Ile Arg Glu Ile Ser Asn Ala Val Asp Phe Ala Ala Thr
 50 55 60
 Val Asn Pro Ala Glu Ala Glu Leu Tyr Arg Arg Val His His Val
 65 70 75 80
 Val Glu Glu Thr Asn Arg Thr Leu Asp Ala Ala Thr Ala Leu Ala Ser
 85 90 95
 Ser Asp Leu Asp Thr Phe Arg Arg Leu Met Arg Glu Ser His Ile Ser
 100 105 110
 Leu Arg Asp Leu Tyr Glu Val Thr Thr Pro Glu Leu Asp Ser Val Phe
 115 120 125
 Thr Ala Ala Gly Glu Leu Gly Ala Arg Met Xaa
 130 135

<210> 2065
 <211> 598
 <212> DNA
 <213> Homo sapiens

<400> 2065
 gccggcgcta tggcctctct gctcgcgcgc gccgcgatg cccttcccg cgcaagggtg
 60

cgcgcgaccg ttactggatc ggccgggattg ggaaccgcag aggcattggg ccttactttc
 120
 attcaggagg tcatagctga gacggccgcc gtccaacgtt ggaatcccga cgccgacgtg
 180
 cttctcgaaac tcggtggtga ggatgccaa atcacctacc ttaagccggt ccccgaaacg
 240
 cgcataaatg gttcgtgtgc tggtaggcacc ggtgccttca tcgaccagat ggctaccctg
 300
 ctgcacacgg acactccggg cctcaatgac ctgcacccc gagccaagac catccatccg
 360
 atcgccctgc gctgtggtgt ttttgccaag tccgaccttc agccctcat taacgagggg
 420
 gcccgccacg aggatctggc tgcctcgggc ctgcaggctg tcgccaactca gtgcattggc
 480
 ggccctggcat gtggtcgccc gattcgagggt aaggtcatct tctctggcgg tccgcttccg
 540
 tttatgccaa gtttgcgaga cgctttctcg cgcgtcctcg acggtaaggt tgacgcgt
 598

<210> 2066

<211> 199

<212> PRT

<213> Homo sapiens

<400> 2066

Ala	Gly	Ala	Met	Ala	Ser	Leu	Leu	Ala	Asp	Ala	Ala	Asp	Ala	Leu	Pro
1			5					10						15	
Gly	Ala	Lys	Val	Arg	Ala	Thr	Val	Thr	Gly	Ser	Ala	Gly	Leu	Gly	Thr
			20					25						30	
Ala	Glu	Ala	Leu	Gly	Leu	Thr	Phe	Ile	Gln	Glu	Val	Ile	Ala	Glu	Thr
			35				40					45			
Ala	Ala	Val	Gln	Arg	Trp	Asn	Pro	Asp	Ala	Asp	Val	Leu	Leu	Glu	Leu
			50			55				60					
Gly	Gly	Glu	Asp	Ala	Lys	Ile	Thr	Tyr	Leu	Lys	Pro	Val	Pro	Glu	Gln
65					70				75					80	
Arg	Met	Asn	Gly	Ser	Cys	Ala	Gly	Gly	Thr	Gly	Ala	Phe	Ile	Asp	Gln
				85				90						95	
Met	Ala	Thr	Leu	Leu	His	Thr	Asp	Thr	Pro	Gly	Leu	Asn	Asp	Leu	Ala
			100				105					110			
Ser	Arg	Ala	Lys	Thr	Ile	His	Pro	Ile	Ala	Ser	Arg	Cys	Gly	Val	Phe
			115				120					125			
Ala	Lys	Ser	Asp	Leu	Gln	Pro	Leu	Ile	Asn	Glu	Gly	Ala	Arg	His	Glu
			130			135					140				
Asp	Leu	Ala	Ala	Ser	Val	Leu	Gln	Ala	Val	Ala	Thr	Gln	Cys	Ile	Ala
145					150				155					160	
Gly	Leu	Ala	Cys	Gly	Arg	Pro	Ile	Arg	Gly	Lys	Val	Ile	Phe	Leu	Gly
			165					170						175	
Gly	Pro	Leu	His	Phe	Met	Pro	Ser	Leu	Arg	Asp	Ala	Phe	Ser	Arg	Val
			180					185						190	
Leu	Asp	Gly	Lys	Val	Asp	Ala									
			195												

<210> 2067

<211> 366

<212> DNA

<213> Homo sapiens

<400> 2067

ttccagcaga tgctgcaaac ctggaccgcg agcggcacgc tgcaggagge cgtggccaaac
 60
 aagatcgccg aatggctgga tgccgacctg caacagtggg acatttcccg cgatgcaccg
 120
 tacttcgggt tcgagatccc gggcgagcca ggcaagtatt tctacgtgtg gctggacgcg
 180
 ccgatcggtt acatggccag tttcaagaac ctgtgctgac gcacgcccga gctggacttc
 240
 gatgctttct gggccaagga ctccaccgcc gagctgtacc atttcacgga caaggacatc
 300
 gtcaacttcc acgccctgtt ctggccggcg atgctcgaag gctcggggcta ccgtaaaccg
 360
 accggt
 366

<210> 2068

<211> 122

<212> PRT

<213> Homo sapiens

<400> 2068

Phe	Gln	Gln	Met	Leu	Gln	Thr	Trp	Thr	Arg	Ser	Gly	Thr	Leu	Gln	Glu
1			5						10					15	
Ala	Val	Ala	Asn	Lys	Ile	Ala	Glu	Trp	Leu	Asp	Ala	Asp	Leu	Gln	Gln
			20				25						30		
Trp	Asp	Ile	Ser	Arg	Asp	Ala	Pro	Tyr	Phe	Gly	Phe	Glu	Ile	Pro	Gly
		35				40					45				
Glu	Pro	Gly	Lys	Tyr	Phe	Tyr	Val	Trp	Leu	Asp	Ala	Pro	Ile	Gly	Tyr
	50					55				60					
Met	Ala	Ser	Phe	Lys	Asn	Leu	Cys	Asp	Arg	Thr	Pro	Glu	Leu	Asp	Phe
65				70					75					80	
Asp	Ala	Phe	Trp	Ala	Lys	Asp	Ser	Thr	Ala	Glu	Leu	Tyr	His	Phe	Ile
			85					90					95		
Gly	Lys	Asp	Ile	Val	Asn	Phe	His	Ala	Leu	Phe	Trp	Pro	Ala	Met	Leu
		100					105						110		
Glu	Gly	Ser	Gly	Tyr	Arg	Lys	Pro	Thr	Gly						
	115						120								

<210> 2069

<211> 280

<212> DNA

<213> Homo sapiens

<400> 2069

ccatagagagg atgggtggaga ctgtgctgtg gcaggggtgt ccggaacctt cctctgggatg
 60
 catggggcct cgccgcaggc catctctcca gacctgggct caccctgccg ctgtgctgtt
 120
 gcctttggct ggaattccac ccagccttc ttgcctcaag aacgcccttc ccccttcaga
 180

tctcatgggc acaggccccc tcttcctaaa cggggtcaga gccccagta atcatgacaa
 240
 agaccctctc ctgcagcaag ctttgggtcaa gctcctaccc
 280

<210> 2070
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 2070
 Met Val Glu Thr Val Arg Val Gln Gly Val Pro Glu Pro Ser Leu Gly
 1 5 10 15
 Cys Met Gly Pro Arg Arg Pro Ser Leu Gln Thr Trp Ala His Pro
 20 25 30
 Ala Pro Val Leu Leu Pro Leu Ala Gly Ile Pro Pro Gln Pro Ser Cys
 35 40 45
 Leu Lys Asn Ala Leu Pro Pro Ser Asp Leu Met Gly Thr Gly Pro Val
 50 55 60
 Phe Leu Asn Gly Val Arg Ala Pro Ser Asn His Asp Lys Asp Pro Leu
 65 70 75 80
 Leu Asp Gln Ala Leu Val Lys Leu Leu Pro
 85 90

<210> 2071
 <211> 399
 <212> DNA
 <213> Homo sapiens

<400> 2071
 acgcgtgtcc agcagactta gaaagcaggt tcctcttctc atacagcacg ttaacatagc
 60
 tgacagggcc tgggtgtctt catcagtact gtgatgactc ttccaccttt gacttcagat
 120
 gctggcgctt ttactttttt gtgccaaact ctacacatga aacacttttg gaataactac
 180
 agacatgact ttctttatct ggggaaaagg agggcattaa accagattag gggctgggag
 240
 gggagggtgt caggggatga gctgctcctg aggaagaggg agagatcaag cttcactcag
 300
 cagctggatt ctcacctagt ttatagactg aaatcctgca aggtggttac aacagtgaac
 360
 aatatgttca tacataaaga ctctaccctc aggtgatca
 399

<210> 2072
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 2072
 Met Thr Leu Ser Pro Leu Thr Ser Asp Ala Gly Ala Phe Tyr Phe Leu
 1 5 10 15
 Cys Gln Thr Leu His Met Lys His Phe Trp Asn Asn Tyr Arg His Asp


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                20                25                30
Phe Leu Tyr Leu Gly Lys Arg Arg Ala Leu Asn Gln Ile Arg Gly Trp
      35                40                45
Glu Gly Arg Leu Ser Gly Asp Glu Leu Leu Leu Arg Lys Arg Gln Arg
      50                55                60
Ser Ser Phe Thr Gln Gln Leu Asp Ser His Leu Val Tyr Arg Leu Lys
      65                70                75                80
Ser Cys Lys Val Val Thr Thr Val Asn Asn Met Phe Ile His Lys Asp
      85                90                95
Ser Thr Leu Arg
      100

```

<210> 2073

<211> 339

<212> DNA

<213> Homo sapiens

<400> 2073

```

ggatccactt ctgtgccttt ccagcttcta gaggcgcct gcgttccttg gctcgtggcc
60
ccttcctcca ccttcaagcc agcagcggag gctgagtcct ttctcatgcc atctctctgt
120
tctctctect gcctectect ccacactgaa ggacccctgt gatcacactg gccccccac
180
cggatgaccc aggataatcc atctccctgt ttgaaggctg gctgattagc aaccttcatt
240
ccatctgcct ccttcattcc ccttggccat gtaatgggat tcacagcttc tggggattag
300
gacatggaca tcttgtggcg ggggcataat tctgtcgac
339

```

<210> 2074

<211> 85

<212> PRT

<213> Homo sapiens

<400> 2074

```

Met Lys Glu Ala Asp Gly Met Lys Val Ala Asn Gln Pro Thr Phe Lys
  1                5                10                15
Gln Gly Asp Gly Leu Ser Trp Val Ile Arg Trp Gly Gly Gln Cys Asp
      20                25                30
His Arg Gly Pro Ser Val Trp Arg Arg Arg Gln Glu Arg Glu Arg
      35                40                45
Asp Gly Met Arg Arg Thr Gln Ala Ser Ala Ala Gly Leu Lys Val Glu
      50                55                60
Glu Gly Ala Thr Ser Gln Gly Thr Gln Ala Ala Ser Arg Ser Trp Lys
      65                70                75                80
Gly Thr Glu Val Asp
      85

```

<210> 2075

<211> 481

<212> DNA

<213> Homo sapiens

<400> 2075

ntggccagggt tgacctcaaa ggtgtacatt gttttatgtg gcgacaatgg actgtcagaa
 60
 accaaggagc tctctgtcc agagaagtcc ctgtttgaaa ggaattccag acacaccttt
 120
 atcctgagcg ctcctgcccc actgggcctg ctgaggaaga tccgcctctg gcacgacagc
 180
 cgtgggcctt cccaggctg gttcatcagc cacgtgatgg tgaaggagct gcacacggga
 240
 cagggctggg tcttccctgc ccagtgtctg ctgtctgccg gcaggcatga tggctcgctg
 300
 gagcgggagc tcacctgtct gcaaggggga ctcggtctct ggaagctttt ctattgcaag
 360
 ttcacagagt acctggagga ttccatgtc tggctgtcgg tgtacagcag gccctctctc
 420
 agccgctacc tgcacacgcc gcgccccacc gtgtctctct cctgtctgtg cgtctacgcg
 480
 t
 481

<210> 2076

<211> 160

<212> PRT

<213> Homo sapiens

<400> 2076

Xaa	Ala	Arg	Leu	Thr	Ser	Lys	Val	Tyr	Ile	Val	Leu	Cys	Gly	Asp	Asn
1				5					10					15	
Gly	Leu	Ser	Glu	Thr	Lys	Glu	Leu	Ser	Cys	Pro	Glu	Lys	Ser	Leu	Phe
		20						25					30		
Glu	Arg	Asn	Ser	Arg	His	Thr	Phe	Ile	Leu	Ser	Ala	Pro	Ala	Gln	Leu
	35					40						45			
Gly	Leu	Leu	Arg	Lys	Ile	Arg	Leu	Trp	His	Asp	Ser	Arg	Gly	Pro	Ser
	50				55					60					
Pro	Gly	Trp	Phe	Ile	Ser	His	Val	Met	Val	Lys	Glu	Leu	His	Thr	Gly
65				70						75				80	
Gln	Gly	Trp	Phe	Phe	Pro	Ala	Gln	Cys	Trp	Leu	Ser	Ala	Gly	Arg	His
		85						90						95	
Asp	Gly	Arg	Val	Glu	Arg	Glu	Leu	Thr	Cys	Leu	Gln	Gly	Gly	Leu	Gly
	100					105						110			
Phe	Trp	Lys	Leu	Phe	Tyr	Cys	Lys	Phe	Thr	Glu	Tyr	Leu	Glu	Asp	Phe
	115					120						125			
His	Val	Trp	Leu	Ser	Val	Tyr	Ser	Arg	Pro	Ser	Ser	Ser	Arg	Tyr	Leu
	130				135					140					
His	Thr	Pro	Arg	Pro	Thr	Val	Ser	Phe	Ser	Leu	Leu	Cys	Val	Tyr	Ala
145				150						155					160

<210> 2077

<211> 1410

<212> DNA

<213> Homo sapiens

<400> 2077

ncagagtgtt ttgagctatc tggatatccca aatgatgtga atacttttcag aaaccaatgg
60
caaattgaac ccaactgttt gcgaattcgg cagcagtaaa gatctttttt tttttttgt
120
ttttttttt ttttttttt ttttgccttc taaagtggct ttaatatcac acaagcggct
180
ctttggctca cagtgcagaga aaacagaggg agccaggaaa ggctccccgc tggcctctgg
240
agtccaggag ccttaggaag gctgaaacaa gccctgacca gcaggcttag ttgtctctgag
300
aagagccagt gaggccacct ggtccagttc accaggtttc ccagggaagc acaggcatct
360
ctgggtcccc gagcacagtgc ccagggaaga ccccccaat ccccatctga acaggccgag
420
ggcagcatgg gaaaggctca gactgcaggt tcatccccga ggatggaag gacacgtgct
480
ctccccctgc aagagcaggc ttgtgcacag cccggcacag ggccagccag ggcgggcccc
540
gcggctgtgc agcgcttacc agggggaggga gttcagccat caggaccttt tccaagtggg
600
tctgctgggc cagcacagcc actcgcagct tgaggggccgc cagggtctgc agctcctggg
660
tgctggagta gacaagcagc tggggnngct ccatgcaggc tccgctctac cccacaggga
720
cggcgaggct ccgggggggc tnnccccaca gacatggtct tggtggtctgt tccgccaccg
780
ctgcacgcag etcctgcagc ctgtgcagac actggccacc catggcctgc agccccctca
840
cgctgagcag gcagcgggtac tcttgcattc agtccatggg ggctgctgag agctctctcc
900
tcatcgcgag tctcagcagc gagcaggcct tccgcaggcg ccccgccctcc gcctccacct
960
ccacagcact gagcctgggc tggggggccgc ctgaagctgt ctgcattgtc tggaggaaat
1020
gggttttggc agcggcggca tccgtggaat cactgggtctg tgtggaactg agctggggcc
1080
acaggctcga gttctgggaa gctgctttcc tgaatgccgc aggcagccgc agcagggtgc
1140
ccttctcctc gagtgtgaag gcttctgggg cctgaggagc agcggatggg gccatttgc
1200
ggctccctgag gcccgcccca ggcctggggg ttcgggctcc catccaaca cgggtcccat
1260
ccccactga cagcagccgc cgctcagggt ggcccttggc aggcaccgtg gtctggcgga
1320
ggcccttggg gggtctctgt tctgaagcat ggccaccagc ttggcctggg gaatgcggtg
1380
ggcgaggagc tgtcgtgcca gaagaggtga
1410

<210> 2078

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2078

Gly His Leu Val Gln Phe Thr Arg Phe Pro Arg Glu Ala Gln Ala Ser
 1 5 10 15
 Leu Gly Pro Arg Ala Gln Cys Gln Gly Arg His Pro Gln Ser Pro Ser
 20 25 30
 Glu Gln Ala Glu Gly Ser Met Gly Lys Ala Gln Thr Ala Gly Ser Ser
 35 40 45
 Arg Arg Met Val Arg Thr Arg Ala Pro Pro Ser Gln Glu Gln Ala Cys
 50 55 60
 Ala Gln Pro Gly Thr Gly Pro Ala Arg Ala Ala Pro Ala Ala Val Gln
 65 70 75 80
 Arg Leu Pro Gly Gly Gly Val Gln Pro Ser Gly Pro Phe Pro Ser Gly
 85 90 95
 Ser Ala Gly Pro Ala Gln Pro Leu Ala Ala
 100 105

<210> 2079

<211> 565

<212> DNA

<213> Homo sapiens

<400> 2079

atttacctcg caaccgaccc tgatcgtgaa ggtgaaagca tcagctggca catccagcag
 60
 gtactggcgg tcaaatccta caaacgcatt accttcaacg agatcactct caagcgcgtt
 120
 gaagaggcac tggccaatcc tcgacaaatc gatctgaaca gagttgcctc acaggaatgc
 180
 cggcgtgtgc ttgaccgctt ggtgggggtac ctgggtgaccc aagagttgcg gcgcctgatg
 240
 ggcaaaccta cttccgctgg ccgcgttcaa tcacccgcgg tggttcttgt ggtcttgccg
 300
 gaacgcgaga tccgcaactt tcaggtgata aatcactttg gcgtgcgtct gttctttgcc
 360
 gatgtaagtc ggggcaccac ttggtatgcc gagtggcaac cggtaccgga tttcgcaagc
 420
 aagcacttcc cctatgttca ggatagcaac ctggctcagc acgtcgccgg cactcgaaat
 480
 gtggctcgtg agtctcgga ggatcgcaag gccgagcgtc atctctctgc accattcatc
 540
 tcatccactc ttcaacaggc cgcca
 565

<210> 2080

<211> 188

<212> PRT

<213> Homo sapiens

<400> 2080

Ile Tyr Leu Ala Thr Asp Pro Asp Arg Glu Gly Glu Ser Ile Ser Trp
 1 5 10 15
 His Ile Gln Gln Val Leu Ala Val Lys Ser Tyr Lys Arg Ile Thr Phe
 20 25 30
 Asn Glu Ile Thr Leu Lys Arg Val Glu Glu Ala Leu Ala Asn Pro Arg

```

          35              40              45
Gln Ile Asp Leu Asn Arg Val Ala Ser Gln Glu Cys Arg Arg Val Leu
   50              55              60
Asp Arg Leu Val Gly Tyr Leu Val Thr Gln Glu Leu Arg Arg Leu Met
65              70              75
Gly Lys Pro Thr Ser Ala Gly Arg Val Gln Ser Pro Ala Val Phe Leu
          85              90              95
Val Val Leu Arg Glu Arg Glu Ile Arg Asn Phe Gln Val Ile Asn His
          100              105              110
Phe Gly Val Arg Leu Phe Phe Ala Asp Val Ser Arg Gly Thr Thr Trp
          115              120              125
Tyr Ala Glu Trp Gln Pro Val Pro Asp Phe Ala Ser Lys His Phe Pro
          130              135              140
Tyr Val Gln Asp Ser Asn Leu Ala Gln His Val Ala Gly Thr Arg Asn
145              150              155
Val Val Val Glu Ser Cys Glu Asp Arg Lys Ala Glu Arg His Pro Pro
          165              170              175
Ala Pro Phe Ile Ser Ser Thr Leu Gln Ala Ala
          180              185

```

<210> 2081

<211> 319

<212> DNA

<213> Homo sapiens

<400> 2081

```

aagcttatgg aaaaacgggg atacggagag gagtatataa atcgctataa aatgatgaca
60
aggttccatc atcaacgggt tccactagta attttggtgt gtggaactgc ctgtactgga
120
aaatcaacaa tcgtacaca acctgctcag aggtcgaatt tgcctaattgt ttgacagacg
180
gacatggtgt atgagctgct gccgacatca acagatgcgc cacttacttc agttcctgtg
240
tggtctcgcg attttaattc acctgaagag cttatcactg aattctgcag agaatgcaga
300
gttgtagcga agggtttgg
319

```

<210> 2082

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2082

```

Lys Leu Met Glu Lys Arg Gly Tyr Gly Glu Glu Tyr Ile Asn Arg Tyr
   1           5           10           15
Lys Met Met Thr Arg Phe His His Gln Arg Val Pro Leu Val Ile Leu
          20           25           30
Val Cys Gly Thr Ala Cys Thr Gly Lys Ser Thr Ile Ala Thr Gln Leu
          35           40           45
Ala Gln Arg Leu Asn Leu Pro Asn Val Leu Gln Thr Asp Met Val Tyr
          50           55           60
Glu Leu Leu Arg Thr Ser Thr Asp Ala Pro Leu Thr Ser Val Pro Val

```

```

65              70              75              80
Trp Ala Arg Asp Phe Asn Ser Pro Glu Glu Leu Ile Thr Glu Phe Cys
            85              90              95
Arg Glu Cys Arg Val Val Arg Lys Gly Leu
            100              105

```

<210> 2083

<211> 382

<212> DNA

<213> Homo sapiens

<400> 2083

```

nngcctgatt ggcacatggc cgtcgagtgc gctgtaacac gcaagcagct atataccatc
60
atacctactg ttgaatgcaa ctgtggccac gttttctgct ttggctgtgg ttgggatgga
120
caccagccgg tcatttgtgc tgtgtgccgc ttgtggctga aaaaatgtgc ggaatgacgt
180
gagacgtcca actggatcgg cgctaatacc aaggaatgcc ccaaactgctg ttcgacgatt
240
gaaaagaatg gcggatgtaa tcatatgacg tgcgcaagt gcaaatacga attttgtgtg
300
atttgctcgg gcccatggtc ggagcacgga aacaactatt acaactgcaa tcggtacgatt
360
gaaaaggcag gagatgaagg tn
382

```

<210> 2084

<211> 127

<212> PRT

<213> Homo sapiens

<400> 2084

```

Xaa Pro Asp Cys Asp Met Ala Val Glu Cys Ala Val Thr Arg Lys Gln
1      5      10      15
Leu Tyr Thr Ile Ile Pro Thr Val Glu Cys Asn Cys Gly His Val Phe
20     25     30
Cys Phe Gly Cys Gly Leu Asp Gly His Gln Pro Val Ile Cys Ala Val
35     40     45
Val Arg Leu Trp Leu Lys Lys Cys Ala Asp Asp Ser Glu Thr Ser Asn
50     55     60
Trp Ile Gly Ala Asn Thr Lys Glu Cys Pro Lys Cys Cys Ser Thr Ile
65     70     75     80
Glu Lys Asn Gly Gly Cys Asn His Met Thr Cys Arg Lys Cys Lys Tyr
85     90     95
Glu Phe Cys Trp Ile Cys Ser Gly Pro Trp Ser Glu His Gly Asn Asn
100    105    110
Tyr Tyr Asn Cys Asn Arg Tyr Asp Glu Lys Ala Gly Asp Glu Gly
115    120    125

```

<210> 2085

<211> 478

<212> DNA

<213> Homo sapiens

<400> 2085

nnggatecca aagaccgcga tattgccatg gtgttccaaa actatgcctt ctaccgcac
 60
 atgactgtcg ccgacaacat ggggttttgc ctcaaatgg cgaaagtggg taagaaagaa
 120
 atccggcgct gcgtggagga agccgcgaa ctctcgacc tcaccgacta tctggaccgc
 180
 aaacccaagg cactctccgg tggccagcgg cagcgcgctg ccattggggcg cgctattgtt
 240
 cgttcccccc gcgtcttctt gatggacgag cctctttcta acctggatgc gcgtctgcgt
 300
 gtccgcaccc gcgcccagat tgcggaactg cagcgccgcc tgggcaccac caccgtttat
 360
 gtcacccatg accaggtgga ggctatgacg atgggggatc gtgtggctgt tctctgtgcc
 420
 gggaaactgc agcaggtgga tactccacgt aatcttttcg accaccccg ctaacgcgt
 478

<210> 2086

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2086

Xaa Asp Pro Lys Asp Arg Asp Ile Ala Met Val Phe Gln Asn Tyr Ala
 1 5 10 15
 Leu Tyr Pro His Met Thr Val Ala Asp Asn Met Gly Phe Ala Leu Lys
 20 25 30
 Leu Ala Lys Val Asp Lys Lys Glu Ile Arg Arg Arg Val Glu Glu Ala
 35 40 45
 Ala Glu Leu Leu Asp Leu Thr Asp Tyr Leu Asp Arg Lys Pro Lys Ala
 50 55 60
 Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala Ile Val
 65 70 75 80
 Arg Ser Pro Arg Val Phe Leu Met Asp Glu Pro Leu Ser Asn Leu Asp
 85 90 95
 Ala Arg Leu Arg Val Arg Thr Arg Ala Gln Ile Ala Glu Leu Gln Arg
 100 105 110
 Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val Glu Ala
 115 120 125
 Met Thr Met Gly Asp Arg Val Ala Val Leu Cys Ala Gly Lys Leu Gln
 130 135 140
 Gln Val Asp Thr Pro Arg Asn Leu Phe Asp His Pro Ala Asn Ala
 145 150 155

<210> 2087

<211> 731

<212> DNA

<213> Homo sapiens

<400> 2087

gataattctc tacacggcat gagctgggga cgtaccccc ttgccaacgt cacctcacgg
 60

tcgtaccgtg gtgattagca gctagccgag gcgctagccg ccatataaga ttcccaaatt
 120
 aaaagaaaaa gcattgcgtc ggccaagaat tgctgtcgct gctgcaacgg ctactgcgt
 180
 ggctcgatca atcgcagcaa tcaccccctc ccccgaggag aagctaactc caataggcca
 240
 cgctcggtag ctcaagccgc tatcgccacg gatggaaagg ggaataatcaa caaggactgc
 300
 cgtgatgcag tcatcaacga tgcaaagctg cgtgccgcga ttgccgggtgc gttggttaag
 360
 gctggtattta gttccgcga cgcggtggct ctagcgcgc gtattgccag agaaatggca
 420
 aaagaggggc tcctcctcat caaccaccac aagctaaagg ctctcatcgg agcccagggtg
 480
 ggtctgctca ctgatgcgaa gatccagcgt gctgccgctg cagtggacct cggcatcaaa
 540
 gccactctag ctgcgacaat cattcccaac gcgctgcatt cagcggcatt caaggatgcg
 600
 gtggctgcgaa atcttgtcgc cgccggtctg acaagaagtt ggcaaaggct acgctgtcg
 660
 ccattgcgc aactgcgctc aatcccgctc tcgggccgat cgcaaagact gaggccatta
 720
 aggctgagat c
 731

<210> 2088

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2088

Met	Ala	Lys	Glu	Gly	Val	Leu	Leu	Ile	Asn	His	His	Lys	Leu	Lys	Ala
1				5				10					15		
Leu	Ile	Gly	Ala	Gln	Val	Gly	Leu	Leu	Thr	Asp	Ala	Lys	Ile	Gln	Arg
		20					25						30		
Ala	Ala	Ala	Ala	Val	Asp	Leu	Gly	Ile	Lys	Ala	Thr	Leu	Ala	Ala	Thr
		35				40						45			
Ile	Ile	Pro	Asn	Ala	Leu	His	Ser	Ala	Ala	Phe	Lys	Asp	Ala	Val	Val
	50					55					60				
Ala	Asn	Leu	Val	Ala	Ala	Gly	Leu	Thr	Arg	Ser	Trp	Gln	Arg	Leu	Arg
	65				70					75				80	
Leu	Ser	Pro	Leu	Pro	Gln	Leu	Arg	Ser	Ile	Pro	Leu	Ser	Gly	Arg	Ser
		85						90						95	
Gln	Arg	Leu	Arg	Pro	Leu	Arg	Leu	Arg							
		100						105							

<210> 2089

<211> 315

<212> DNA

<213> Homo sapiens

<400> 2089

accggtgtgg accagggtca gctgcgcgac gccatgtttt cctaccttcc ccaccacaag
 60

ctcggggaat tcgacatcga tctgttgctg gaccatcgcg attccccgca gcccatcatc
 120
 ttcgacacccg accacttcga ggggtacgag cgcccccgcc tcgtgtgtgca cgaagtcacc
 180
 gatcaacttg gccaaagcgtt ccttgatttg gaaggcccag agccggctct cggctgggaa
 240
 tcgttggtgg cgtctctcac gagtcttgct gactctatgg ggatccgtct gaccggcatt
 300
 accgattcga tcccg
 315

<210> 2090

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2090

Thr	Gly	Val	Asp	Gln	Ala	Gln	Leu	Arg	Asp	Ala	Met	Phe	Ser	Tyr	Leu
1			5						10					15	
Pro	His	His	Lys	Leu	Gly	Glu	Phe	Asp	Ile	Asp	Leu	Leu	Leu	Asp	His
			20				25						30		
Arg	Asp	Ser	Arg	Gln	Pro	Ile	Ile	Phe	Asp	Thr	Asp	His	Phe	Glu	Gly
			35				40					45			
Tyr	Glu	Arg	Pro	Arg	Leu	Val	Leu	His	Glu	Val	Thr	Asp	Gln	Leu	Gly
	50					55				60					
Gln	Ala	Phe	Leu	Val	Leu	Glu	Gly	Pro	Glu	Pro	Ala	Leu	Gly	Trp	Glu
65					70					75				80	
Ser	Leu	Val	Ala	Ser	Leu	Thr	Ser	Leu	Val	Asp	Ser	Met	Gly	Ile	Arg
				85					90					95	
Leu	Thr	Gly	Ile	Thr	Asp	Ser	Ile	Pro							
		100					105								

<210> 2091

<211> 322

<212> DNA

<213> Homo sapiens

<400> 2091

actcttgccc attgtctctg tctctgcggt tttctctctg tctctctgtg tctctgtctc
 60
 tgtgtccctg tccagttctg tnnctgtgtg tgcgcgcata tctctctgtg tctctgtgng
 120
 agtctctctg tcttttgtct ctgtctctct ctgtgtctct gccattttg gtctctgctt
 180
 tctttctctg gtgtgtctct ccattttctg ctctctctct ctgtctctct ccattttctg
 240
 cctctctctt tttctctctg tgtgtctctt ttgtctctct gtttctctgc gtgtctctgt
 300
 ccattttctg ccttccagc gt
 322

<210> 2092

<211> 107

<212> PRT

<213> Homo sapiens

<400> 2092

```

Thr Leu Val His Cys Leu Cys Leu Cys Val Phe Leu Ser Val Ser Leu
1      5      10      15
Cys Leu Cys Leu Cys Val Pro Val Gln Phe Cys Xaa Cys Val Cys Ala
20      25      30
His Leu Ser Leu Cys Leu Cys Xaa Ser Leu Cys Leu Phe Cys Leu Cys
35      40      45
Leu Ser Leu Cys Leu Cys Pro Phe Trp Ser Leu Leu Ser Phe Leu Cys
50      55      60
Val Ser Leu His Phe Cys Leu Ser Ser Ser Val Ser Leu His Phe Cys
65      70      75      80
Leu Cys Ser Phe Ser Leu Cys Val Ser Leu Leu Ser Leu Cys Phe Ser
85      90      95
Ala Cys Leu Cys Pro Phe Leu Ser Leu His Ala
100      105

```

<210> 2093

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2093

```

gccggcggtca tcgaaacgat caaggtggcg caatttcgcc tctgccatag tcgaaaaaatg
60
tttgggtgg cctaccgcg agagaccag gagatggtgc tcgatgcgca taaccgcgcc
120
tttgcgttct ttggcggcgt accgcagcgg gttatctacg acaaccttaa aaccgcagtg
180
gatgcgatct tggtcggcaa ggatcgaatc ttcaaccggc gcttcctggc gttggctaata
240
cattacctgt ttgaacctgt agcctgtacg cctgctgctg gctgggagaa gggccaagtt
300
gagaatcaag ttcgcaacat acgc
324

```

<210> 2094

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2094

```

Ala Gly Val Met Gln Thr Ile Lys Val Ala Gln Phe Arg Leu Cys His
1      5      10      15
Ser Arg Lys Met Phe Val Val Ala Tyr Pro Arg Glu Thr Gln Glu Met
20      25      30
Val Leu Asp Ala His Asn Arg Ala Phe Phe Gly Gly Val Pro
35      40      45
Gln Arg Val Ile Tyr Asp Asn Leu Lys Thr Ala Val Asp Ala Ile Leu
50      55      60
Val Gly Lys Asp Arg Ile Phe Asn Arg Arg Phe Leu Ala Leu Ala Asn
65      70      75      80
His Tyr Leu Phe Glu Pro Val Ala Cys Thr Pro Ala Ala Gly Trp Glu

```

```

      85                      90                      95
Lys Gly Gln Val Glu Asn Gln Val Arg Asn Ile Arg
      100                      105

<210> 2095
<211> 402
<212> DNA
<213> Homo sapiens

<400> 2095
cccggtcacag accaggaaga agcagacaat atgatcgctt ctttcgacac ttatgttcgc
60
accctgcccc ccgcccga aa tcttctgctt aaacaattcc atattgtgga tgttgccccg
120
cgcggtggtgg gcgtgggttc agtgggcacc cactccctgg tactgctact gtcggcccc
180
aatgatgaac ctcttctgct gcaagtga aa gaagccctcc ccagtgtcct caccacccat
240
gggaaactgc cggatgcttt ttcggaaactg tccgctgggg actcctccgg gtcctcccc
300
gataatcttg ataagcatat taaagccggc aatggctacc ggggtggtggc gtgccagcag
360
attctgcagg ccactcgga tccgctgctg gggtagacgc gt
402

<210> 2096
<211> 134
<212> PRT
<213> Homo sapiens

<400> 2096
Pro Val Thr Asp Gln Glu Glu Ala Asp Asn Met Ile Ala Ser Phe Asp
1 5 10 15
Thr Tyr Val Arg Thr Leu Pro Pro Ala Ala Asn Leu Leu Leu Lys Gln
20 25 30
Phe His Ile Val Asp Val Ala Arg Arg Val Val Gly Val Gly Ser Val
35 40 45
Gly Thr His Ser Leu Val Leu Leu Leu Ser Gly Pro Asn Asp Glu Pro
50 55 60
Leu Val Leu Gln Val Lys Glu Ala Leu Pro Ser Val Leu Thr Thr His
65 70 75 80
Gly Lys Leu Pro Asp Ala Phe Ser Glu Leu Ser Ala Gly Asp Ser Ser
85 90 95
Gly Leu Leu Pro Asp Asn Leu Asp Lys His Ile Lys Ala Gly Asn Gly
100 105 110
Tyr Arg Val Val Ala Cys Gln Gln Ile Leu Gln Ala His Ser Asp Pro
115 120 125
Leu Leu Gly Trp Thr Arg
130

<210> 2097
<211> 641
<212> DNA
<213> Homo sapiens

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<400> 2097
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 120
 gccatgagca aggaggaggc cgaccaggta ctgggcgtgc agctggggct gtctgtccgc
 180
 caccgcctcc cagcctcac ttcaggctcc ctcccagcca ggctggggcc tggccctcac
 240
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 300
 cgtccctct gcgtgtcact ctctgcctgt cctcactggt tcagggaacc ccagcctctc
 360
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 420
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 480
 ctccagctgg ccttagttt gagccgagaa gagcatgata aggtcagagc agcctccctg
 540
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 641

<210> 2098
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 2098
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 Pro Pro Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu
 20 25 30
 Glu Leu Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp
 35 40 45
 Gln Val Leu Gly Val Gln Leu Gly Leu Ser Val Arg His Pro Pro Pro
 50 55 60
 Arg Leu Thr Ser Gly Ser Leu Pro Ala Arg Arg Gly Pro Gly Pro His
 65 70 75 80
 Cys Arg Cys Ser Thr Cys Cys His Ser Ser Pro Pro Gln Ser Cys Leu
 85 90 95
 Ile Leu Thr Pro Pro Ser Leu Cys Val Ser Leu Ser Ala Cys Pro His
 100 105 110
 Trp Phe Arg Asp Pro Gln Pro Leu Phe Ile Arg Leu Tyr Leu Thr Leu
 115 120 125
 Ala Leu Pro Leu Thr Leu Pro Leu Ala Pro Pro Val Met Pro Leu Thr
 130 135 140
 Leu Ser Leu Pro Gln Pro Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln
 145 150 155 160
 Leu Gln Leu Ala Leu Ser Leu Ser Arg Glu Glu His Asp Lys Val Arg
 165 170 175
 Ala Ala Ser Leu Ser Leu Pro Leu Pro Gly Ala Pro Leu Arg Pro Ala

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          180          185          190
Pro Ser Pro Leu Pro Lys Ser Pro Pro Thr Ile Leu Leu Gly Pro Lys
      195          200          205
Pro Thr Gly Ser Arg
      210

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<210> 2099
 <211> 347
 <212> DNA
 <213> Homo sapiens

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<400> 2099
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120
agcacctgcc caccgggtgc tcagtggagg cagtgtccag ggctgctgtg cccacgtgtg
180
tgccctcaga catccctccc cagacacttg ctgcatgacc caggagggtg caggcagtg
240
cagtattctg ttcaggtgag ctcagaggtg gcagggtgct ggctgcggcc ctgcctcact
300
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347

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<210> 2100
 <211> 106
 <212> PRT
 <213> Homo sapiens

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<400> 2100
Met Asp Ser Thr Cys Pro Gln Gly Cys Ser Val Glu Ala Val Pro Arg
  1          5          10          15
Ala Ala Val Pro Met Arg Val Pro Cys Pro Leu Pro Asp Ala Asp Ser
      20          25          30
Thr Cys Pro Arg Gly Ala Gln Trp Arg Gln Cys Pro Gly Leu Leu Cys
      35          40          45
Pro Arg Val Cys Pro Gln Thr Ser Leu Pro Arg His Leu Leu His Asp
      50          55          60
Pro Gly Gly Gly Arg Gln Trp Gln Tyr Ser Val Gln Val Ser Ser Glu
      65          70          75          80
Val Ala Gly Ala Trp Leu Arg Pro Cys Leu Thr Pro Thr Ala Ser Ala
      85          90          95
Ser Ser Pro Leu Ala His Pro Thr Trp Pro
      100          105

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<210> 2101
 <211> 549
 <212> DNA
 <213> Homo sapiens

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<400> 2101
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60

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 120
 gggtgaacca cgacaagaat gagttgtggg ccagccttct catccaccctt gacgagctat
 180
 taacagtgtg gttggagacc ggaacgggtg gggatcagta tgtggcccgc tgtgacacca
 240
 ttggtactcc ggtccgtctg accttcgacc cagaaatcgt ggggtggtgt gagggggcca
 300
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 360
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 420
 ggcgtcctga gcgttcccac catctagact gctgactatg acgaccacaca ttttggccct
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 540
 ccctgacct
 549

<210> 2102
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 2102
 Met Gly Arg Asp Glu Leu Pro Leu Pro Thr Ala Thr Ser Leu Ala Leu
 1 5 10 15
 Cys Gly Leu Asn His Asp Lys Asn Glu Leu Leu Ala Ser Leu Leu Ile
 20 25 30
 His Leu Asp Glu Leu Leu Thr Val Trp Leu Glu Thr Gly Thr Val Arg
 35 40 45
 Asp Gln Tyr Val Ala Arg Cys Asp Thr Ile Gly Thr Pro Val Arg Leu
 50 55 60
 Thr Phe Asp Pro Glu Ile Val Gly Gly Gly Glu Gly Ala Ile Glu Gly
 65 70 75 80
 Ile Gly Val Asp Val Asp Val Asp Gly Ala Ile Val Val Glu Thr Ser
 85 90 95
 Asp Gly Arg Arg Ser Phe Asn Ala Ala Asp Val His His Leu Arg Thr
 100 105 110
 Arg

<210> 2103
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 2103
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 60
 atgattatgg cggcagtgcg acagatcccc gccaccatg agttactcgc ttcagggggt
 120
 tgggaggggg acgcatatcg gtacgaccag gttggtatgg aatcaaagg gaatgacgtc
 180

ggtatcgtcg gatcgaggc ggtcgggtgc cgggttgagg ctgtgatggc ggccatgggt
 240
 gcgaccgtgc gtgtcttcga cccgtggggc actcctgatt cttttccagc tggcgtgatg
 300
 gcatgtgatg atctcgatga ggttctgagg ctcagccgca tcctcactct ccacgctcgt
 360
 gccaacgagg acaaccgtca catgattggc gttgaacaat tagctgagat gcctgatggc
 420
 tccgtcctcg tcaactgtgc ccgtgggtcg ctgggtcgac
 459

<210> 2104

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2104

Xaa	Arg	Val	Thr	Tyr	Thr	Pro	Gly	Arg	Asn	Ala	Thr	Ala	Thr	Ala	Glu
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His	Thr	Ile	Ala	Met	Ile	Met	Ala	Ala	Val	Arg	Gln	Ile	Pro	Ala	His
		20					25					30			
His	Glu	Leu	Leu	Ala	Ser	Gly	Val	Trp	Glu	Gly	Asp	Ala	Tyr	Arg	Tyr
		35				40					45				
Asp	Gln	Val	Gly	Met	Glu	Ile	Lys	Gly	Asn	Asp	Val	Gly	Ile	Val	Gly
	50				55					60					
Cys	Gly	Ala	Val	Gly	Cys	Arg	Val	Ala	Ala	Val	Met	Ala	Ala	Met	Gly
65				70					75					80	
Ala	Thr	Val	Arg	Val	Phe	Asp	Pro	Trp	Ala	Thr	Pro	Asp	Ser	Phe	Pro
			85					90					95		
Ala	Gly	Val	Met	Ala	Cys	Asp	Asp	Leu	Asp	Glu	Val	Leu	Arg	Leu	Ser
		100				105						110			
Arg	Ile	Leu	Thr	Leu	His	Ala	Arg	Ala	Asn	Glu	Asp	Asn	Arg	His	Met
	115					120					125				
Ile	Gly	Val	Glu	Gln	Leu	Ala	Glu	Met	Pro	Asp	Gly	Ser	Val	Leu	Val
	130				135						140				
Asn	Cys	Ala	Arg	Gly	Ser	Leu	Val	Asp							
145					150										

<210> 2105

<211> 4057

<212> DNA

<213> Homo sapiens

<400> 2105

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 120
 cccctatatg gctccagtcg gttttggggg gggcagctaa gtgggggagg ggaacacaa
 180
 aagtttgggc aaaacattaa cctgacaaa cttgattccg gaaaaaaatc cctcaagagc
 240
 gcaaggccag cttagccaac tggcagctga gtggaaaagt tcagtcctct cgggcagctc
 300

cggtggcacc tagaggggag aggggtgcagg ctttgaagcc agaaagacat gsgatgcaagt
360
cttactttgc ttcttgctgt taccagttgg cctgacctta ggaatgtta tttaatctct
420
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480
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540
tgagcgacag gccatgggac tctgtcgtga taaccaagct tcaggggtgtg ggaagaggac
600
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660
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720
ctagaagctc cgagttctct tactcccagc agtgaactca gcagcccagg ccaaagtgag
780
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840
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960
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1020
acagcagcca cgttcttga gcagggcagc ttcagtgtgg atgacgtgca gactgtgagt
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1140
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1200
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ccttctcgcc caggagcagt tgggcagcag gaaggaagcc atgggctgcc ccagtcacag
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1380
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1860
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1920

ctttatatca attatacatt taatataatt taatttataaa taattttaaag attcttagga
 1980
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 2340
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 2580
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 2640
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 2700
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 3300
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 3360
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 3420
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 3540

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 3780
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 3900
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 4020
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 4057

<210> 2106

<211> 240

<212> PRT

<213> Homo sapiens

<400> 2106

Ser	Asn	Gln	Ser	Val	Phe	Leu	Leu	Phe	Ser	Asp	Leu	Leu	Pro	Gln	Leu
1				5					10				15		
Glu	Ala	Pro	Ser	Ser	Leu	Thr	Pro	Ser	Ser	Glu	Leu	Ser	Ser	Pro	Gly
			20					25					30		
Gln	Ser	Glu	Leu	Thr	Asn	Met	Asp	Leu	Ala	Ala	Leu	Phe	Ser	Asp	Thr
		35				40						45			
Pro	Ala	Asn	Ala	Ser	Gly	Ser	Ala	Gly	Gly	Ser	Asp	Glu	Ala	Leu	Asn
		50				55					60				
Ser	Gly	Ile	Leu	Thr	Ile	Asp	Val	Thr	Ser	Val	Ser	Ser	Ser	Leu	Gly
65				70				75						80	
Gly	Asn	Leu	Pro	Ala	Asn	Asn	Ser	Ser	Leu	Gly	Pro	Met	Glu	Pro	Leu
				85				90					95		
Val	Leu	Val	Ala	His	Ser	Asp	Ile	Pro	Pro	Ser	Leu	Asp	Ser	Pro	Leu
			100					105					110		
Val	Leu	Gly	Thr	Ala	Ala	Thr	Val	Leu	Gln	Gln	Gly	Ser	Phe	Ser	Val
		115				120						125			
Asp	Asp	Val	Gln	Thr	Val	Ser	Ala	Gly	Ala	Leu	Gly	Cys	Leu	Val	Ala
		130				135					140				
Leu	Pro	Met	Lys	Asn	Leu	Ser	Asp	Asp	Pro	Leu	Ala	Leu	Thr	Ser	Asn
145				150					155					160	
Ser	Asn	Leu	Ala	Ala	His	Ile	Thr	Thr	Pro	Thr	Ser	Ser	Ser	Thr	Pro
				165					170					175	
Arg	Glu	Asn	Ala	Ser	Val	Pro	Glu	Leu	Leu	Ala	Pro	Ile	Lys	Val	Glu
			180					185					190		
Pro	Asp	Ser	Pro	Ser	Arg	Pro	Gly	Ala	Val	Gly	Gln	Gln	Glu	Gly	Ser
		195				200						205			
His	Gly	Leu	Pro	Gln	Ser	Thr	Leu	Pro	Ser	Pro	Ala	Glu	Gln	His	Gly
	210					215					220				
Ala	Gln	Asp	Thr	Glu	Leu	Ser	Ala	Gly	Thr	Gly	Asn	Phe	Tyr	Leu	Val

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225                230                235                240

<210> 2107
<211> 305
<212> DNA
<213> Homo sapiens

<400> 2107
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agtcctggct tggtctctgt tccagatctt aatgattctt tgagtcagct ctcaggggag
120
gcctcaggcc tgggtgtctga aaacaccccc agacctgatg acagcagagc tatcgctcca
180
gcctccctcc aaatcaccag ttcttgttct ggtgaacccc tggacctgga ttccaaggat
240
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300
ccnccn
305

<210> 2108
<211> 92
<212> PRT
<213> Homo sapiens

<400> 2108
Met Ala Gln Val Pro Met Leu Asn Leu Leu Pro Ser Pro Gly Leu Ala
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Leu Val Pro Asp Leu Asn Asp Ser Leu Ser Pro Val Ser Gly Glu Ala
20      25      30
Ser Gly Leu Val Ser Glu Asn Thr Pro Arg Pro Asp Asp Ser Arg Ala
35      40      45
Ile Ala Pro Ala Ser Leu Gln Ile Thr Ser Ser Cys Ser Gly Glu Pro
50      55      60
Leu Asp Leu Asp Ser Lys Asp Val Ser Arg Pro Asp Ser Gln Gly Arg
65      70      75      80
Leu Cys Pro Ala Ser Asn Pro Ile Leu Ala Xaa Pro
85      90

<210> 2109
<211> 700
<212> DNA
<213> Homo sapiens

<400> 2109
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acgtttctcca gacgtccccc agcccaggcg agtcggcaag caaaggctac gaaaagaaaa
120
taccaagcgt ccagtgaggc tccccagcgc aaacggagga acgaaacttc atttctccca
180
gccaagaaaa ctagtgttaa agaaactcag aggactttta aggggaacgc acaaaaaaatg
240

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tttttccaa agaagcattc ggtagcaca agttagataga accaggagga gagacagtgc
 300
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 360
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 420
 ccacatttaa tttccacaat aaatacggtc ttaaaaatgt ctatgatgac cagtgttcag
 480
 aagcaaaagta ttcctgtggt gctggaaggc agagatgctc tcgtgagatc ccagacgggc
 540
 tcaggtaaaa ttcttgcccta ttgcatccct gtggtccagt cccctcaagc aatggagtca
 600
 aaaatacagc gcagtgatgg cccctatgcc ctggtgctcg tgccaacgag agaggtaagc
 660
 agggtccctt ttgggacaag tttaagcac atgctttcat
 700

<210> 2110

<211> 233

<212> PRT

<213> Homo sapiens

<400> 2110

Xaa	Ala	Ser	Pro	Thr	Gln	Thr	Met	Ala	Ala	Ala	Asp	Gly	Ser	Leu	Phe
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Asp	Asn	Pro	Arg	Thr	Phe	Ser	Arg	Arg	Pro	Pro	Ala	Gln	Ala	Ser	Arg
			20					25					30		
Gln	Ala	Lys	Ala	Thr	Lys	Arg	Lys	Tyr	Gln	Ala	Ser	Ser	Glu	Ala	Pro
		35					40					45			
Pro	Ala	Lys	Arg	Arg	Asn	Glu	Thr	Ser	Phe	Leu	Pro	Ala	Lys	Lys	Thr
		50				55				60					
Ser	Val	Lys	Glu	Thr	Gln	Arg	Thr	Phe	Lys	Gly	Asn	Ala	Gln	Lys	Met
					70					75				80	
Phe	Ser	Pro	Lys	Lys	His	Ser	Val	Ser	Thr	Ser	Asp	Arg	Asn	Gln	Glu
				85					90					95	
Glu	Arg	Gln	Cys	Ile	Lys	Thr	Ser	Ser	Leu	Phe	Lys	Asn	Asn	Pro	Asp
			100					105					110		
Ile	Pro	Glu	Leu	His	Arg	Pro	Val	Val	Lys	Gln	Val	Gln	Glu	Lys	Val
			115				120					125			
Phe	Thr	Ser	Ala	Ala	Phe	His	Glu	Leu	Gly	Leu	His	Pro	His	Leu	Ile
			130			135					140				
Ser	Thr	Ile	Asn	Thr	Val	Leu	Lys	Met	Ser	Ser	Met	Thr	Ser	Val	Gln
				150					155					160	
Lys	Gln	Ser	Ile	Pro	Val	Leu	Leu	Glu	Gly	Arg	Asp	Ala	Leu	Val	Arg
				165					170					175	
Ser	Gln	Thr	Gly	Ser	Gly	Lys	Ile	Leu	Ala	Tyr	Cys	Ile	Pro	Val	Val
			180				185						190		
Gln	Ser	Leu	Gln	Ala	Met	Glu	Ser	Lys	Ile	Gln	Arg	Ser	Asp	Gly	Pro
			195				200					205			
Tyr	Ala	Leu	Val	Leu	Val	Pro	Thr	Arg	Glu	Val	Ser	Arg	Leu	Pro	Phe
			210			215						220			
Gly	Thr	Ser	Phe	Lys	His	Met	Leu	Ser							
225							230								

<210> 2111
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 2111
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 180
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 300
 cggggcaacg aagtggatga aagctggacc gacgcactg
 339

<210> 2112
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 2112
 Thr Arg Cys Ala Gly Pro Asp Pro Ile Ile Ala Ala Gln Arg Phe Gly
 1 5 10 15
 Ala Val Ser Asp Gln Met Glu Ile Thr Arg Lys Ala Leu Lys Lys His
 20 25 30
 Gly Arg Gly Asn Lys Leu Ala Ile Ala Glu Leu Val Ala Leu Ala Glu
 35 40 45
 Leu Phe Met Pro Ile Lys Leu Val Pro Lys Gln Phe Glu Gly Leu Val
 50 55 60
 Glu Arg Val Arg Ser Ala Leu Glu Arg Leu Arg Ala Gln Glu Arg Ala
 65 70 75 80
 Ile Met Gln Leu Cys Val Arg Asp Ala Arg Met Pro Arg Ala Asp Phe
 85 90 95
 Leu Arg Gln Phe Pro Gly Asn Glu Val Asp Glu Ser Trp Thr Asp Ala
 100 105 110
 Leu

<210> 2113
 <211> 2329
 <212> DNA
 <213> Homo sapiens

<400> 2113
 nnatacaaaa agcttttcat gtttgaacgt gttccaccatg gcgaggagct ccacatgccc
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 atcacagtaa tctggggcgt gtccccagaa gacaatggca acccactaaa tcccaagagt
 120
 aaagggaagt tgacattaga tagcagtttt aacatcgcca gcccgcttc ccaggcctgg
 180

atTTTgcact tctgtcaaaa actgagaaaac caaacattct tttaccagac tgatgaacag
240
gaacttcacca gctgcttcat tgagacattc aaacagtgga tggaaaacca ggactgtgat
300
gagccctgcc tgtacccatg ctgcagccac tggagcttcc cctacaagca agagattttt
360
gaactgtgca tcaagagagc tatcatggag ctggaaaagga gtacagggta ccatttggat
420
agcaaaaacc cagggccgag gtttgatata aatgatacta tcagggcagt ggtgttagag
480
ttccagagta cctacctctt cactctggct tatgaaaaga tgcatacagt ttataaagag
540
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600
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720
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780
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840
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900
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1020
cagcttggga cttcatgat gctcatcatg tgtatcagtt gggctttcgc caccctcttt
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1140
aaaaaactac agtcagtgct cttttcccat gccttgtcta caagtcaccg tgacaaggga
1200
caaagcaaaa cacataccat aaatgcttat catttagatc ccagggggccc aaaatctgaa
1260
ctggagcatg agttttatga attagaacct ctggcttccc acagctgcac tgcccctgag
1320
aagaccactt atgaagagac ccacatctgc tctgaatttt tcaacagcca agcaagaat
1380
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1440
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1560
tgccagcaga tgggggactg cttgtgccaac cagtgtcttc ctaccactag cagctttgtc
1620
cagatccaaa acggcggtggc acctctgaag gccacacacc aagctgtcga gggctttgtg
1680
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1740
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1800

gaaaaaattg gcaagaccaa tgtacacagt cttcagagga gcatagaaga gcattctcca
 1860
 aagatggcag agccatcgtc atttgtctgc agaagcactg gatcggtact caaaacgtgt
 1920
 tgcgaccccg agaataaaca aagggaaactc tgtaaaaata gagacgtgag caatctggag
 1980
 agcagtgtag ggactgaaaa caaggcagga gggaaagtgg agctgagctt gtcacagacg
 2040
 gatgcaagtg tgaactcaga acatttcaat cagaatgaac caaaagtctt atttaatcat
 2100
 ttaaatggggg aggtgtggtg taggtcttgc ccaaataatt cacaaagttg tggcagaatt
 2160
 gtgagagtga agtgcaattc tgtggactgt caaatgccaa acatggaagc caatgtgcct
 2220
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 2280
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 2329

<210> 2114

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2114

Xaa	Tyr	Lys	Lys	Leu	Phe	Met	Phe	Glu	Arg	Val	His	His	Gly	Glu	Glu
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Leu	His	Met	Pro	Ile	Thr	Val	Ile	Trp	Gly	Val	Ser	Pro	Glu	Asp	Asn
			20					25					30		
Gly	Asn	Pro	Leu	Asn	Pro	Lys	Ser	Lys	Gly	Lys	Leu	Thr	Leu	Asp	Ser
			35				40				45				
Ser	Phe	Asn	Ile	Ala	Ser	Pro	Ala	Ser	Gln	Ala	Trp	Ile	Leu	His	Phe
	50				55				60						
Cys	Gln	Lys	Leu	Arg	Asn	Gln	Thr	Phe	Phe	Tyr	Gln	Thr	Asp	Glu	Gln
65				70				75					80		
Asp	Phe	Thr	Ser	Cys	Phe	Ile	Glu	Thr	Phe	Lys	Gln	Trp	Met	Glu	Asn
			85				90						95		
Gln	Asp	Cys	Asp	Glu	Pro	Ala	Leu	Tyr	Pro	Cys	Cys	Ser	His	Trp	Ser
			100				105					110			
Phe	Pro	Tyr	Lys	Gln	Glu	Ile	Phe	Glu	Leu	Cys	Ile	Lys	Arg	Ala	Ile
			115				120					125			
Met	Glu	Leu	Glu	Arg	Ser	Thr	Gly	Tyr	His	Leu	Asp	Ser	Lys	Thr	Pro
			130			135					140				
Gly	Pro	Arg	Phe	Asp	Ile	Asn	Asp	Thr	Ile	Arg	Ala	Val	Val	Leu	Glu
145				150				155						160	
Phe	Gln	Ser	Thr	Tyr	Leu	Phe	Thr	Leu	Ala	Tyr	Glu	Lys	Met	His	Gln
			165				170						175		
Phe	Tyr	Lys	Glu	Val	Asp	Ser	Trp	Ile	Ser	Ser	Glu	Leu	Ser	Ser	Ala
			180				185					190			
Pro	Glu	Gly	Leu	Ser	Asn	Gly	Trp	Phe	Val	Ser	Asn	Leu	Glu	Phe	Tyr
			195				200					205			
Asp	Leu	Gln	Asp	Ser	Leu	Ser	Asp	Gly	Thr	Leu	Ile	Ala	Met	Gly	Leu
			210			215					220				
Ser	Val	Ala	Val	Ala	Phe	Ser	Val	Met	Leu	Leu	Thr	Thr	Trp	Asn	Ile

225 230 235 240
 Ile Ile Ser Leu Tyr Ala Ile Ile Ser Ile Ala Gly Thr Ile Phe Val
 245 250 255
 Thr Val Gly Ser Leu Val Leu Leu Gly Trp Glu Leu Asn Val Leu Glu
 260 265 270
 Ser Val Thr Ile Ser Val Ala Val Gly Leu Ser Val Asp Phe Ala Val
 275 280 285
 His Tyr Gly Val Ala Tyr Arg Leu Ala Pro Asp Pro Asp Arg Glu Gly
 290 295 300
 Lys Val Ile Phe Ser Leu Ser Arg Val Gly Ser Ala Met Ala Met Ala
 305 310 315 320
 Ala Leu Thr Thr Phe Val Ala Gly Ala Met Met Ile Pro Ser Thr Val
 325 330 335
 Leu Ala Tyr Thr Gln Leu Gly Thr Phe Met Met Leu Ile Met Cys Ile
 340 345 350
 Ser Trp Ala Phe Ala Thr Phe Phe Gln Cys Met Cys Arg Cys Leu
 355 360 365
 Gly Pro Gln Gly Thr Cys Gly Gln Ile Pro Leu Pro Lys Lys Leu Gln
 370 375 380
 Cys Ser Ala Phe Ser His Ala Leu Ser Thr Ser Pro Ser Asp Lys Gly
 385 390 395 400
 Gln Ser Lys Thr His Thr Ile Asn Ala Tyr His Leu Asp Pro Arg Gly
 405 410 415
 Pro Lys Ser Glu Leu Glu His Glu Phe Tyr Glu Leu Glu Pro Leu Ala
 420 425 430
 Ser His Ser Cys Thr Ala Pro Glu Lys Thr Thr Tyr Glu Glu Thr His
 435 440 445
 Ile Cys Ser Glu Phe Phe Asn Ser Gln Ala Lys Asn Leu Gly Met Pro
 450 455 460
 Val His Ala Ala Tyr Asn Ser Glu Leu Ser Lys Ser Thr Glu Ser Asp
 465 470 475 480
 Thr Gly Ser Ala Leu Leu Gln Pro Pro Leu Glu Gln His Thr Val Cys
 485 490 495
 His Phe Phe Ser Leu Asn Gln Arg Cys Ser Cys Pro Asp Ala Tyr Lys
 500 505 510
 His Leu Asn Tyr Gly Pro His Ser Cys Gln Gln Met Gly Asp Cys Leu
 515 520 525
 Cys His Gln Cys Ser Pro Thr Thr Ser Ser Phe Val Gln Ile Gln Asn
 530 535 540
 Gly Val Ala Pro Leu Lys Ala Thr His Gln Ala Val Glu Gly Phe Val
 545 550 555 560
 His Pro Ile Thr His Ile His His Cys Pro Cys Leu Gln Gly Arg Val
 565 570 575
 Lys Pro Ala Gly Met Gln Asn Ser Leu Pro Arg Asn Phe Phe Leu His
 580 585 590
 Pro Val Gln His Ile Gln Ala Gln Glu Lys Ile Gly Lys Thr Asn Val
 595 600 605
 His Ser Leu Gln Arg Ser Ile Glu Glu His Leu Pro Lys Met Ala Glu
 610 615 620
 Pro Ser Ser Phe Val Cys Arg Ser Thr Gly Ser Leu Leu Lys Thr Cys
 625 630 635 640
 Cys Asp Pro Glu Asn Lys Gln Arg Glu Leu Cys Lys Asn Arg Asp Val
 645 650 655
 Ser Asn Leu Glu Ser Ser Gly Gly Thr Glu Asn Lys Ala Gly Gly Lys


```

        660                665                670
Val Glu Leu Ser Leu Ser Gln Thr Asp Ala Ser Val Asn Ser Glu His
        675                680                685
Phe Asn Gln Asn Glu Pro Lys Val Leu Phe Asn His Leu Met Gly Glu
        690                695                700
Ala Gly Cys Arg Ser Cys Pro Asn Asn Ser Gln Ser Cys Gly Arg Ile
        705                710                715                720
Val Arg Val Lys Cys Asn Ser Val Asp Cys Gln Met Pro Asn Met Glu
        725                730                735
Ala Asn Val Pro Ala Val Leu Thr His Ser Glu Leu Ser Gly Glu Ser
        740                745                750
Leu Leu Ile Lys Thr Leu
        755

```

<210> 2115

<211> 461

<212> DNA

<213> Homo sapiens

<400> 2115

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acgcgtctctt ggctctgggag cgggctcccc cgacacgcca ccttcctctgc cagatgggtgc
60
ttctgggtat tccagaatct ggaatggggg atgcctatcc ccctcctgag cccacctgct
120
ggctcttgggt ccttggagcc caccaagtcc acaaccacct gctctgaata gaaagctgac
180
attgaaccga acagccgcgt cggaggggga tatctgtgga gagctgtgac tgggagccgg
240
tgtgtgcctt tctgtgttca tttctcgagt cctctgccgg ctgctgccag gtgaaggcat
300
ctccatgccc agccggtggg cagctggggc ggggtggacat ccagcttctg cccgacgggg
360
ttcagatgac cgagatccta cgggattgcc aatgtgtggg gacggggggc tttcaggggc
420
gggaaaaacat gtccccatcc gtgggaagtg gagccacgtg g
461

```

<210> 2116

<211> 146

<212> PRT

<213> Homo sapiens

<400> 2116

```

Met Gly Thr Cys Phe Pro Ala Pro Glu Ser Pro Pro Ser Pro His Ile
1      5      10      15
Gly Asn Pro Val Gly Ser Arg Ser Ser Glu Pro Arg Arg Ala Glu Ala
20      25      30
Gly Gly Pro Pro Ala Pro Ala Ala His Arg Leu Gly Met Glu Met Pro
35      40      45
Ser Pro Gly Ser Ser Arg Gln Arg Thr Arg Glu Met Thr Thr Glu Arg
50      55      60
His Thr Pro Ala Pro Ser His Ser Ser Pro Gln Ile Ser Pro Ser Asp
65      70      75      80
Ala Ala Val Arg Phe Asn Val Ser Phe Leu Phe Arg Ala Gly Gly Cys

```

```

      85              90              95
Gly Leu Gly Gly Leu Gln Gly Pro Lys Thr Ser Arg Trp Ala Gln Glu
      100              105              110
Gly Asp Arg His Pro Pro Phe Gln Ile Leu Glu Tyr Pro Glu Ala Pro
      115              120              125
Ser Gly Arg Glu Gly Gly Val Ser Gly Glu Pro Ala Pro Arg Pro Glu
      130              135              140
Thr Arg
145

```

```

<210> 2117
<211> 360
<212> DNA
<213> Homo sapiens

```

```

<400> 2117
nnacgcgcttg gggagacgac ggtgaccttc ccagcaagct catcgaggga tgaacaatc
60
cgcgccagcg ttaagacctt ctccggggct gtcaccgccc atctggagaa gtgtggaccg
120
atcaggtgac actcgcggta gactgaatag atgcctgagt ctgaagacac tgtgtggctg
180
accctaagagg ccttcgataa gctcaccgag gagctggagt acctcaaagg cgaaggccgc
240
accgtcattg ccaacaagat tgcgcagccc cgctcgggaag gcgaccttcc tgagaacggc
300
ggctaccatg ccgcccgtag ggagcagggg caggccgagg cccgcatccc tcaactcgag
360

```

```

<210> 2118
<211> 70
<212> PRT
<213> Homo sapiens

```

```

<400> 2118
Met Pro Glu Ser Glu Asp Thr Val Trp Leu Thr Gln Glu Ala Phe Asp
1      5      10      15
Lys Leu Thr Gln Glu Leu Glu Tyr Leu Lys Gly Glu Gly Arg Thr Val
      20      25      30
Ile Ala Asn Lys Ile Ala Asp Ala Arg Ser Glu Gly Asp Leu Ser Glu
      35      40      45
Asn Gly Gly Tyr His Ala Ala Arg Glu Glu Gln Gly Gln Ala Glu Ala
      50      55      60
Arg Ile Arg Gln Leu Glu
65              70

```

```

<210> 2119
<211> 465
<212> DNA
<213> Homo sapiens

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```

<400> 2119
nacgcgtgaa gggcgctgt cgccctctca ctggcgcagc ctgcactgcc gctgccgcct
60

```

cgccccgcc ttgccttggc gttgtctctg gcactgtggc ggactgacca cggccccggc
 120
 atgggctgca agggagacgc gagcggagtt tgctataaaa tgggagttct ggttggtactc
 180
 actgtttctgt ggctgttctc ctacgtaaag gccgactcaa aagccattac aacctctctt
 240
 acaacaaaat ggttttccac tccattgttg ttagaagcca gtgagttttt agcagaagac
 300
 agtcaagaga aattttggaa tttttagtaa gccagtcaaa atattggatc atcagatcat
 360
 gacgggtaccg attattccta ctatcatgca atattggagg ctgcatttca gtttctgtca
 420
 ccctccagc agaatttgtt taaatttgtt ctgtcccttc acgcg
 465

<210> 2120

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2120

Met	Gly	Cys	Lys	Gly	Asp	Ala	Ser	Gly	Val	Cys	Tyr	Lys	Met	Gly	Val
1				5					10				15		
Leu	Val	Val	Leu	Thr	Val	Leu	Trp	Leu	Phe	Ser	Ser	Val	Lys	Ala	Asp
			20					25					30		
Ser	Lys	Ala	Ile	Thr	Thr	Ser	Leu	Thr	Thr	Lys	Trp	Phe	Ser	Thr	Pro
		35					40					45			
Leu	Leu	Leu	Glu	Ala	Ser	Glu	Phe	Leu	Ala	Glu	Asp	Ser	Gln	Glu	Lys
	50				55						60				
Phe	Trp	Asn	Phe	Val	Glu	Ala	Ser	Gln	Asn	Ile	Gly	Ser	Ser	Asp	His
65				70					75					80	
Asp	Gly	Thr	Asp	Tyr	Ser	Tyr	Tyr	His	Ala	Ile	Leu	Glu	Ala	Ala	Phe
			85					90					95		
Gln	Phe	Leu	Ser	Pro	Leu	Gln	Gln	Asn	Leu	Phe	Lys	Phe	Cys	Leu	Ser
		100						105					110		
Leu	His	Ala													
			115												

<210> 2121

<211> 336

<212> DNA

<213> Homo sapiens

<400> 2121

ccggacaagg tcaatggaat gaaaacctcc cgccgacag acaatagtat aaatgttaca
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 tgtggtcctc cttatgaaac taatggccct aaaacctttt acatttttgt agtcagaagt
 120
 ggagggttctt ttgttacaaa atacaacaag acaaaactgtc agttttatgt agataatctc
 180
 tactattcaa ctgactatga gtttctggtc tcttttcaca atggagtgtg cgaggagagt
 240
 tcagttataa gaaatgagtc aacaaatttt aatgctaaag ccctgattat attcctgggtg
 300

ttttctgatta ttgtgacatc aatagccttg cttgtt
336

<210> 2122
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2122
Pro Asp Lys Val Asn Gly Met Lys Thr Ser Arg Pro Thr Asp Asn Ser
1 5 10 15
Ile Asn Val Thr Cys Gly Pro Pro Tyr Glu Thr Asn Gly Pro Lys Thr
20 25 30
Phe Tyr Ile Leu Val Val Arg Ser Gly Gly Ser Phe Val Thr Lys Tyr
35 40 45
Asn Lys Thr Asn Cys Gln Phe Tyr Val Asp Asn Leu Tyr Tyr Ser Thr
50 55 60
Asp Tyr Glu Phe Leu Val Ser Phe His Asn Gly Val Tyr Glu Gly Asp
65 70 75 80
Ser Val Ile Arg Asn Glu Ser Thr Asn Phe Asn Ala Lys Ala Leu Ile
85 90 95
Ile Phe Leu Val Phe Leu Ile Ile Val Thr Ser Ile Ala Leu Leu Val
100 105 110

<210> 2123
<211> 426
<212> DNA
<213> Homo sapiens

<400> 2123
aactgggccc agttcggcaa cctgcacccg ttcgccccgg ccgagcaaaag cgctgggttat
60
cagcaactga ccgacgaact ggaagcgaat ctctgcgcgc ccacaggtta tgacgcgac
120
tccttcgcgc cgaacgctgg ctcccagggc gagtacgcgc gctcgtctggc gatccgcgct
180
taccaccaga gccgtggcga tgagcgtcgc gacatctgcc tgattccgtc ctctgcccc
240
ggcaccacaac cggaaccgc caacatggcc ggcatgcgcg tggtcgtgac cgcttgcgac
300
gcccgcgcca acgtcgacat cgaagacctg cgcgccaagg ctatcgagca ccgcgaacac
360
ctcgcgcgcg tgatgatcac ctaccgcgtc acccacggcg tgttcgaaga aggcattccgc
420
gagatc
426

<210> 2124
<211> 142
<212> PRT
<213> Homo sapiens

<400> 2124
Asn Trp Ala Glu Phe Gly Asn Leu His Pro Phe Ala Pro Ala Glu Gln

```

      1           5           10           15
Ser Ala Gly Tyr Gln Gln Leu Thr Asp Glu Leu Glu Ala Met Leu Cys
      20           25           30
Ala Ala Thr Gly Tyr Asp Ala Ile Ser Leu Gln Pro Asn Ala Gly Ser
      35           40           45
Gln Gly Glu Tyr Ala Gly Leu Leu Ala Ile Arg Ala Tyr His Gln Ser
      50           55           60
Arg Gly Asp Glu Arg Arg Asp Ile Cys Leu Ile Pro Ser Ser Ala His
      65           70           75           80
Gly Thr Asn Pro Ala Thr Ala Asn Met Ala Gly Met Arg Val Val Val
      85           90           95
Thr Ala Cys Asp Ala Arg Gly Asn Val Asp Ile Glu Asp Leu Arg Ala
      100          105          110
Lys Ala Ile Glu His Arg Glu His Leu Ala Ala Leu Met Ile Thr Tyr
      115          120          125
Pro Ser Thr His Gly Val Phe Glu Gly Ile Arg Glu Ile
      130          135          140

```

<210> 2125

<211> 285

<212> DNA

<213> Homo sapiens

<400> 2125

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ngtatggcat ctgctgcttc aagttttgtg gtgacaccaa atgtcacttc taacacaacc
60
acagtcaagc ccaatatggt tatgttacct attcaaaaca caagagggttc aagattggtt
120
ctaaaggcgg ctgaagacgc ggcaccaccg gctgtcaccg ttgaagcggc caaggaagag
180
aagccgaagc caccaccaat tggacctaa agaggagcca aggtgagaat tcttaggaag
240
gagtcatact ggttcaaagg agtgggatca gttgtgactg ttgat
285

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<210> 2126

<211> 95

<212> PRT

<213> Homo sapiens

<400> 2126

```

Xaa Met Ala Ser Ala Ala Ser Ser Phe Val Val Thr Pro Asn Val Thr
1           5           10           15
Ser Asn Thr Thr Thr Val Lys Pro Asn Met Val Met Leu Pro Ile Gln
      20           25           30
Asn Thr Arg Gly Ser Arg Leu Val Leu Lys Ala Ala Glu Asp Ala Ala
      35           40           45
Pro Pro Ala Val Thr Val Glu Ala Ala Lys Glu Glu Lys Pro Lys Pro
      50           55           60
Pro Pro Ile Gly Pro Lys Arg Gly Ala Lys Val Arg Ile Leu Arg Lys
      65           70           75           80
Glu Ser Tyr Trp Phe Lys Gly Val Gly Ser Val Val Thr Val Asp
      85           90           95

```

<210> 2127
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 2127
 atggcagcca agatgcttgc attgttcgct ctcctagctc tttgtgcaag cgccactagt
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 gcgacgcata ttccagggca cttgtcacca gtcatgccat tgggtaccat gaacccatgc
 120
 atgcagtact gcatgatgca acaggggctt gccagcttga tggcggtgcc gtccttgatg
 180
 ctgcagcaac tgttggcctt accgcttcag acgatgccag tgatgatgcc acagatgatg
 240
 acgcctaaca tgatgtcacc attgatgatg ccgagcatga tgtcaccaat ggtcttgccg
 300
 agcatgatgt cgcaaatgat gatgccacaa tgtcactgcg acgccgtctc gcagattatg
 360
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 420
 ttacagcaac cctttgttgg tgctgcattc taga
 454

<210> 2128
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 2128
 Met Ala Ala Lys Met Leu Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
 1 5 10 15
 Ser Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Val Met
 20 25 30
 Pro Leu Gly Thr Met Asn Pro Cys Met Gln Tyr Cys Met Met Gln Gln
 35 40 45
 Gly Leu Ala Ser Leu Met Ala Cys Pro Ser Leu Met Leu Gln Gln Leu
 50 55 60
 Leu Ala Leu Pro Leu Gln Thr Met Pro Val Met Met Pro Gln Met Met
 65 70 75 80
 Thr Pro Asn Met Met Ser Pro Leu Met Met Pro Ser Met Met Ser Pro
 85 90 95
 Met Val Leu Pro Ser Met Met Ser Gln Met Met Pro Gln Cys His
 100 105 110
 Cys Asp Ala Val Ser Gln Ile Met Leu Gln Gln Gln Leu Pro Phe Met
 115 120 125
 Phe Asn Pro Met Ala Met Thr Ile Pro Pro Met Phe Leu Gln Gln Pro
 130 135 140
 Phe Val Gly Ala Ala Phe
 145 150

<210> 2129
 <211> 354
 <212> DNA
 <213> Homo sapiens

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<400> 2129
acgcgtgact tggatgaacaa acccatatcc atcaccacct tcggtgttga tacggaaaata
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ctcacgcccc ttgacaagcg gcgtgatgcy aacggcggtg acgggggtgt gcgcatcggg
120
actatcaagg ctctccactc caaatatggg atcgggtgaac tcattccgtgc cttcagtcgg
180
gtccatgatg aacggcctaa taccgtcctt cgtatctggg gcggcgggccc agacgagaat
240
ccccccaagg tcttggtcgc cgtcttctgc ccggacggtt cgggtggagt tcgcggtgccc
300
attgatcatt ctgaggtcag aaatgccttg gtagtttgg acatctttgc cgcc
354

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<210> 2130

<211> 118

<212> PRT

<213> Homo sapiens

<400> 2130

```

Thr Arg Asp Leu Val Asn Lys Pro Ile Ser Ile Thr Pro Phe Gly Val
1           5           10          15
Asp Thr Glu Ile Leu Thr Pro Phe Asp Lys Arg Arg Asp Ala Asn Gly
20          25          30
Gly Asp Gly Val Val Arg Ile Gly Thr Ile Lys Ala Leu His Ser Lys
35          40          45
Tyr Gly Ile Gly Glu Leu Ile Arg Ala Phe Ser Arg Val His Asp Glu
50          55          60
Arg Pro Asn Thr Val Leu Arg Ile Trp Gly Gly Gly Pro Asp Glu Asn
65          70          75          80
Pro Leu Lys Val Leu Ala Arg Arg Leu Val Pro Asp Gly Ser Val Glu
85          90          95
Phe Arg Gly Ala Ile Asp His Ser Glu Val Arg Asn Ala Leu Gly Ser
100         105         110
Leu Asp Ile Phe Ala Ala
115

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<210> 2131

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2131

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gcatacgccg cattggttat gtgtgcctat tccattgggt atgtggaagg ttgggatcag
60
ccagacagtc attatgatgg ttgtttacag ctgggcgagt ggggctttcg aatcaatgac
120
ctgatgaaga cggtagaggg gcgcgcaggg tgcattgagt attatgaaat gctcaacgaa
180
caacgccccg acttgtctta tgacatagac ggtattgttt ataaagtga tcagattgac
240
ctgcaagaag agcttggttt tattgctcgt gcgccacgct gggcaattgc tcgaaaaattt
300

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cctgctcaag aagaagttac gcgt
324

<210> 2132
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2132
Ala Ser Arg Pro Leu Val Met Cys Ala Tyr Ser Ile Gly Tyr Val Glu
1 5 10 15
Gly Trp Asp Gln Pro Asp Ser His Tyr Asp Gly Leu Leu Gln Leu Gly
20 25 30
Glu Trp Gly Phe Arg Ile Asn Asp Leu Met Lys Thr Val Glu Gly Ala
35 40 45
Ala Gly Cys Ile Glu Tyr Tyr Glu Met Leu Asn Glu Gln Arg Pro Asp
50 55 60
Leu Ser Tyr Asp Ile Asp Gly Ile Val Tyr Lys Val Asp Gln Ile Asp
65 70 75 80
Leu Gln Glu Glu Leu Gly Phe Ile Ala Arg Ala Pro Arg Trp Ala Ile
85 90 95
Ala Arg Lys Phe Pro Ala Gln Glu Glu Val Thr Arg
100 105

<210> 2133
<211> 292
<212> DNA
<213> Homo sapiens

<400> 2133
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gtggctgtct ttagaggacc cggcgaactt ttcctgcttt ttccacttg ctccatcaca
120
taccatcacat caccaacacc catcacatac atacacagtc atgaacggcc atcaggccac
180
accagattac atcgctgtgg atccaaccct gcatttttct gccctctctt tactgcgagt
240
gtcacctcta cccggaaagg tcttcaacct ccaagtttcc cagtaattta tt
292

<210> 2134
<211> 93
<212> PRT
<213> Homo sapiens

<400> 2134
Met Val Leu His Asp Met Asn Lys Phe Phe Leu Thr Leu Asn Ser Leu
1 5 10 15
Val Ala Val Phe Arg Gly Pro Gly Glu Leu Phe Leu Leu Phe Pro Thr
20 25 30
Cys Ser Ile Thr Tyr Ile Thr Ser Pro Thr Pro Ile Thr Tyr Ile His
35 40 45
Ser His Glu Arg Pro Ser Gly His Thr Arg Leu His Arg Cys Gly Ser

50	55	60
Asn Pro Ala Phe Ser Cys Pro Ser Phe Thr Ala Ser Val Thr Ser Thr		
65	70	75
Arg Lys Gly Leu Gln Pro Pro Ser Phe Pro Val Ile Tyr		80
85	90	

<210> 2135

<211> 439

<212> DNA

<213> Homo sapiens

<400> 2135

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actccgagcg tcgaccaaact cgagatgcat ccctcgttca accaggcgac cttccgcgca
120
gagctggcgg agcgcggcat taaccggag gcctggagcc cgctggggcca gtcgaaggac
180
ctcgacaatc ccgtcctcac cgatatattcc aaggcgactg gaaagacgcc tgcccagggtg
240
gtcattcgct ggcacctgca gatcggcaac gtggtattcc ccaagtcggt gacaccatca
300
cgaattgcgg agaactttga tgtgttcgat ttcgagctgt ctgacagagca gatcggccgca
360
attgatggcc tggatcacgg caacaggctc ggtgggtgacc cttctaccgc cgacttctga
420
ttctgcaaca ataaccggt
439

<210> 2136

<211> 139

<212> PRT

<213> Homo sapiens

<400> 2136

Thr Arg Ser Ile Gly Val Ser Asn Phe Lys Thr Glu His Leu Asp Ala		
1	5	10
Ile Glu Gly Ala Thr Pro Ser Val Asp Gln Ile Glu Met His Pro Ser		
20	25	30
Phe Asn Gln Ala Thr Phe Arg Ala Glu Leu Ala Glu Arg Gly Ile Asn		
35	40	45
Pro Glu Ala Trp Ser Pro Leu Gly Gln Ser Lys Asp Leu Asp Asn Pro		
50	55	60
Val Leu Thr Asp Ile Ser Lys Ala Thr Gly Lys Thr Pro Ala Gln Val		
65	70	75
Val Ile Arg Trp His Leu Gln Ile Gly Asn Val Val Phe Pro Lys Ser		
85	90	95
Val Thr Pro Ser Arg Ile Ala Glu Asn Phe Asp Val Phe Asp Phe Glu		
100	105	110
Leu Ser Asp Glu Gln Ile Ala Ala Ile Asp Gly Leu Asp His Gly Asn		
115	120	125
Arg Leu Gly Gly Asp Pro Ser Thr Ala Asp Phe		
130	135	

<210> 2137
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 2137
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 tccgggacag agatggctgg cggagcctgg ggccgcctgg cctgttactt ggagttcctg
 120
 aagaaggagg agctgaagga gttccagctt ctgctcgcca ataaagcgca ctccaggagc
 180
 tcttcgggtg agacacccgc tcagccagag aagacgagtg gcatggagggt ggcctcgtag
 240
 ctggtggctc agtatgggga gcagcgggccc tgggacctag cctccatac ctgggagcag
 300
 atgggggtga ggctactgtg cgccaagcc
 330

<210> 2138
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 2138
 Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
 1 5 10 15
 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
 20 25 30
 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
 35 40 45
 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
 50 55 60
 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
 65 70 75 80
 Ser Leu Cys Ala Gln Ala
 85

<210> 2139
 <211> 433
 <212> DNA
 <213> Homo sapiens

<400> 2139
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 gtgaacaagc tggcgagtag catcgccag tacaacgatc agatttccaa agtcaccacc
 120
 gccgcgggtg ccccgaaaga cctgctggac cagcgcagcg aggcgggtgc ccagttgtcc
 180
 gagctggtgc ggaccagggt ggtccagcgc ggttcgagtt atgacgtcta tateggcagc
 240
 ggtcagcgcc tgggtgatggg caacagcacc aacacctgt cgcgagtgc gagcaaggac
 300

gaccgcgagcc agtcggcctt gcagctggat cgcgccacca gcaccgtcga tatcacctcc
 360
 acggtgacccg gtggcgagat cgggtggtctg ctgcgctatc gcagcgatgt gctcgacccg
 420
 tcgatcaacg cgt
 433

<210> 2140

<211> 144

<212> PRT

<213> Homo sapiens

<400> 2140

Glu	Gln	Leu	Ser	Ala	Gln	Asn	Thr	Gly	Ile	Asn	Ser	Asn	Leu	Ser	Asp
1				5					10				15		
Met	Ala	Gly	Gln	Val	Asn	Lys	Leu	Ala	Ser	Thr	Ile	Ala	Gln	Tyr	Asn
			20					25					30		
Asp	Gln	Ile	Ser	Lys	Val	Thr	Thr	Ala	Ala	Gly	Ala	Pro	Asn	Asp	Leu
		35					40				45				
Leu	Asp	Gln	Arg	Ser	Glu	Ala	Val	Arg	Gln	Leu	Ser	Glu	Leu	Val	Gly
	50					55					60				
Thr	Gln	Val	Val	Gln	Arg	Gly	Ser	Ser	Tyr	Asp	Val	Tyr	Ile	Gly	Ser
65					70					75				80	
Gly	Gln	Arg	Leu	Val	Met	Gly	Asn	Ser	Thr	Asn	Thr	Leu	Ser	Ala	Val
			85						90					95	
Pro	Ser	Lys	Asp	Asp	Pro	Ser	Gln	Ser	Ala	Leu	Gln	Leu	Asp	Arg	Gly
			100					105						110	
Thr	Ser	Thr	Val	Asp	Ile	Thr	Ser	Thr	Val	Thr	Gly	Gly	Glu	Ile	Gly
		115				120						125			
Gly	Leu	Leu	Arg	Tyr	Arg	Ser	Asp	Val	Leu	Asp	Pro	Ser	Ile	Asn	Ala
	130					135						140			

<210> 2141

<211> 426

<212> DNA

<213> Homo sapiens

<400> 2141

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 gtttatccctt atctttctttt ccgcttgatc aatgatattg tggataaagg cgaagtgtta
 120
 ggtgacccaa ttgcttgatc tgttaaatat cgtaaaagga ttaacaaagg cttgatgaaa
 180
 atcctgtcta aaatgggtat ttcaacgatt gcctcttata gtggtgcgca attggttgaa
 240
 gcggttggtc tggatactaa agtggctgac ctttgtttca aaggcgttgc aagtcgtatc
 300
 aaagggtgctc gttttgaaga tttccagcgt gatcaagcaa cgattgccaa taatgcttgg
 360
 aagttacgta aacctattca acagggcggt tatcttaaat acgtacatga ctctgagtat
 420
 cagcgcg
 426

<210> 2142
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 2142
 Xaa Tyr Pro Cys Ser Asp Pro His Gln Phe Ala Val Leu Leu Gly Phe
 1 5 10 15
 Gly Ala Thr Ala Val Tyr Pro Tyr Leu Ser Phe Arg Leu Ile Asn Asp
 20 25 30
 Met Val Asp Lys Gly Glu Val Leu Gly Asp Pro Ile Ala Cys His Val
 35 40 45
 Lys Tyr Arg Lys Gly Ile Asn Lys Gly Leu Met Lys Ile Leu Ser Lys
 50 55 60
 Met Gly Ile Ser Thr Ile Ala Ser Tyr Arg Gly Ala Gln Leu Phe Glu
 65 70 75 80
 Ala Val Gly Leu Asp Thr Lys Val Val Asp Leu Cys Phe Lys Gly Val
 85 90 95
 Ala Ser Arg Ile Lys Gly Ala Arg Phe Glu Asp Phe Gln Arg Asp Gln
 100 105 110
 Ala Thr Ile Ala Asn Asn Ala Trp Lys Leu Arg Lys Pro Ile Gln Gln
 115 120 125
 Gly Gly Tyr Leu Lys Tyr Val His Asp Ser Glu Tyr His Ala
 130 135 140

<210> 2143
 <211> 1008
 <212> DNA
 <213> Homo sapiens

<400> 2143
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 tgtcatattg tacgcagtat gtcttttcaa cgattcttgg cgggggtggc agccatcttg
 120
 cttctcctgc ctactcgtg cgctgatgat gcgcaggcgc ccgttgcga taacctcggg
 180
 acggctctca gcccctccaa etccctcatt cgcgagccgg cgaattcgtc agtcaacggg
 240
 acgctcaaga gcacatatga gtacctccgg ctcatcgacg gtcacgatct acccgacgac
 300
 gatggctacg etcatgatca tctggtcggc gctttgcgcc cgtatttggg gaatgggtga
 360
 gacagtcggc agggccacgt caccacaact atggcggcgt catccctgaa aacctcAAC
 420
 gcgttgcctg acaaggagag atcagaggtc gacaaacgta cccgcctgcc gaagggtgc
 480
 atcacgagaa agacggtgat gacggatctg cccatcgaga cgatgaggcg ggagatcggc
 540
 ctgtccaacg acgggttgtg cctcacaccg tggaagggtca agacgacttc ttccgaggag
 600
 gctcgggtgg cgatgcaggc gctggccagt gccgacctat tcagcaatgc taaggacgcc
 660

gagaaatggg ggtgggagtc gatctcggac gggattttgc gccatctcga gacctacagt
 720
 ggccccagta cgactatcgc gatggccttg tcggcggcga ataccgtctc tacattgtct
 780
 cgttcccaagt tgcaacgcat cggcgacagt ctgcgggtagt cgccatatcc gaggaaggac
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 900
 gcgtacctgt tgaggttattc cgggaattgg gcgtggtgac atgacggttt cttggcaagg
 960
 tgtgaccaag acattccctt cgggcgattc cgcgcgtggg ggggtgcac
 1008

<210> 2144

<211> 307

<212> PRT

<213> Homo sapiens

<400> 2144

Met	Phe	Thr	Gly	Asp	Ala	Val	Val	Ile	Val	Glu	Val	Ser	Gln	Leu	Cys
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His	Ile	Val	Arg	Ser	Met	Ser	Phe	Gln	Arg	Phe	Leu	Ala	Gly	Val	Ala
			20					25					30		
Ala	Ile	Leu	Leu	Leu	Pro	Thr	Ala	Cys	Ala	Asp	Asp	Ala	Gln	Ala	
		35				40					45				
Pro	Val	Val	Asp	Asn	Leu	Gly	Thr	Val	Leu	Ser	Pro	Ser	Asn	Ser	Leu
		50				55					60				
Ile	Arg	Glu	Pro	Ala	Asn	Ser	Ser	Val	Asn	Gly	Thr	Leu	Lys	Ser	Thr
65					70					75				80	
Tyr	Glu	Tyr	Leu	Arg	Leu	Ile	Asp	Gly	His	Asp	Leu	Pro	Asp	Asp	Asp
				85					90					95	
Gly	Tyr	Ala	His	Asp	His	Leu	Val	Ala	Ala	Leu	Arg	Pro	Tyr	Leu	Val
		100						105					110		
Asn	Gly	Gly	Asp	Ser	Arg	Gln	Ala	His	Val	Thr	Gln	Leu	Met	Ala	Ala
		115				120						125			
Ser	Ser	Leu	Lys	Thr	Leu	Asn	Ala	Leu	Ser	Asp	Lys	Glu	Arg	Ser	Glu
		130				135					140				
Val	Asp	Lys	Arg	Thr	Arg	Leu	Pro	Lys	Gly	Cys	Ile	Thr	Arg	Lys	Thr
145					150					155				160	
Val	Met	Thr	Asp	Leu	Pro	Ile	Ala	Thr	Met	Arg	Arg	Glu	Ile	Gly	Leu
				165					170					175	
Ser	Asn	Asp	Gly	Leu	Cys	Leu	Thr	Pro	Trp	Lys	Val	Lys	Thr	Thr	Ser
		180						185					190		
Ser	Glu	Glu	Ala	Arg	Trp	Ala	Met	Gln	Ala	Leu	Ala	Ser	Ala	Asp	Leu
		195					200					205			
Phe	Ser	Asn	Ala	Lys	Asp	Ala	Glu	Lys	Trp	Gly	Trp	Glu	Ser	Ile	Ser
		210				215					220				
Asp	Gly	Tyr	Leu	Arg	His	Leu	Glu	Thr	Tyr	Ser	Gly	Pro	Ser	Thr	Thr
225					230					235				240	
Ile	Ala	Met	Ala	Leu	Ser	Ala	Ala	Asn	Thr	Val	Ser	Thr	Leu	Ser	Arg
			245						250					255	
Ser	Gln	Leu	Gln	Arg	Ile	Gly	Asp	Ser	Leu	Ala	Asp	Ala	Pro	Tyr	Pro
		260					265						270		
Arg	Lys	Asp	Leu	Gly	Pro	Ala	Leu	Ile	Arg	Asn	Gly	Lys	Pro	Val	Lys

275
Asp Lys Cys Ser Ile Glu Ser Ala Tyr Leu Leu Arg Tyr Ser Gly Asn
290 295 300

Trp Ala Trp
305

<210> 2145
<211> 389
<212> DNA
<213> Homo sapiens

<400> 2145
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atgacaaccc ttgaacaatc attatctcaa attcccgcat tttcgattat tcatgaacat
120
ttatttagct cggcccagcc tcttgcgtgaa caactaaaat tgattaaaga gtttggttgt
180
agcacagtca ttaaccttgc tttaactaat gcttcaaatc atcttgagaa tgaagaccgt
240
atttcttttag accttgggtt aaattatatt catattccaa ttgattggga gatgccttct
300
gctgagcagt gcttattagt tttagatttg attgatcatt tagtgcaaaa tgaattgttt
360
tggatacatt gcgcaaaaaa taaacgcgt
389

<210> 2146
<211> 109
<212> PRT
<213> Homo sapiens

<400> 2146
Met Thr Thr Leu Glu Gln Ser Leu Ser Gln Ile Pro Ala Phe Ser Ile
1 5 10 15
Ile His Glu His Leu Phe Ser Ser Ala Gln Pro Ser Ala Glu Gln Leu
20 25 30
Lys Leu Ile Lys Glu Phe Gly Cys Ser Thr Val Ile Asn Leu Ala Leu
35 40 45
Thr Asn Ala Ser Asn His Leu Glu Asn Glu Asp Arg Ile Cys Leu Asp
50 55 60
Leu Gly Leu Asn Tyr Ile His Ile Pro Ile Asp Trp Glu Met Pro Ser
65 70 75 80
Ala Glu Gln Cys Leu Leu Val Leu Asp Leu Ile Asp His Leu Val Gln
85 90 95
Asn Glu Ile Val Trp Ile His Cys Ala Lys Asn Lys Arg
100 105

<210> 2147
<211> 235
<212> DNA
<213> Homo sapiens

<400> 2147

ctccctgctg gctgcgtctc cgaggacatg tgcagtcctg acccctgttt caatgggtggg
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 acttgccctg tcacctggaa tgacttccac tgtacctgcc ctgccaatTT cagggggcct
 120
 acatgtgccc agcagctgtg gtgtcccgcc cagccctgtc tccacactgc cagtggtgtg
 180
 gcggaggcca cgttccgcga gggteccccc gccgcgttca gcgggcacaa cgcgt
 235

<210> 2148

<211> 78

<212> PRT

<213> Homo sapiens

<400> 2148

Leu	Pro	Ala	Gly	Cys	Val	Ser	Glu	Asp	Met	Cys	Ser	Pro	Asp	Pro	Cys
1				5					10					15	
Phe	Asn	Gly	Gly	Thr	Cys	Leu	Val	Thr	Trp	Asn	Asp	Phe	His	Cys	Thr
			20					25					30		
Cys	Pro	Ala	Asn	Phe	Thr	Gly	Pro	Thr	Cys	Ala	Gln	Gln	Leu	Trp	Cys
		35					40					45			
Pro	Gly	Gln	Pro	Cys	Leu	Pro	Pro	Ala	Thr	Cys	Val	Ala	Glu	Ala	Thr
		50				55					60				
Phe	Arg	Glu	Gly	Pro	Pro	Ala	Ala	Phe	Ser	Gly	His	Asn	Ala		
65					70						75				

<210> 2149

<211> 1474

<212> DNA

<213> Homo sapiens

<400> 2149

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 120
 caacacgtgg gagtaagact tctcctgtctc tttgccagtg gtctgagggtg atgaaccacc
 180
 ctggcttggt gtgctgtgtc cagcaaaacta caggggtgcc gctggtagtt atgggtgaaac
 240
 cagacacttt tcttatccac gagattaaga ctcttctctgc taaagcgaag atccaagaca
 300
 tggttgtctat taggcacacg gcctgcaatg agcagcagcg gacaacaatg attctgctgt
 360
 gtgaggatgg cagcctgcgc atttaccatgg ccaacgtgga gaacacctcc tactgggtgc
 420
 agccatccct gcagcccagc agtgtcatca gcatcatgaa gcctgttcga aagcgcaaaa
 480
 cagctacaat cacaaccng cagctctagc caggtgactt tcccattga cttttttgaa
 540
 cacaaccagc agctgacaga tgtggagttt ggtggtaacg acctctaca ggtctataat
 600
 gcacaacaga taaaacaccg gctgaattcc actggcatgt atggggccaa caccaagccc
 660

ggaggcttca ccattgagat tagtaacaac aatagcacta tggatgatgac aggcattgcgg
 720
 atccagattg ggactcaagc aatagaacgg gccccgtcat atatcgagat ctctggcaga
 780
 actatgcagc tcaacctgag tcgctcacgc tggtttgact tccccctcac cagagaagaa
 840
 gccctgcagg ctgataagaa gctgaacctc ttcattgggg cctcggtgga tccagcaggt
 900
 gtcacataga tagatgctgt aaaaatttat ggcaagacta aggagcagtt tggctggcct
 960
 gatgagcccc cagaagaatt cccttctgcc tctgtcagca acatctgccc ttcaaatctg
 1020
 aaccagagca acggcactgg agatagcgac tcagctgccc ccaactacgac cagtggaaact
 1080
 gtcttgagga ggctggttgt gagttcttta gaagccctgg aaagctgctt tgcggttgcc
 1140
 ccaatcatcg agaaggagag aaacaagaat gctgctcagg agctggccac ttgtctgtg
 1200
 tccctgccag cactgccag tgtccagcag cagtccaaga gccttctggc cagcctgcac
 1260
 accagccgtg cggcctacca cagccacaag gtaactgttc tctcaggaaa aggaaattgc
 1320
 agtgctgaca gggaatcaaa taagttagct ctctattgta aagcaacagc acagcaaatg
 1380
 aaggtagagg gaggatagca ttcagattag acctacattt tacagagttt ctctcgagaa
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 attctcaagt gccactcaaa actgagggta agcc
 1474

<210> 2150

<211> 312

<212> PRT

<213> Homo sapiens

<400> 2150

Ser	Leu	Phe	Glu	Ser	Ala	Lys	Gln	Leu	Gln	Ser	Gln	Pro	Xaa	Thr	Ser
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Ser	Gln	Val	Thr	Phe	Pro	Ile	Asp	Phe	Phe	Glu	His	Asn	Gln	Gln	Leu
		20						25					30		
Thr	Asp	Val	Glu	Phe	Gly	Gly	Asn	Asp	Leu	Leu	Gln	Val	Tyr	Asn	Ala
		35					40					45			
Gln	Gln	Ile	Lys	His	Arg	Leu	Asn	Ser	Thr	Gly	Met	Tyr	Val	Ala	Asn
		50				55				60					
Thr	Lys	Pro	Gly	Gly	Phe	Thr	Ile	Glu	Ile	Ser	Asn	Asn	Asn	Ser	Thr
65				70						75				80	
Met	Val	Met	Thr	Gly	Met	Arg	Ile	Gln	Ile	Gly	Thr	Gln	Ala	Ile	Glu
				85				90					95		
Arg	Ala	Pro	Ser	Tyr	Ile	Glu	Ile	Phe	Gly	Arg	Thr	Met	Gln	Leu	Asn
		100						105				110			
Leu	Ser	Arg	Ser	Arg	Trp	Phe	Asp	Phe	Pro	Phe	Thr	Arg	Glu	Glu	Ala
		115				120						125			
Leu	Gln	Ala	Asp	Lys	Lys	Leu	Asn	Leu	Phe	Ile	Gly	Ala	Ser	Val	Asp
		130				135					140				
Pro	Ala	Gly	Val	Thr	Met	Ile	Asp	Ala	Val	Lys	Ile	Tyr	Gly	Lys	Thr


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145              150              155              160
Lys Glu Gln Phe Gly Trp Pro Asp Glu Pro Glu Glu Phe Pro Ser
              165              170              175
Ala Ser Val Ser Asn Ile Cys Pro Ser Asn Leu Asn Gln Ser Asn Gly
              180              185              190
Thr Gly Asp Ser Asp Ser Ala Ala Pro Thr Thr Thr Ser Gly Thr Val
              195              200              205
Leu Glu Arg Leu Val Val Ser Ser Leu Glu Ala Leu Glu Ser Cys Phe
              210              215              220
Ala Val Gly Pro Ile Ile Glu Lys Glu Arg Asn Lys Asn Ala Ala Gln
              225              230              235              240
Glu Leu Ala Thr Leu Leu Leu Ser Leu Pro Ala Pro Ala Ser Val Gln
              245              250              255
Gln Gln Ser Lys Ser Leu Leu Ala Ser Leu His Thr Ser Arg Ser Ala
              260              265              270
Tyr His Ser His Lys Val Thr Val Leu Ser Gly Lys Gly Asn Cys Ser
              275              280              285
Ala Asp Arg Glu Ser Asn Lys Leu Ala Leu His Cys Lys Ala Thr Ala
              290              295              300
Gln Gln Ser Lys Val Glu Gly Gly
305              310

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<210> 2151
<211> 511
<212> DNA
<213> Homo sapiens

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<400> 2151
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120
gtgcatcagc gctcctttca gttgaccggg atcgccgac cattgcgggc gctggctcgt
180
gagctggcgg ccgaggtgcg ggtgctgtgt ttcgatgagc tggctcgtcaa tgacatcggt
240
gacgcgatca ttctcggggc cctgtttcag gtgatgttcg acgcaggcgt ggtggtggtc
300
tgcacctcca atctgccgcc ggatcagctg tatgccgacg gtttcaaccg cgaccgcttc
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420
gatcatcgct tgcattccgg cgccatcgag cagcgttact gggctcgtct gccgggagcag
480
ggtagcgcgt tgagccaggt gttcgacgcg t
511

```

```

<210> 2152
<211> 170
<212> PRT
<213> Homo sapiens

```

```

<400> 2152
Ala Gly Val Tyr Leu Trp Gly Pro Val Gly Arg Gly Lys Thr Trp Leu

```

1	5	10	15
Met Asp Gln Phe His Gln Ser Leu Xaa Gly Cys Arg Arg Xaa Arg Gln			
20	25	30	
His Phe His His Phe Met Gly Trp Val His Gln Arg Ser Phe Gln Leu			
35	40	45	
Thr Gly Ile Ala Asp Pro Leu Arg Ala Leu Ala Arg Glu Leu Ala Ala			
50	55	60	
Glu Val Arg Val Leu Cys Phe Asp Glu Leu Phe Val Asn Asp Ile Gly			
65	70	75	80
Asp Ala Ile Ile Leu Gly Arg Leu Phe Gln Val Met Phe Asp Ala Gly			
85	90	95	
Val Val Val Val Cys Thr Ser Asn Leu Pro Pro Asp Gln Leu Tyr Ala			
100	105	110	
Asp Gly Phe Asn Arg Asp Arg Phe Leu Pro Ala Ile Thr Ala Ile Lys			
115	120	125	
Gln His Met Gln Val Val Ala Val Asn Gly Ala Glu Asp His Arg Leu			
130	135	140	
His Pro Gly Ala Ile Glu Gln Arg Tyr Trp Val Ala Leu Pro Glu Gln			
145	150	155	160
Gly Ser Ala Leu Ser Gln Val Phe Asp Ala			
165	170		

<210> 2153

<211> 528

<212> DNA

<213> Homo sapiens

<400> 2153

nnaccggtgc caaagagctg gggatcaacc tgccgaacac cgccggtacg cagcaggtgt
 60
 tcagttacgtg cagcgcgatt ggcggcgcca attgggacca ctccgcgctg atcaagggcc
 120
 tggagcatat ggccaacttt tcgattcgcg atcaataagc cacaccgctc ccacctttga
 180
 tggcattcca agtctgaaat tgatccatct ctaataacaa aaatccccgg gagcccgtt
 240
 atgtcggtcg atccgcaaca cctgcttcgc gagctgtttg ccacagccat cgatgccgcc
 300
 caccgccggc atgtccttga accttatctg ccgctgacc gcacaggccg tgtgattgtg
 360
 attgggcccg gcaaaaccgc acccgccatg gccctcgctg tcgagaaagg ctggcaaggc
 420
 gaagtccagg gccttggtgt caccgcgtac ggccacggcg cgccgtgcaa aaaaatcgaa
 480
 gtggtcgagg ccgctcaccc ggtgcgggat gccgcgggcc tggcggtg
 528

<210> 2154

<211> 96

<212> PRT

<213> Homo sapiens

<400> 2154

Met Ser Val Asp Pro Gln His Leu Leu Arg Glu Leu Phe Ala Thr Ala

```

      1           5           10           15
Ile Asp Ala Ala His Pro Arg His Val Leu Glu Pro Tyr Leu Pro Ala
      20           25           30
Asp Arg Thr Gly Arg Val Ile Val Ile Gly Pro Gly Lys Thr Ala Pro
      35           40           45
Ala Met Ala Leu Val Val Glu Asn Gly Trp Gln Gly Glu Val Thr Gly
      50           55           60
Leu Val Val Thr Arg Tyr Gly His Gly Ala Pro Cys Lys Lys Ile Glu
      65           70           75           80
Val Val Glu Ala Ala His Pro Val Pro Asp Ala Ala Gly Leu Ala Val
      85           90           95

```

<210> 2155

<211> 297

<212> DNA

<213> Homo sapiens

<400> 2155

```

gtgcacgcgc acggcacacc cgccatgccg cgccgctatt tcgaggccct gctgcaggag
60
ttcgcccccg actgcgaggt gctcaccgtc accgattcag agggcaaccc cctcagttcg
120
gtgctcagtt tctacttcg tgatgaagt ctgccctact atcgggcgca cgccgtcgcg
180
gcgcgcgaac tggcggccaa tgacttcaaa tactgggagc tgatgcgacg cgcctgtgcg
240
cgcgccctca agtggtttga ctacggccgc agcaagcagg gcacgggctc ctacgcn
297

```

<210> 2156

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2156

```

Met Pro Arg Arg Tyr Phe Glu Ala Leu Leu Gln Glu Phe Gly Pro Asp
      1           5           10           15
Cys Glu Val Leu Thr Val Thr Asp Ser Glu Gly Asn Pro Leu Ser Ser
      20           25           30
Val Leu Ser Phe Tyr Phe Arg Asp Glu Val Leu Pro Tyr Tyr Ala Gly
      35           40           45
Asp Ala Val Ala Ala Arg Glu Leu Ala Ala Asn Asp Phe Lys Tyr Trp
      50           55           60
Glu Leu Met Arg Arg Ala Cys Ala Arg Gly Leu Lys Val Phe Asp Tyr
      65           70           75           80
Gly Arg Ser Lys Gln Gly Thr Gly Ser Tyr Ala
      85           90

```

<210> 2157

<211> 711

<212> DNA

<213> Homo sapiens

<400> 2157

naccgagata acgaggtcgt catcatctcc actgggtccc aaggtgagcc actttcggcc
 60
 ctagcaagga tcgccaaccg agagcaccga gacatcgagg tgggggaggg agataccgtt
 120
 ttgctggcat cctctctcat cccgggtaat gagaatgccg tctatcgagt gattaatggc
 180
 ctgacgaagc ttggcgccgc cgtggtacat aagggaacg ctttggtcca cgttccggc
 240
 catgccgagc ceggagagct gctgtacgag tataacatcg tgcggccacg cgctgtgatg
 300
 ccgattcatg gtgaggtgag tcattctgtc gctaattgcc atctggccaa agcaaccggt
 360
 gtcgatgaga acaacgtggt gcttgtcgag gacggcgggg ttattgacct tgttgacgga
 420
 gtaccgcgag ttgttgccaa ggtcgatgcc tcgtacatcc ttgttgacgg atctgggggtg
 480
 ggggagctta ccgaggacac gctcactgat cgcggtatcc tcggtaggga gggattcttg
 540
 tcagtcgtca ccgtgggtcga caccgctcgc gcgtcagtgg tgtctcgccc ggcatccag
 600
 gcgcgtggtt ttgccgaggg cgactcggtc ttcgcggaga tcaccgacca gatcgtcacc
 660
 gagctagaga aggcgatggc cgggtggtatg gacgataccc accggttgca a
 711

<210> 2158

<211> 237

<212> PRT

<213> Homo sapiens

<400> 2158

Xaa Arg Asp Asn Glu Val Val Ile Ile Ser Thr Gly Ser Gln Gly Glu
 1 5 10 15
 Pro Leu Ser Ala Leu Ala Arg Ile Ala Asn Arg Glu His Arg Asp Ile
 20 25 30
 Glu Val Gly Glu Gly Asp Thr Val Leu Leu Ala Ser Ser Leu Ile Pro
 35 40 45
 Gly Asn Glu Asn Ala Val Tyr Arg Val Ile Asn Gly Leu Thr Lys Leu
 50 55 60
 Gly Ala Ala Val Val His Lys Gly Asn Ala Leu Val His Val Ser Gly
 65 70 75 80
 His Ala Ala Ala Gly Glu Leu Leu Tyr Ala Tyr Asn Ile Val Arg Pro
 85 90 95
 Arg Ala Val Met Pro Ile His Gly Glu Val Arg His Leu Val Ala Asn
 100 105 110
 Ala Asp Leu Ala Lys Ala Thr Gly Val Asp Glu Asn Asn Val Val Leu
 115 120 125
 Val Glu Asp Gly Gly Val Ile Asp Leu Val Asp Gly Val Pro Arg Val
 130 135 140
 Val Gly Lys Val Asp Ala Ser Tyr Ile Leu Val Asp Gly Ser Gly Val
 145 150 155 160
 Gly Glu Leu Thr Glu Asp Thr Leu Thr Asp Arg Arg Ile Leu Gly Glu
 165 170 175
 Glu Gly Phe Leu Ser Val Val Thr Val Val Asp Thr Arg Ser Ala Ser

```

      180              185              190
Val Val Ser Arg Pro Ala Ile Gln Ala Arg Gly Phe Ala Glu Gly Asp
      195              200              205
Ser Val Phe Ala Glu Ile Thr Asp Gln Ile Val Thr Glu Leu Glu Lys
      210              215              220
Ala Met Ala Gly Gly Met Asp Asp Thr His Arg Leu Gln
      225              230              235

```

<210> 2159
 <211> 322
 <212> DNA
 <213> Homo sapiens

```

<400> 2159
tcgcgagcac actccagcct ctggagagac gacaacgcgt gaagggggcac cagcttgcgg
60
ggcagcagct ccagggggcgg cctgggaggg ctttgtgcag aagaagcctg ttctcttcta
120
cctgttttga aaagttgtct ctgcagatgg tgggtgagag ttcgctgcc gggccactgt
180
cttcctgcc ctgcggacac ttcttcccca ccttcctaaa gctgtgggag acctggagcc
240
gtgggagcatc aatggctctt tgactcagga atcttaaaaa atcacaccct ggggctacca
300
tgggggcctt ctggttctcc tt
322

```

<210> 2160
 <211> 100
 <212> PRT
 <213> Homo sapiens

```

<400> 2160
Met Val Ala Pro Gly Cys Asp Phe Leu Arg Phe Leu Ser Gln Arg Ala
1      5      10      15
Ile Asp Ala Pro Arg Leu Gln Val Ser His Ser Phe Arg Lys Val Gly
      20      25      30
Lys Lys Cys Pro Gln Gly Arg Glu Asp Ser Gly Pro Gly Ser Glu Leu
      35      40      45
Ser Pro Thr Ile Cys Arg Asp Asn Phe Ser Lys Gln Val Glu Gly Asn
      50      55      60
Arg Leu Leu Leu His Lys Ala Leu Pro Gly Arg Pro Trp Ser Cys Cys
      65      70      75      80
Pro Ala Ser Trp Cys Pro Phe Thr Arg Cys Arg Leu Ser Arg Gly Trp
      85      90      95
Ser Val Leu Ala
      100

```

<210> 2161
 <211> 1070
 <212> DNA
 <213> Homo sapiens

<400> 2161

tcttagggga aggggaaggct tatctgaaga gtagacctct ggttttgaat gagggagaca
 60
 gtgggggatat gaggggggga aacctcaaaa agaatatgta tccatcacta tgaagggta
 120
 ggctatacag gggaagcctc caaagggaaa tctggaaaaa tgttctgaga gggacattaa
 180
 ggatgtactc agaaattaag aaaacatatt aggacttgcc aaaagtgaga gaagcaactg
 240
 aggagactta tatgcaaaaa tcgcaaaaga ggagagaaca aaagatggag gttggatgct
 300
 aaatagggaa agagaacgcg tgaatgaggt agggggcaga acatgcagtg cagaaaaaca
 360
 acagatatgg aagggcatta aagagggcta aatgggaata ttaggaaatg agagttggga
 420
 atttgtcaga gttgtgtatt aacaaggaga gggtaaggta agaaggtggc aaagtaagag
 480
 ccagggcata aggttttgct gtccaggaag ctttgttgga aaaatgttag aagtaatggg
 540
 tttggtcagt atggtgagag gtgagagagg ctaaatggga tgggcataaa gggcaggcca
 600
 gtgggaagaa tcctatgaaa gtgtaggcag atctgagagc acagacaaat acagtggaga
 660
 atgtggcaca gggcagaggg cagtgggctg agcagcgagt gcccatgggg agggggagat
 720
 ccagaagaac ccattgagtc cctaagaatg acacacaggt gacagctgaa agaaggaggg
 780
 acacagaaga tatagcagca tgattctctg gggcaaaatg aggaagaaaag gaatggaaga
 840
 agaaaagtga gggttcctgc tgatgtgagg ggatgactgg aggaagggca ggtattgact
 900
 gggggggtaaa ggaaccattc ttggatcaag gttatgatgg aataagaagg aagagagagc
 960
 tggctagctg agtaaggac catcgataa aacagacaaa agttaagact agatggagtg
 1020
 gcaactaggc agatcagatg tattttttaa aggggaaact gctaagatct
 1070

<210> 2162

<211> 145

<212> PRT

<213> Homo sapiens

<400> 2162

Met Val Leu Tyr Ser Ala Ser Gln Leu Ser Leu Pro Ser Tyr Ser Ile
 1 5 10 15
 Ile Thr Leu Ile Gln Glu Trp Phe Leu Tyr Pro Pro Val Asn Thr Cys
 20 25 30
 Leu Ser Ser Ser His Pro Leu Thr Ser Ala Gly Thr Leu His Phe Leu
 35 40 45
 Leu Pro Phe Leu Ser Ser Ser Phe Cys Pro Arg Glu Ser Cys Cys Tyr
 50 55 60
 Ile Phe Cys Val Pro Pro Ser Phe Ser Cys His Leu Cys Val Ile Leu
 65 70 75 80
 Arg Asp Ser Met Gly Ser Ser Gly Tyr Ser Pro Pro His Gly His Ser

```

      85              90              95
Leu Leu Ser Pro Leu Pro Ser Ala Leu Cys His Ile Leu His Cys Ile
      100              105              110
Cys Leu Cys Ser Gln Ile Cys Leu His Phe His Arg Ile Leu Ala Thr
      115              120              125
Gly Leu Pro Phe Met Pro Ile Pro Phe Ser Leu Ser His Leu Ser Pro
      130              135              140
Tyr
145

```

<210> 2163

<211> 657

<212> DNA

<213> Homo sapiens

<400> 2163

```

tattttaaattc ttataaaaa aggtaggagg atcaggactt cgacccccctt aaaacgcggc
60
ggcctccctc caatccacct ccacttecta caccaccccc gctctcccc ccccccttt
120
tgggtccggg ttggaagggt ggggtgaaatg ggaaccgaat accaatttca cccgggaacc
180
agtaatgcc atgataaccg ccaagttggg accgaagtgt ggatccataa gtacgggagg
240
ccagtggggg ggaattgggt taagccccct cccagccttt ctccgacgc gtgctcgcgc
300
agacatgccca agaggctctc tctccaggag agccacctgt gaaacccacc cgcatgctc
360
ctccccacc tgtgcacaga cgagtgcctg ggctccagag agggaggagg ctgaaggcct
420
cagacaggag tccgtcccgt ccagtcccat catccaaga aatccggc cgcactccct
480
gcagctccat ggctcaacaa ggtgcggatg cctgctggac ctggctgctt tccatccaac
540
tttgatccct tcccaagag gaagagtgt acctaggag aagtgtgtgt cgcacaggca
600
tgcagcctgg tctcttgctc aggcggcttg cgcagattcc tagaggaatc tgcagcg
657

```

<210> 2164

<211> 152

<212> PRT

<213> Homo sapiens

<400> 2164

```

Met Pro Met Ile Thr Ala Lys Leu Gly Pro Lys Leu Gly Ser Ile Ser
  1              5              10              15
Thr Gly Gly Gln Trp Gly Gly Ile Gly Leu Ser Pro Leu Pro Ala Phe
      20              25              30
Leu Arg Pro Arg Ala Pro Ser Asp Met Pro Arg Gly Ser Leu Ser Arg
      35              40              45
Arg Ala Thr Cys Glu Thr His Pro Ala Cys Ser Ser His His Cys Ala
      50              55              60
Gln Thr Ser Ala Trp Ala Pro Glu Arg Glu Gly Ala Glu Gly Leu Arg

```

```

65          70          75          80
Gln Glu Ser Val Pro Ser Ser Pro Ile Ile Pro Arg Asn Ile Arg Pro
      85          90          95
Asp Ser Leu Gln Leu His Gly Ser Thr Arg Cys Gly Cys Leu Leu Asp
      100          105          110
Leu Ala Ala Phe His Pro Thr Leu Ile Pro Ser Pro Arg Gly Arg Val
      115          120          125
Leu Pro Arg Asp Lys Cys Gly Ala His Arg His Ala Ala Trp Ser Leu
      130          135          140
Ala Gln Ala Ala Cys Ala Asp Ser
145          150

<210> 2165
<211> 962
<212> DNA
<213> Homo sapiens

<400> 2165
nctttctcat cgacagcgac gcacaaccgg cgacatcacc ggtgacgggt caaggtggga
60
gcccgagggc ccgcggtgaa cttattgtgt cgtcttatgg aagaaaagtc actcggaagt
120
accgtaaatc accccagcgc ctcatccccc gaatctgttc gccatctgct gtcgccccgt
180
cgcttaaggc atcacccac tagactgacc gaagtctcgc cgaggggaggc tagggagggt
240
taggttgcca ggaatgacat cgggacgacg tctacgcgtc gaataggcag cggacgtacg
300
tcgagtagccg gccgtacggt ggtgtcttct gaccgcacac gcagagctat cgctaaaaga
360
ttgatggccc gcacctcagc tatgacgacg gccactctag aggaatatgg tcgtcgacac
420
tcttggttcc gtgatctgtc agccgaagaa agatcgtgga tctcgatcgt ggctcgctca
480
ggatttagcg gcttcgtcca gtggtttgct gacgatgacg ccgagcccta ctccccacc
540
gacgtcttcg acgtggcgcc ccggtccatg acccgcaaga tctccttgca ccagacagtc
600
gagctcgtcc gcaccacgat tgacgtcgtt gaggcacaaa ttgagaccga aatgccacgc
660
ggtgatcgcc aagtgtctgc cactgccatc gttcactact ccgcgcagggt ggccttcgcc
720
gccgcccagc ttacgcgcg agccgcgcaa cgtcgcgcta cctgggagta acgtctggaa
780
tcctcgtcgc ttgatgccgt cgtgcgagcc gacgccgatg aacagctcat ctccgcagct
840
tctactctcg gctggcgccc gggcatcaac ctctcgctcg ttgtcgggcg gggcccgagc
900
accgagcatg aactccacgt gctgcgacgt gatggagaac gcatgcagat gacggtgcta
960
gc
962

<210> 2166

```


<211> 239

<212> PRT

<213> Homo sapiens

<400> 2166

```

Val Ala Arg Asn Asp Ile Gly Thr Thr Ser Thr Arg Arg Ile Gly Ser
 1              5              10              15
Gly Arg Thr Ser Ser Thr Gly Arg Thr Val Val Ser Ser Asp Arg Thr
      20              25              30
Arg Arg Ala Ile Ala Lys Arg Leu Met Ala Arg Thr Ser Ala Met Thr
      35              40              45
Thr Ala Thr Leu Glu Glu Met Gly Arg Arg His Ser Trp Phe Arg Asp
      50              55              60
Leu Ser Ala Glu Glu Arg Ser Trp Ile Ser Ile Val Ala Arg Ser Gly
      65              70              75              80
Ile Asp Gly Phe Val Gln Trp Phe Ala Asp Asp Ala Glu Pro Tyr
      85              90              95
Ser Pro Thr Asp Val Phe Asp Val Ala Pro Arg Ser Met Thr Arg Lys
      100             105             110
Ile Ser Leu His Gln Thr Val Glu Leu Val Arg Thr Thr Ile Asp Val
      115             120             125
Val Glu Ala Gln Ile Glu Thr Glu Met Pro Arg Gly Asp Arg Gln Val
      130             135             140
Leu Arg Thr Ala Ile Val His Tyr Ser Arg Glu Val Ala Phe Ala Ala
      145             150             155             160
Ala Glu Val Tyr Ala Arg Ala Ala Glu Arg Arg Gly Thr Trp Asp Glu
      165             170             175
Arg Leu Glu Ser Leu Val Val Asp Ala Val Val Arg Ala Asp Ala Asp
      180             185             190
Glu Gln Leu Ile Ser Arg Ala Ser Thr Leu Gly Trp Arg Pro Gly Ile
      195             200             205
Asn Leu Cys Val Val Val Gly Arg Ala Pro Thr Thr Glu His Glu Leu
      210             215             220
His Val Leu Arg Arg Asp Gly Glu Arg Met Gln Met Thr Val Leu
      225             230             235

```

<210> 2167

<211> 325

<212> DNA

<213> Homo sapiens

<400> 2167

```

accggtgcag tttgtgaggg gttggtgacg ccgcatcggg aggttcacgc cgtcacggcg
60
catccacatt atccccgactg gaagatctcg ccagggttacg gacagtggtc gcgtacgcgaa
120
cagatgcaga gtgtgactgt gacgcgagtc agacacttcg tcccgcggcg tcccacggcg
180
attcttcgag cgggtgtctga ggtgacgttc gggttgcgtc tctgcgcgt cgttgggcga
240
agcaccgcgg cgattgtggc tgtgtcgcgg gccttgcctc cgacgcggtc gcgcgggctg
300
tgcgctgac tcccacagca taccc
325

```

<210> 2168
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 2168
 Thr Gly Ala Val Cys Glu Gly Leu Val Thr Pro Asp Arg Glu Val His
 1 5 10 15
 Ala Val Thr Ala His Pro His Tyr Pro Asp Trp Lys Ile Ser Pro Gly
 20 25 30
 Tyr Gly Gln Trp Ser Arg Ser Glu Gln Ile Asp Ser Val Thr Val Thr
 35 40 45
 Arg Val Arg His Phe Val Pro Arg Arg Pro Thr Ala Ile Leu Arg Ala
 50 55 60
 Val Ser Glu Val Thr Phe Gly Leu Arg Leu Cys Ala Val Arg Trp Arg
 65 70 75 80
 Ser Thr Ala Ala Ile Val Ala Val Ser Pro Ala Leu Leu Ser Thr Arg
 85 90 95
 Ser Arg Gly Ser Cys Ala Asp Leu Pro Gln His Thr
 100 105

<210> 2169
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 2169
 gaggacgcct acgtgctcat caccagggc aagatctcgg cgatcgccga cgtcctgccg
 60
 atcctggaga aggtcgtaaa ggccggcaag ccgctgctcg tcacgcgcca ggacatcgac
 120
 ggggaggccc ttgtcacccct cgtcgtcaat aagatccgcg gtaccttcag ctccgtggca
 180
 gtcaaggcgc ccggtctcgg tgaccgcgc aaggcaatgc tcgaggacat cgccaccctc
 240
 accggtggtc aggtcgtcgc tcccagaggt gggtcaagc tcgaccaggt gggcctcgag
 300
 gttcagggc
 309

<210> 2170
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 2170
 Glu Asp Ala Tyr Val Leu Ile Thr Gln Gly Lys Ile Ser Ala Ile Ala
 1 5 10 15
 Asp Val Leu Pro Ile Leu Glu Lys Val Val Lys Ala Gly Lys Pro Leu
 20 25 30
 Leu Val Ile Ala Glu Asp Ile Asp Gly Glu Ala Leu Ser Thr Leu Val
 35 40 45
 Val Asn Lys Ile Arg Gly Thr Phe Ser Ser Val Ala Val Lys Ala Pro

```

      50              55              60
Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Thr Leu
65              70              75              80
Thr Gly Gly Gln Val Val Ala Pro Glu Val Gly Leu Lys Leu Asp Gln
      85              90              95
Val Gly Leu Glu Val Gln Gly
      100

```

```

<210> 2171
<211> 518
<212> DNA
<213> Homo sapiens

```

```

<400> 2171
cgcgtaatgt gtattaaggt ccttggtggc tcgcatcgcc gttatgcagc aatcggtgat
60
atcatcaaaag tttagtgaa ggaagcaatt cctcgaggaa aaattaaaaa aggtaatggt
120
cattcagctg tggtagtgcg taccagaaaa ggtgtacgtc gtcccgatgg ttctgttatt
180
cgttttgatc gcaacgcagc ggttatcttg aatgcaaaca accagccagt cggtacacgt
240
atcttttgcc ctgtaacccg tgagcttcga aatgaaaatt tcattgaagt tgtttcactg
300
gcgcagaag tactgtaagg aaccgaaaaa ggcagcaaaa ataaacgtg acgatgaagt
360
aattgttatt gccggttaaag ataaaggtaa aactgggaaa gttctcraag ttttaactaa
420
cggtaaagta attattgaag gtgtaaatgt tcaaaagaaa caccaaaaac caaacctca
480
agcggggcgtg gaaggcggaa tcattgaaca gaatgcac
518

```

```

<210> 2172
<211> 105
<212> PRT
<213> Homo sapiens

```

```

<400> 2172
Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr Ala
1              5              10              15
Ala Ile Gly Asp Ile Ile Lys Val Ser Val Lys Glu Ala Ile Pro Arg
20              25              30
Gly Lys Ile Lys Lys Gly Asn Val His Ser Ala Val Val Arg Thr
35              40              45
Arg Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp Arg
50              55              60
Asn Ala Ala Val Ile Leu Asn Ala Asn Asn Gln Pro Val Gly Thr Arg
65              70              75              80
Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Asn Glu Asn Phe Met Lys
85              90              95
Ile Val Ser Leu Ala Pro Glu Val Leu
      100              105

```

<210> 2173
 <211> 475
 <212> DNA
 <213> Homo sapiens

<400> 2173
 nntggggaag aaatgccggt gcatgcactt tgtgcagcat taggtgcagg ggtgatgcag
 60
 cgggcgctgt ccttttgcgg cggggtttcg agcattcatc tgggtcatgc attttcgcac
 120
 gcattttctg taccctcgtc atgcgtttct ccccatgcac acacattatc gcctttgcac
 180
 ccgcaggagc gcatggaata cctcgtgaaa tggaagggat ggtcgcagaa gtacagcaca
 240
 tgggaaccgg aggaaaacat cctggatgct cgcttgctcg cagcctttga ggaaagggaa
 300
 agagagatgg agctctatgg ccccaaaaag cgtggaccca agcccaaac ctctctctc
 360
 aaagcgcagg ccaaggcaaa ggccaaaact tacgagtttc gaagtgactc agccaggggc
 420
 atccggatcc cctaccctgg ccgctcgccc caggacctgg cctccacttc ccggg
 475

<210> 2174
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 2174
 Xaa Gly Glu Glu Met Pro Val His Ala Leu Cys Ala Ala Leu Gly Ala
 1 5 10 15
 Gly Val Met Gln Arg Ala Arg Ala Phe Cys Gly Gly Val Ser Ser Ile
 20 25 30
 His Leu Val His Ala Phe Ser His Ala Phe Leu Val Ser Ser Ser Cys
 35 40 45
 Val Ser Pro His Ala His Thr Leu Ser Pro Leu His Pro Gln Gly Arg
 50 55 60
 Met Glu Tyr Leu Val Lys Trp Lys Gly Trp Ser Gln Lys Tyr Ser Thr
 65 70 75 80
 Trp Glu Pro Glu Glu Asn Ile Leu Asp Ala Arg Leu Leu Ala Ala Phe
 85 90 95
 Glu Glu Arg Glu Arg Glu Met Glu Leu Tyr Gly Pro Lys Lys Arg Gly
 100 105 110
 Pro Lys Pro Lys Thr Phe Leu Leu Lys Ala Gln Ala Lys Ala Lys Ala
 115 120 125
 Lys Thr Tyr Glu Phe Arg Ser Asp Ser Ala Arg Gly Ile Arg Ile Pro
 130 135 140
 Tyr Pro Gly Arg Ser Pro Gln Asp Leu Ala Ser Thr Ser Arg
 145 150 155

<210> 2175
 <211> 462
 <212> DNA
 <213> Homo sapiens

<400> 2175
 cgcgacaccc tctttgtgg gcgccttcc tctccgaatt cgcgaaccct ccagactctg
 60
 gccccaggagg ttgtcgagcg tggagccgat atcggcattg ccaactgatgg tgacgcagac
 120
 cgcctcggtg tcattgatga ccagggggcat ttcttgcac ccaaccagat cctcgtattg
 180
 ctgtacacat accttctgga ggacaaggga tggcaggtgc cctgcgtgcg taacctcgcg
 240
 acgacccacc tgcttgaccg tgtcgccgag gccacgggc agacctgtta cgaggtaccg
 300
 gtcggattta agtgggtgtc gtccaagatg gccgagacca acgccgtcat cgggtggtgag
 360
 tcttcgggtg gtttgacctg ccagggggcat attgcaggca aggatggtgt ctatgctggc
 420
 accctgctgg tggaaatgat cgccaagcgg ggtaagaagc tt
 462

<210> 2176
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 2176
 Arg Asp Thr Leu Phe Gly Gly Arg Leu Pro Ser Pro Asn Ser Arg Thr
 1 5 10 15
 Leu Gln Thr Leu Ala Gln Glu Val Val Glu Arg Gly Ala Asp Ile Gly
 20 25 30
 Ile Ala Thr Asp Gly Asp Ala Asp Arg Leu Gly Ile Ile Asp Asp Gln
 35 40 45
 Gly His Phe Leu His Pro Asn Gln Ile Leu Val Leu Leu Tyr Thr Tyr
 50 55 60
 Leu Leu Glu Asp Lys Gly Trp Gln Val Pro Cys Val Arg Asn Leu Ala
 65 70 75 80
 Thr Thr His Leu Leu Asp Arg Val Ala Glu Ala His Gly Gln Thr Cys
 85 90 95
 Tyr Glu Val Pro Val Gly Phe Lys Trp Val Ser Ser Lys Met Ala Glu
 100 105 110
 Thr Asn Ala Val Ile Gly Gly Glu Ser Ser Gly Gly Leu Thr Val Gln
 115 120 125
 Gly His Ile Ala Gly Lys Asp Gly Val Tyr Ala Gly Thr Leu Leu Val
 130 135 140
 Glu Met Ile Ala Lys Arg Gly Lys Lys Leu
 145 150

<210> 2177
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 2177
 ctcgagaatc atgacggcga cgacgtgact atctccacc gtgtgcctcg tgacggcggg
 60

accttggact cgattgtcgg cgtgctggcc ggggcatacct ggtatcagcg ggagatccac
 120
 gacttttttt gtgtgaggtt tgtcggccct ggggcagatg atcgtgcctt cttgtccac
 180
 gatgcaccga aaccgccct gcgcaaggaa gctgtgttgg cgcagcgagc tgacaccgtg
 240
 tggccgggtg cggtgacga ggctggctcg aagtccgcga gtcgacgtt cccgtgcggc
 300
 gttcctgacc ctgagacgtg gcggcgatc aaagacggcg aggatattcc ggatgccgag
 360
 gtcacgcggg ccatgtctgg ccggcgcccg cgatcagctg cccgtcgaat ggcaagcacg
 420
 gcgtcaggca ggcaggcatg agacattcga ctatcaacct tgacgtcgac gcgtgcac
 478

<210> 2178

<211> 146

<212> PRT

<213> Homo sapiens

<400> 2178

Leu	Glu	Asn	His	Asp	Gly	Asp	Asp	Val	Thr	Ile	Ser	Thr	Arg	Val	Pro
1				5				10					15		
Arg	Asp	Gly	Gly	Thr	Leu	Asp	Ser	Ile	Val	Gly	Val	Leu	Ala	Gly	Ala
		20						25					30		
Ser	Trp	Tyr	Gln	Arg	Glu	Ile	His	Asp	Phe	Phe	Gly	Val	Arg	Phe	Val
		35				40						45			
Gly	Pro	Gly	Ala	Asp	Asp	Arg	Ala	Leu	Leu	Val	His	Asp	Ala	Pro	Lys
	50					55				60					
Pro	Pro	Leu	Arg	Lys	Glu	Ala	Val	Leu	Ala	Gln	Arg	Ala	Asp	Thr	Val
	65			70					75				80		
Trp	Pro	Gly	Ala	Ala	Asp	Gln	Ala	Gly	Ser	Lys	Ser	Ala	Ser	Arg	Arg
			85					90					95		
Leu	Pro	Val	Gly	Val	Pro	Asp	Pro	Glu	Thr	Trp	Arg	Arg	Ile	Lys	Asp
			100					105					110		
Gly	Glu	Asp	Ile	Pro	Asp	Ala	Glu	Val	Ile	Ala	Ala	Met	Ser	Gly	Arg
		115				120						125			
Arg	Pro	Arg	Ser	Ala	Ala	Arg	Arg	Met	Ala	Ser	Thr	Ala	Ser	Gly	Arg
	130					135						140			
Gln	Ala														
145															

<210> 2179

<211> 296

<212> DNA

<213> Homo sapiens

<400> 2179

gtgcacttcc gaggaggacgt cgagcgtcgc attaacgggg ccggcgcggt gggcgcacac
 60
 aagacgtcga tgctgcagga tctggaacng gaccgcgcga tggagatcga cccgctcgtc
 120
 tccgctcgtc aggagatggg acgctggcc aacgtgccga cgccacgct cgatgctgtg
 180

ctcccactga tcaagcaacg tgaattcatg acgaagccgg atgccgtggc ggccgcgcag
 240
 gaacgtctgg ctaaagcggc ataaaccagc cgccgaaacc agcggcataa cgcggg
 296

<210> 2180
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 2180
 Val His Phe Arg Val Asp Val Glu Arg Arg Ile Asn Gly Ala Gly Ala
 1 5 10 15
 Val Gly Ala His Lys Thr Ser Met Leu Gln Asp Leu Asp Xaa Asp Arg
 20 25 30
 Ala Met Glu Ile Asp Pro Leu Val Ser Val Val Gln Glu Met Gly Arg
 35 40 45
 Leu Ala Asn Val Pro Thr Pro Thr Leu Asp Val Val Leu Pro Leu Ile
 50 55 60
 Lys Gln Arg Glu Phe Met Thr Lys Pro Asp Ala Val Ala Ala Ala Gln
 65 70 75 80
 Glu Arg Leu Ala Lys Ala Ala
 85

<210> 2181
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 2181
 ngcgcgccgg gatggatcat agtctggctc gatgcatcac gtgcgcgcgc ggcgcgcgtg
 60
 tcgattcccg acggcatgat cgcggcactc gaccgtaccg gcaaggcgca aacgcacctc
 120
 acgctggcat cgccggaagc ggggtgctgc agcgaactga acgtgcgcga cgggtgcgatg
 180
 gtgcgcgcgg ggcagacgct cgcaagatt tcgggcctct cgaagctctg gctgatcgct
 240
 gagattccgg aagcgctcgc gctcgatcgc cgtccgggca tgaccgtcga cgcgacgttc
 300
 tcggggcgatc cgacgcagca ttccaccggg cgtatccgcg agatcctgcc gggcatcacc
 360
 accagtagcc gcacgcttca ggcgcgc
 387

<210> 2182
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 2182
 Xaa Ala Pro Gly Trp Ile Ile Val Trp Leu Asp Ala Ser Arg Ala Arg
 1 5 10 15
 Met Arg Ala Leu Ser Ile Pro Asp Gly Met Ile Ala Ala Leu Asp Arg

```

                20                25                30
Thr Gly Lys Ala Gln Thr His Leu Thr Leu Ala Ser Pro Glu Ala Gly
   35                40                45
Val Val Ser Glu Leu Asn Val Arg Asp Gly Ala Met Val Ala Pro Gly
   50                55                60
Gln Thr Leu Ala Lys Ile Ser Gly Leu Ser Lys Leu Trp Leu Ile Val
   65                70                75                80
Glu Ile Pro Glu Ala Leu Ala Leu Asp Ala Arg Pro Gly Met Thr Val
   85                90                95
Asp Ala Thr Phe Ser Gly Asp Pro Thr Gln His Phe Thr Gly Arg Ile
  100                105                110
Arg Glu Ile Leu Pro Gly Ile Thr Thr Ser Ser Arg Thr Leu Gln Ala
  115                120                125
Arg

```

<210> 2183
 <211> 310
 <212> DNA
 <213> Homo sapiens

```

<400> 2183
aagcttgaaa aacaaatttg tgcacagtct gataacccaa aaatgactga tggattggct
60
ctgcattttc caagcagggg ggggtcgggc atggagaatg aaacattctg agaaaagact
120
taaatgtgga aacttttggg tcaagagggg attctaggag atacaagaaa tatctcctgg
180
gggcatccaa agggaataac actgtaatct tgagtgatgt atggttccat tgcccagagga
240
atagggatga aaaccataaa ctcccttggg tgggtattaa cttatcanc aaagttacca
300
tanataatgg
310

```

<210> 2184
 <211> 100
 <212> PRT
 <213> Homo sapiens

```

<400> 2184
Met Val Thr Leu Xaa Asp Lys Leu Ile Pro Thr Gln Arg Ser Leu Trp
1      5      10      15
Phe Ser Ser Leu Phe Leu Gly Gln Trp Asn His Thr Ser Leu Lys Ile
20     25     30
Thr Val Leu Phe Pro Leu Asp Ala Pro Arg Arg Tyr Phe Leu Tyr Leu
35     40     45
Leu Glu Tyr Pro Leu Glu Pro Lys Val Ser Thr Phe Lys Ser Phe Leu
50     55     60
Arg Met Phe His Ser Pro Cys Pro Thr Pro Pro Cys Leu Glu Asn Ala
65     70     75     80
Glu Pro Ile His Gln Ser Phe Leu Gly Tyr Gln Thr Val His Lys Phe
85     90     95
Val Phe Gln Ala

```


100

<210> 2185

<211> 723

<212> DNA

<213> Homo sapiens

<400> 2185

ngaatatcca tgcagcagct cgtcgacaat tttagcgggt ccattccctga cgaatcttgac
 60
 tctcttgtga ccctgcccggt agtcgggtcgt aagaccgcca atgttgtttt aggtaatgcc
 120
 ttccggatccc ccggaatcac cccggacacc cagctcatgc ggggtatctcg acgtctgggc
 180
 tggaccgatg cgactacccc cgccaagggt gaaaccgacc tggctgagct ttttgacccg
 240
 tctgaatggg tgatgtttgt tcaccgcctc atctggcacg ggcggcgccg ctgtcactcg
 300
 cgccgtcctg cctgcgggggt atgcccggtt gccgagtggt gcccgctcct cggggaaggc
 360
 ccaacggatc ccgaggaggc cgccacgtta gtccgggagc cgcgtcgatg agggggatga
 420
 acgttttcgg cgcggtgatg gccgccttga tgtttgctgg ctgcggggga gatcggggca
 480
 tagctcatca gcgtgaaaaat gccggaatac cggggtgctc gcatttgccg tcggggccga
 540
 ttgcgaaaaa ttccggggccg gccacagagg gccggcccat gcccgatcac ggcttgcaat
 600
 gccttggtga ggggcccagc atctccatgt ctccggcgac atcgaggggc gtgaccgtcg
 660
 tgacgatctg ggcgtcgtgg tgtcgacatc gtcgtagtga ggctccgctc attgcgaacg
 720
 cgt
 723

<210> 2186

<211> 136

<212> PRT

<213> Homo sapiens

<400> 2186

Xaa Ile Ser Met Gln Gln Leu Val Asp Asn Phe Asp Gly Ala Ile Pro
 1 5 10 15
 Asp Asp Leu Asp Ser Leu Val Thr Leu Pro Gly Val Gly Arg Lys Thr
 20 25 30
 Ala Asn Val Val Leu Gly Asn Ala Phe Gly Ile Pro Gly Ile Thr Pro
 35 40 45
 Asp Thr His Val Met Arg Val Ser Arg Arg Leu Gly Trp Thr Asp Ala
 50 55 60
 Thr Thr Pro Ala Lys Val Glu Thr Asp Leu Ala Glu Leu Phe Asp Pro
 65 70 75 80
 Ser Glu Trp Val Met Leu Cys His Arg Leu Ile Trp His Gly Arg Arg
 85 90 95
 Arg Cys His Ser Arg Arg Pro Ala Cys Gly Val Cys Pro Val Ala Glu

```

                100                105                110
Trp Cys Pro Ser Phe Gly Glu Gly Pro Thr Asp Pro Glu Glu Ala Ala
      115                120                125
Thr Leu Val Arg Glu Pro Arg Arg
      130                135

```

<210> 2187

<211> 342

<212> DNA

<213> Homo sapiens

<400> 2187

```

nnacgcgtga aggatgcgcc ccggtcgacc ggccatccgt cttgcctcgc aggcattccag
60
cccgccatat gctgcaaccg caacaccgct ttgccgtcgc atggcatctc cactccggat
120
cgcctcgatc cacgagggct atcggcgcga aagaagtgtc cggggcaaaa tcccgcgag
180
gaaagcccga tggagtggaa gacgctgtc aacgacacc gcttcggagg ggctgccaggc
240
ctcgatggga cgcgcggacg gtcggagttc cagaaggacc acgaccggat catcttctcc
300
gaagccttcc gcaagctggg ccgcaagacc caggtgcacc cg
342

```

<210> 2188

<211> 51

<212> PRT

<213> Homo sapiens

<400> 2188

```

Met Glu Trp Lys Thr Leu Leu Asn Asp Thr Arg Phe Gly Gly Val Ala
  1          5          10          15
Ser Leu Asp Gly Thr Arg Gly Arg Ser Glu Phe Gln Lys Asp His Asp
      20          25          30
Arg Ile Ile Phe Ser Glu Ala Phe Arg Lys Leu Gly Arg Lys Thr Gln
      35          40          45
Val His Pro
      50

```

<210> 2189

<211> 1412

<212> DNA

<213> Homo sapiens

<400> 2189

```

ntcgcttcat ggtgcgcaat tacgacaacg ccaagtctca gaatgccgag gcttacaccg
60
cgtttcttcca cgcgatgcta gatgccgggg tcaacctgcc gccatcgtgc tttgaggcct
120
ggttctctctc ggacgctcac gacgacgaag ctttcgaggt tttccgcgcc gccctgccga
180
gggctgcccc ggcggctgcc caggtgatca gtgcctgaca ccgggctgac ttcgcaggtc
240

```

atcgaaggcaa tctgtgacctg gttcgacgcc aacggacgcg atctgccgtg ggcgcgaccc
 300
 ggcaacctccg cgtggggcggt ccttggttagc gaggtcatga gccaacagac ccgcatgtcc
 360
 cgggtgatcg ggccgtggca cgagtggatg aaccgctggc ccacccctga tgatttggcg
 420
 gaggaaggact ctggggaagc ggttgcccgcg tgggggcgcc tgggttaccg gcgtcggggc
 480
 ttacgcctcg attcctgtgc cgtcacgac gccaccgagc acgacggggg tgtgcccaac
 540
 agtgacgacg agctcgtcgc cctcccggtt attggcgact acaccgcgag cgcagtcgtc
 600
 tcttttgcgt ttggcggccg cgccacagt cttgacacca atgtacgtcg cctcatcgct
 660
 agagcagagt ctgggatcgc aaactgtcca acctcgggtg cgagggctga gcggttagtc
 720
 gccgacgcgt tgggtcccg cgaagacgac cgagcggcca agtgggcggt ggcgtcgatg
 780
 gaattggggg cactgggtatg caccggcgcg tctccgcagt gtgaggtctg ccgcatccgg
 840
 gatggctgca ggtgggtgat cgacggtagg ccggacaatg ccccgggccc tcgaggacag
 900
 ccatggaagg gcacggatcg ccagtgcgcg ggctgtatta tggacgtggt gcgcaacagc
 960
 cctcacgggg tgaaggtcca gatggctctt tccgcctggc ccgagctcga tcaggcatca
 1020
 aggtgccttg aatccttact cgatgacggt ttagtgacac gacgaggtaa ccttattagc
 1080
 ctgtgacctg agaaattctt ggccccgacc acccaaacag accgagtcca gcagtgatgc
 1140
 cgctgggcta tccttagagg cggctcctca attggatcag ccaaaccacg tcaccgatca
 1200
 agacaccatg agcacaacac ccaaacagcc gcgcacggcg acagctgccc gacgccgaca
 1260
 cattgtcgac catctgcgtt ctttggggca ctccgagtc atcgagatc tttaaccaat
 1320
 gttcgggtgc tctacatcga cgattcgccg cgatgtcgat gccctctcgg atgaatccaa
 1380
 gatctggaag atttcggggg gagacgtcat ga
 1412

<210> 2190

<211> 292

<212> PRT

<213> Homo sapiens

<400> 2190

Ser	Val	Pro	Asp	Thr	Gly	Leu	Thr	Ser	Gln	Val	Ile	Glu	Ala	Ile	Cys
1				5				10						15	
Ala	Trp	Phe	Asp	Ala	Asn	Gly	Arg	Asp	Leu	Pro	Trp	Arg	Arg	Pro	Gly
			20					25					30		
Thr	Ser	Ala	Trp	Gly	Val	Leu	Val	Ser	Glu	Val	Met	Ser	Gln	Gln	Thr
		35				40					45				
Pro	Met	Ser	Arg	Val	Ile	Gly	Pro	Trp	His	Glu	Trp	Met	Asn	Arg	Trp

[illegible]

gctgggattg ccggtgggtgc ac
502

<210> 2192
<211> 104
<212> PRT
<213> Homo sapiens

<400> 2192
Leu Asn Leu Ala Asp Met Thr Glu Arg Gly Leu Arg Gly Glu Ser Ile
1 5 10 15
Thr Arg Glu Glu Ala Leu Glu Ile Leu Arg Ser Ser Asp Asp Glu Leu
20 25 30
Met Ser Ile Ile Ala Ala Ala Gly Lys Val Arg Arg His Phe Phe Asp
35 40 45
Asn Arg Val Arg Leu Asn Tyr Leu Val Asn Leu Lys Ser Gly Leu Cys
50 55 60
Pro Glu Asp Cys Ser Tyr Cys Ser Gln Arg Leu Gly Ser Arg Ala Glu
65 70 75 80
Ile Thr Lys Tyr Ser Trp Ala Asp Pro Gln Lys Val His Asp Ala Val
85 90 95
Glu Ala Gly Ile Ala Gly Gly Ala
100

<210> 2193
<211> 321
<212> DNA
<213> Homo sapiens

<400> 2193
ccatggggaa tgcagagcac ggacagtcac acagactgtc ctctctgtgcc ttctggaccc
60
aacatactcc tcttgccaac tgggtattac tggaccttac tgggccttac tggacccaac
120
atactcctct tgccaactgg ggatttaaaa attttaaaag cccctttatc tccctccaca
180
agtcattgtac tgccaacagg gacacactgt tttctttgga aaccctgtct gtgtgccaga
240
cagaggtccc actgccctgg gacagctccc ttgcctanag gggaaggagg gtgtgtgtgc
300
tgtgtgtgt taggttgggg a
321

<210> 2194
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2194
Met Gly Asn Ala Glu His Gly Gln Ser His Arg Leu Ser Ser Leu Ala
1 5 10 15
Phe Trp Thr Gln His Thr Pro Leu Ala Asn Trp Val Leu Leu Asp Leu
20 25 30
Thr Gly Pro Tyr Trp Thr Gln His Thr Pro Leu Ala Asn Trp Gly Phe


```

                100                105                110
Arg Val Ala Ser Gly Asn Leu Val Thr Ala Arg Pro Ile Gly Val Leu
                115                120                125
Asp Gly Val Asp Phe His His Thr Gly Glu Val Arg Arg Val Asp Arg
                130                135                140
Lys Gly Ile Asn Arg Leu Leu Asp Glu Arg Ser Ile Val Leu Leu Ser
145                150                155                160
Pro Leu Gly Tyr Ser Pro Thr Gly
                165

```

<210> 2197

<211> 351

<212> DNA

<213> Homo sapiens

<400> 2197

```

acaagtcggt cgacgattcg ctttccggag gcggggcccag gaatggtaat gaaaccgcgag
60
ttatgggggcc ctgcgctcga cgagattgcc gcgggaaaac gtgccggagg gggtgaacag
120
ttagattccg cagtgcagca catccacggt gctactcacg ataaactgtc cggtgtctgtt
180
ccgaaacgct acgatggtcg ggatgtcttg gcaggcgagg acccgaatgc accgttctgtg
240
cttgtgccta gcccggctgg tgcagtgttt agtcaaaata aggcacaagc ctggtccaat
300
gaagaccaca ttgtttttgc ctgtgggcgc tatgaaggta ttgatcaacg c
351

```

<210> 2198

<211> 117

<212> PRT

<213> Homo sapiens

<400> 2198

```

Thr Ser Pro Ser Thr Ile Arg Phe Pro Glu Ala Gly Pro Gly Met Val
1         5         10        15
Met Lys Pro Glu Leu Trp Gly Pro Ala Leu Asp Glu Ile Ala Ala Gly
20        25        30
Lys Arg Ala Gly Gly Ala Glu Gln Leu Asp Ser Ala Val Gln His Ile
35        40        45
His Gly Ala Thr His Asp Lys Leu Ser Gly Ala Val Pro Lys Arg Tyr
50        55        60
Asp Gly Arg Asp Val Leu Ala Gly Glu Asp Pro Asn Ala Pro Leu Leu
65        70        75        80
Leu Val Pro Ser Pro Ala Gly Ala Val Phe Ser Gln Asn Lys Ala Gln
85        90        95
Ala Trp Ser Asn Glu Asp His Ile Val Phe Ala Cys Gly Arg Tyr Glu
100       105       110
Gly Ile Asp Gln Arg
115

```

<210> 2199

<211> 457

<212> DNA

<213> Homo sapiens

<400> 2199

agacgcccgc cgccaagatc tgcattcccta ggccacgcta agaccctggg gaagagcgca
 60
 ggagcccggg agaagggtctg gaaggagggg actggacgtg cggagaattc cccctaaaa
 120
 ggcagaagcc cccgccccca cctcccgagc tccgttcggg cagagcgctc gctgcctgc
 180
 cgttgctggg ggcgcccacc tcgcccagcc atgccaggcc cggccaccga cgcggggaag
 240
 atccctttct gcgacgcca ggaagaaatc cgtgccgggc tcgaaagctc tgaggcgggc
 300
 ggcggcccg agaggccagg cgcgcgagg cagcggcaga acatcgctct gaggaatgtc
 360
 gtctgatga gcttgctcca cttgggggccc gtgtactccc tgggtgctcat ccccaaagcc
 420
 aagccactca ctctgctctg gggtaagtcc cgccggc
 457

<210> 2200

<211> 152

<212> PRT

<213> Homo sapiens

<400> 2200

Arg	Arg	Arg	Pro	Pro	Arg	Ser	Ala	Ser	Leu	Gly	His	Ala	Lys	Thr	Leu
1			5						10					15	
Gly	Lys	Ser	Ala	Gly	Ala	Arg	Glu	Lys	Gly	Trp	Lys	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Ala	Glu	Asn	Ser	Pro	Leu	Lys	Gly	Arg	Ser	Pro	Arg	Pro	His	Pro
			35					40				45			
Pro	Ser	Ser	Val	Arg	Ala	Glu	Arg	Leu	Pro	Ala	Cys	Arg	Cys	Trp	Gly
			50			55					60				
Arg	Pro	Pro	Arg	Pro	Ala	Met	Pro	Gly	Pro	Ala	Thr	Asp	Ala	Gly	Lys
65				70					75					80	
Ile	Pro	Phe	Cys	Asp	Ala	Lys	Glu	Glu	Ile	Arg	Ala	Gly	Leu	Glu	Ser
			85						90					95	
Ser	Glu	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Pro	Gly	Ala	Arg	Gly	Gln	Arg
			100					105					110		
Gln	Asn	Ile	Val	Trp	Arg	Asn	Val	Val	Leu	Met	Ser	Leu	Leu	His	Leu
			115			120						125			
Gly	Ala	Val	Tyr	Ser	Leu	Val	Leu	Ile	Pro	Lys	Ala	Lys	Pro	Leu	Thr
			130			135					140				
Leu	Leu	Trp	Gly	Lys	Ser	Arg	Arg								
145						150									

<210> 2201

<211> 336

<212> DNA

<213> Homo sapiens

<400> 2201

agtactgcga tggacagcta tgctgtggat ggtgggtcgca aattacatgt ttgtggtaac
 60
 aaccctgatt gcgatgggta tgaagtcgaa gaaggcgaat tcaagatcaa ggggttatgat
 120
 ggtccgacta tcccatgcga taaatgtgat ggtgagatgc agcttaaaac gggtcgtttt
 180
 ggtccatatt tcgcatgtac tagctgtgac aatactcgta aggtactcaa gagtgggtcaa
 240
 cctgctccgc cactgtgtaga cccaatcaaa atggagcacc tacgttcaac gaagcatgat
 300
 gattttcttcg tcttacgtga gggcgctgct ggttta
 336

<210> 2202
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 2202
 Ser Thr Ala Met Asp Ser Tyr Val Val Asp Gly Gly Arg Lys Leu His
 1 5 10 15
 Val Cys Gly Asn Asn Pro Asp Cys Asp Gly Tyr Glu Val Glu Glu Gly
 20 25 30
 Glu Phe Lys Lys Gly Tyr Asp Gly Pro Thr Ile Pro Cys Asp Lys
 35 40 45
 Cys Asp Gly Glu Met Gln Leu Lys Thr Gly Arg Phe Gly Pro Tyr Phe
 50 55 60
 Ala Cys Thr Ser Cys Asp Asn Thr Arg Lys Val Leu Lys Ser Gly Gln
 65 70 75 80
 Pro Ala Pro Pro Arg Val Asp Pro Ile Lys Met Glu His Leu Arg Ser
 85 90 95
 Thr Lys His Asp Asp Phe Phe Val Leu Arg Glu Gly Ala Ala Gly Leu
 100 105 110

<210> 2203
 <211> 273
 <212> DNA
 <213> Homo sapiens

<400> 2203
 ctcgagagat gcagtcaccag ccgggggtggg aagctgtgca gacagccccg gatctggggac
 60
 gtgatggaaa actcaacaga ctggttcaga tcttggtccc gagccccagag gcaccggggga
 120
 cccccagggc tgtttctccc tggccacacc agtaccaccac ttccaaatgc cctgtaggtg
 180
 accaccaggc cacacaggcc cgtctgaggg gccacaggct gtgcaccatg ggacgcaggc
 240
 ctgtccctgc ctccctccga tgtcctgatg gtg
 273

<210> 2204
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 2204

```

Met Gln Ser Gln Pro Gly Trp Glu Ala Val Gln Thr Ala Pro Asp Leu
 1           5           10           15
Gly Arg Asp Gly Lys Leu Asn Arg Leu Val Gln Ile Leu Ala Arg Ser
          20           25           30
Pro Glu Ala Pro Gly Thr Pro Arg Ala Val Ser Pro Trp Pro His Gln
          35           40           45
Tyr Pro Thr Ser Lys Cys Pro Val Gly Asp His Gln Ala Thr Gln Ala
          50           55           60
Arg Leu Arg Gly His Arg Leu Cys Thr Met Gly Arg Arg Pro Val Pro
65           70           75           80
Ala Ser Leu Arg Cys Pro Asp Gly
          85

```

<210> 2205

<211> 387

<212> DNA

<213> Homo sapiens

<400> 2205

```

gnnnnnngng nnnnactggt gtgcatggtt aaaatcctgc aagctactgg gttgccacag
60
catctgtccc actttgtggt ctgcaaatac agcttctggg atcaacagga gccggtgatt
120
gtcgctcctg aagtggacac ctctcctctt tccgtcagca aggagccgca ctgcatggtt
180
gtctttgatc attgcaatga gttttctggt aacatcaccc aagactttat cgagcatctt
240
tccgaaggag cattggcaat tgaagtatat ggacataaaa taaacgatcc ccggaaaaac
300
ccgcacctgt gggatttggg aatcatccaa gcaaagacac gtagtcttcg ggacagatgg
360
agtgaagtgc ccaggaaatt ggaattc
387

```

<210> 2206

<211> 129

<212> PRT

<213> Homo sapiens

<400> 2206

```

Xaa Xaa Gly Xaa Xaa Leu Val Cys Met Val Lys Ile Leu Gln Ala Thr
 1           5           10           15
Gly Leu Pro Gln His Leu Ser His Phe Val Phe Cys Lys Tyr Ser Phe
          20           25           30
Trp Asp Gln Gln Glu Pro Val Ile Val Ala Pro Glu Val Asp Thr Ser
          35           40           45
Ser Ser Ser Val Ser Lys Glu Pro His Cys Met Val Val Phe Asp His
          50           55           60
Cys Asn Glu Phe Ser Val Asn Ile Thr Glu Asp Phe Ile Glu His Leu
65           70           75           80
Ser Glu Gly Ala Leu Ala Ile Glu Val Tyr Gly His Lys Ile Asn Asp

```

```

      85              90              95
Pro Arg Lys Asn Pro Ala Leu Trp Asp Leu Gly Ile Ile Gln Ala Lys
      100              105              110
Thr Arg Ser Leu Arg Asp Arg Trp Ser Glu Val Pro Arg Lys Leu Glu
      115              120              125
Phe

```

<210> 2207
 <211> 667
 <212> DNA
 <213> Homo sapiens

```

<400> 2207
atctccaacc ccgagaccct ctccaatata gccggcttcg agggctacat cgacctgggc
60
cgcgagctct ccagcctgca ctcaactgtc tgggaggccg tcagccagct ggagcagagc
120
atagtatcca aactgggacc cctgcctcgg atcctgaggg acgtccacac agcactgagc
180
accccaggta gcgggcagct cccagggacc aatgacctgg cctccacacc gggctctggc
240
agcagcagca tctcagctgg gctgcagaag atggtgattg agaacgatct ttccggtctg
300
atagatttca cccggttacc gtctccaacc cccgaaaaca aggacttggt ttttgtcaca
360
aggctcctcg gggctccagc ctcacctgcc cgcagctcga gttactcgga agccaacgag
420
cctgatcttc agatggccaa cggtggcaag agcctctcca tgggtggacct ccaggacgcc
480
cgcacgctgg atggggaggc aggcctcccc gcggggcccc acgtcctccc cacagatggg
540
caggccgctg cagctcagct ggtggccggg tggccggccc gggcaacccc agtgaacctg
600
gcagggctgg ccacggtgcg gcgggcaggc cagacaccaa ccacaccagg cacctccgag
660
ggcgcg
667

```

<210> 2208
 <211> 222
 <212> PRT
 <213> Homo sapiens

```

<400> 2208
Ile Ser Asn Pro Glu Thr Leu Ser Asn Thr Ala Gly Phe Glu Gly Tyr
1      5      10      15
Ile Asp Leu Gly Arg Glu Leu Ser Ser Leu His Ser Leu Leu Trp Glu
20     25     30
Ala Val Ser Gln Leu Glu Gln Ser Ile Val Ser Lys Leu Gly Pro Leu
35     40     45
Pro Arg Ile Leu Arg Asp Val His Thr Ala Leu Ser Thr Pro Gly Ser
50     55     60
Gly Gln Leu Pro Gly Thr Asn Asp Leu Ala Ser Thr Pro Gly Ser Gly

```

```

65              70              75              80
Ser Ser Ser Ile Ser Ala Gly Leu Gln Lys Met Val Ile Glu Asn Asp
      85              90
Leu Ser Gly Leu Ile Asp Phe Thr Arg Leu Pro Ser Pro Thr Pro Glu
      100              105              110
Asn Lys Asp Leu Phe Phe Val Thr Arg Ser Ser Gly Val Gln Pro Ser
      115              120              125
Pro Ala Arg Ser Ser Ser Tyr Ser Glu Ala Asn Glu Pro Asp Leu Gln
      130              135              140
Met Ala Asn Gly Gly Lys Ser Leu Ser Met Val Asp Leu Gln Asp Ala
      145              150              155
Arg Thr Leu Asp Gly Glu Ala Gly Ser Pro Ala Gly Pro Asp Val Leu
      165              170              175
Pro Thr Asp Gly Gln Ala Ala Ala Ala Gln Leu Val Ala Gly Trp Pro
      180              185              190
Ala Arg Ala Thr Pro Val Asn Leu Ala Gly Leu Ala Thr Val Arg Arg
      195              200              205
Ala Gly Gln Thr Pro Thr Thr Pro Gly Thr Ser Glu Gly Ala
      210              215              220

```

<210> 2209

<211> 353

<212> DNA

<213> Homo sapiens

<400> 2209

```

ngggaagtgtg tgactagcct cccaaagcca ctctcctgag tgacattgag agcatcctat
60
agagaaggcc atgagagaga tagcactggg acagatgggtg tcagcagagg ggactccaga
120
ccacagcaga agtgaccaag ctgtagcttc cttagatggc cccaagggtg ggagggttca
180
cacagcagag cctgggtctg gaggcacctt ggggatgttt ttccccatta ggccccgtgag
240
ctctatggaa gcaacttaact gcctgttccc cgcttattct gtgtttaaac caaggaaaca
300
acatgcctgg ggtctgaaat cctggattca aatcctgact gtgtgtgtgtg ctt
353

```

<210> 2210

<211> 94

<212> PRT

<213> Homo sapiens

<400> 2210

```

Met Arg Glu Ile Ala Leu Gly Gln Met Val Ser Ala Glu Gly Thr Pro
1      5      10      15
Asp His Ser Arg Ser Asp Gln Ala Val Ala Ser Leu Asp Gly Pro Lys
      20      25      30
Gly Gly Arg Leu His Thr Ala Glu Pro Gly Ser Gly Gly Thr Leu Gly
      35      40      45
Met Phe Phe Pro Ile Arg Pro Leu Ser Ser Met Glu Ala Leu Asn Cys
      50      55      60
Leu Phe Pro Ala Tyr Ser Val Phe Lys Pro Arg Lys Gln His Ala Trp

```

```

65              70              75              80
Gly Leu Lys Ser Trp Ile Gln Ile Leu Thr Val Leu Cys Ala
      85              90

<210> 2211
<211> 493
<212> DNA
<213> Homo sapiens

<400> 2211
ctgaccacat ctcgcacgat cctagacctc tgttctgcat ctccggacacc accgactgct
60
cactgtaccc tgggactgca cagagggaaa cgattaccaa acccagagac ggggaccgga
120
aggaaggagg ggaaggggat ggatccatgt actttggggt tggagaaatg ggggacagca
180
agtctctcca acccaaatac agcccccctg ggaggctcct gccccgtctc tgtggatagt
240
gagcccagct gcaagggcgg cctgccaggg acaaacccac caaaaggaaa gatgttgtag
300
aaccaaagag aggtccctcg aaagaggcgt ctccgggggc ctccaagccc gggagcgccc
360
ggcggacagg gggcagtggc caagtctgtg cggaccctga ccgcctcaga gaacgagagc
420
atgcgcaaa gtcgtcccat caccaagtcc agcagaggcg ccggctggag gcgaccagag
480
ctgtcatccc ggg
493

<210> 2212
<211> 126
<212> PRT
<213> Homo sapiens

<400> 2212
Met Gly Met Thr Leu Arg Met Leu Ser Phe Ser Glu Ala Val Arg Val
1      5      10      15
Arg Thr Asp Leu Ala Thr Ala Pro Cys Pro Pro Gly Ala Pro Gly Leu
20     25     30
Gly Gly Pro Gly Arg Arg Leu Phe Gln Gly Ala Ser Leu Trp Phe Tyr
35     40     45
Asn Ile Phe Pro Phe Gly Gly Phe Val Pro Gly Arg Pro Pro Leu Gln
50     55     60
Leu Gly Ser Leu Ser Thr Glu Thr Gly Gln Glu Pro Pro Arg Gly Ala
65     70     75     80
Val Phe Gly Leu Arg Arg Leu Ala Val Pro His Phe Ser Asn Pro Lys
85     90     95
Val His Gly Ser Ile Pro Phe Pro Ser Phe Leu Pro Val Pro Val Ser
100    105    110
Gly Phe Gly Asn Arg Phe Pro Leu Cys Ser Pro Arg Val Gln
115    120    125

<210> 2213
<211> 327

```

<212> DNA

<213> Homo sapiens

<400> 2213

acgcgtccga cggcagttc cggcagctgc gggaaagctg cgaatgcgtc gccgagcatt
 60
 gccggtgctt cgacacactg gggtatatcg cctctaaagc acaggtctac gaaggttctg
 120
 acggaaggcc cggccaatcc gatcgcgccg tcggcgctgc gcatcatccg ggcgcgcgtg
 180
 tcgcagctct ggggcacgtc gctgctccgc aacggacggg cggaacagag tgtggtggag
 240
 atcgcccggt tggtcgacgc gatcacgtca cgggacgagg aagccgccca gcgtgcactg
 300
 ctgcaccaca atcgacgcgc gttggaa
 327

<210> 2214

<211> 95

<212> PRT

<213> Homo sapiens

<400> 2214

Met Arg Ser Pro Ser Ile Ala Gly Ala Ser Thr His Trp Val Ile Ser
 1 5 10 15
 Pro Ser Lys His Arg Ser Thr Lys Val Leu Thr Glu Gly Pro Ala Asn
 20 25 30
 Pro Ile Ala Ala Ser Ala Leu Arg Ile Ile Arg Ala Arg Val Ser Gln
 35 40 45
 Leu Trp Gly Thr Ser Leu Leu Arg Asn Gly Arg Ala Glu Gln Ser Val
 50 55 60
 Val Glu Ile Ala Arg Leu Val Asp Ala Ile Thr Ser Arg Asp Glu Glu
 65 70 75 80
 Ala Ala Gln Arg Ala Leu Leu Asp His Asn Arg Ser Ala Leu Glu
 85 90 95

<210> 2215

<211> 430

<212> DNA

<213> Homo sapiens

<400> 2215

ctggggatca tgccctacat cactgcgtcg atcatcctgc agctgctgac agtcgtgatc
 60
 ccgaagctgg aaacccttaa gaaggaggcg gcgtccggtc agaacaagat caccagctac
 120
 acccggtacc tcactctcgt gcttgccctg ttgcaggcaa cggccttcgt cagcgttggc
 180
 acctccggcc gtctattcac cnmtgcagct ntgcagctg tctactccac ctcggtcttc
 240
 gaagtcgtcg tcatgatcct gactatgacg gccggtacga ccatcgctcat gtggatgggt
 300
 gagctcatca ccgaccgagg tatcggcaac ggtatgtcga tcatgatctt cactcagatt
 360

gcggcgcgtt tccctgactc gctgtggtct atcaaggctc ctcgaaatgg cgccgggtcag
420

gctcacgcgt

430

<210> 2216

<211> 143

<212> PRT

<213> Homo sapiens

<400> 2216

Leu	Gly	Ile	Met	Pro	Tyr	Ile	Thr	Ala	Ser	Ile	Ile	Leu	Gln	Leu	Leu
1			5						10				15		
Thr	Val	Val	Ile	Pro	Lys	Leu	Glu	Thr	Leu	Lys	Lys	Glu	Gly	Ala	Ser
			20					25					30		
Gly	Gln	Asn	Lys	Ile	Thr	Gln	Tyr	Thr	Arg	Tyr	Leu	Thr	Leu	Val	Leu
		35					40					45			
Gly	Leu	Leu	Gln	Ala	Thr	Ala	Phe	Val	Thr	Leu	Ala	Thr	Ser	Gly	Arg
	50				55					60					
Leu	Phe	Thr	Xaa	Ala	Ala	Xaa	Pro	Val	Val	Tyr	Ser	Thr	Ser	Val	Phe
65					70					75				80	
Glu	Val	Val	Val	Met	Ile	Leu	Thr	Met	Thr	Ala	Gly	Thr	Thr	Ile	Val
			85						90				95		
Met	Trp	Met	Gly	Glu	Leu	Ile	Thr	Asp	Arg	Gly	Ile	Gly	Asn	Gly	Met
		100						105					110		
Ser	Ile	Met	Ile	Phe	Thr	Gln	Ile	Ala	Ala	Arg	Phe	Pro	Asp	Ser	Leu
		115					120					125			
Trp	Ser	Ile	Lys	Val	Ala	Arg	Asn	Gly	Ala	Gly	Gln	Ala	His	Ala	
	130					135					140				

<210> 2217

<211> 444

<212> DNA

<213> Homo sapiens

<400> 2217

accagggcgc cttcgaagga cctctctcca gctatcgtga cgacgacggc gaagcgggct
60
atgacgtggc tcgatgacga cgtgggcgcc gacctgttga atcaggctga ttccatggac
120
catgccctgg aggccaccgt ccaggtcgg gtcaccacgc cggacgcccc agtcatccag
180
acctgtgcgc tgttgcgtga ccttgctcgc gtggcagtc gccagctggg ccgaaatgac
240
gaggactcta gggaaccagt cgaatgcggag agagtacagg ctcaagcgnc gatgcgggag
300
gttttcgaga ccgccgaacg catgggtggg ctggccgcgc ccgacgtggt gtgggtctct
360
gagttctgaga agggataaccg cagcattcac gtcgctccgc tgagtggttg cggcttgcta
420
cgagagaatg tctttgctca gtcc
444

<210> 2218

<211> 148

<212> PRT

<213> Homo sapiens

<400> 2218

```

Thr Arg Ala Ala Ser Lys Asp Leu Ser Pro Ala Ile Val Thr Thr Thr
 1           5           10           15
Ala Lys Arg Ala Met Thr Trp Leu Asp Asp Val Gly Ala Asp Leu
      20           25           30
Leu Asn Gln Ala Asp Ser Met Asp His Ala Leu Glu Ala Thr Val Pro
 35           40           45
Gly Arg Val Thr Thr Pro Asp Ala Gln Val Ile Gln Thr Cys Ala Val
 50           55           60
Leu Arg Asp Leu Ala Arg Val Ala Val Ser Gln Leu Gly Arg Asn Asp
65           70           75           80
Glu Asp Ser Arg Glu Pro Val Asp Ala Glu Arg Val Gln Ala Gln Ala
      85           90           95
Xaa Met Arg Glu Val Phe Glu Thr Ala Glu Arg Met Val Gly Leu Ala
      100           105           110
Ala Ala Asp Val Val Trp Val Ser Glu Ser Glu Lys Gly Tyr Arg Ser
      115           120           125
Ile His Val Ala Pro Leu Ser Val Gly Gly Leu Leu Arg Glu Asn Val
      130           135           140
Phe Ala Gln Ser
145

```

<210> 2219

<211> 688

<212> DNA

<213> Homo sapiens

<400> 2219

```

acgcgtaccg tcggtggcat gagcgtcctg ccactggaaa ttggtgtgtc attcagctac
60
ggcattacga atatggcgtg gatgtggcta tggttcgacg agcccggaag ccgttgggag
120
tggtcgatcc ttttccccgc tgggtggctg accagcgctt tggtcagtca ggggttcggt
180
ggaatgttcc atagtgtgca gattgcgcgt catgtcagca gttaccacgg catcatggtc
240
gcttttcgcg tcggtgggta cggatggcct gcgatgcaca acttcgctca cctgatgatg
300
cgctattcga ttcgctcggc cttgataatc ggcatcgcca tccagttcac ctggggaggca
360
gtgctgatga tctcgggtat caggccgttg acatggcgcg cgcttggtaa cgattctctc
420
atcgagacga atctcggcgc tccgttcatt ttgctcattg tgaaagcttg gcgcgcgcga
480
cccgaaggaa ttcctggctc taccagtcgg cgcgccacgg ccggtggcac agcgcgagtc
540
tatatgaggg atgatcttgt ttctcgacgc cttctacagc gtccttgaga gcctctgcga
600
gcgaaggggc cggggtgtagg tctccccggg gctcgttgtg gtccctctct tcggtgacgc
660

```


agagccgtgt gatgaggcga agtcatga
688

<210> 2220

<211> 189

<212> PRT

<213> Homo sapiens

<400> 2220

```
Met Ser Val Leu Pro Leu Glu Ile Trp Leu Ser Phe Ser Tyr Gly Ile
 1           5           10          15
Thr Asn Met Ala Trp Met Trp Leu Trp Phe Asp Glu Pro Gly Asn Arg
      20           25           30
Trp Glu Trp Ser Ile Leu Phe Pro Ala Gly Trp Leu Thr Ser Ala Leu
      35           40           45
Val Ser Gln Gly Phe Gly Gly Met Phe His Ser Val Gln Ile Ala Arg
 50           55           60
His Val Ser Ser Tyr His Gly Ile Met Val Ala Phe Ala Leu Val Gly
 65           70           75           80
Tyr Gly Trp Leu Ala Met His Asn Leu Arg His Pro Asp Glu Arg Tyr
      85           90           95
Ser Ile Arg Ser Ala Leu Ile Ile Gly Ile Gly Ile Gln Phe Thr Trp
      100          105          110
Glu Ala Val Leu Met Ile Ser Gly Ile Arg Pro Leu Thr Trp Arg Pro
      115          120          125
Leu Val Ile Asp Ser Leu Ile Glu Thr Asn Leu Gly Ala Pro Phe Met
      130          135          140
Leu Leu Ile Val Lys Ala Trp Arg Ala Pro Pro Glu Gly Ile Pro Gly
      145          150          155          160
Ser Thr Ser Pro Arg Pro Thr Ala Arg Gly Thr Ala Arg Val Tyr Met
      165          170          175
Arg Asp Asp Leu Val Ser Arg Arg Leu Leu Gln Arg Pro
      180          185
```

<210> 2221

<211> 530

<212> DNA

<213> Homo sapiens

<400> 2221

```
actagtgtag ctgcaatata tactcgggat ttactacagt taagccttat ccttccaccc
 60
aaagaagagc aaaccgccat cgctaacgtc ctttccgaca tggacaccga actcgacgcc
      120
ctacaacaac gcctcagtaa aacaaaaacc atcaagcaag gcgatgatgca agaactactc
      180
acaggggaaaa cgagggttggt atgagccaca aggtgaattt agtgcgatgag ctggataaagc
      240
gtattatctc ggtaaatacgt ttattgtcac agcctgagct tgctattccg gcttatcagc
      300
ggccttataa atggtcacia gagaacctaa atgcgctgat gagtgattta cgaatttacc
      360
gtaacaaatc ggcttatcgg ctggggacgg tgggtttttca ttatcataat gaaccgtag
      420
```

acaacgagaa taccacaaag ctggatattg tagacgggtca gcaacgtacc ttaaccttgt
 480
 tgctgctagt caaagccatt ttagaagaac ggttgctctgc gttacgcgt
 530

<210> 2222
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 2222
 Thr Ser Val Ala Ala Ile Tyr Thr Arg Asp Leu Leu Gln Leu Ser Leu
 1 5 10 15
 Ile Leu Pro Pro Lys Glu Glu Gln Thr Ala Ile Ala Asn Val Leu Ser
 20 25 30
 Asp Met Asp Thr Glu Leu Asp Ala Leu Gln Gln Arg Leu Ser Lys Thr
 35 40 45
 Lys Thr Ile Lys Gln Gly Met Met Gln Glu Leu Leu Thr Gly Lys Thr
 50 55 60
 Arg Leu Val
 65

<210> 2223
 <211> 482
 <212> DNA
 <213> Homo sapiens

<400> 2223
 cggccgcgcg ggtagtgagc cctgcgtcgg tggcgtaaatg gaaaatgctg cgctggttgg
 60
 acaggcgcca gacattgttg tggacgatgc cgctgtcgcg cggtggcagc ccggtgaaga
 120
 tgcattttatc caacggcccg gacagggccg gcagttcaca gtccagtttg taaagcgctg
 180
 cgctgctcgc gctgatatag gcctggagat gccccatggc gtgtcgggca acctcgtagt
 240
 tcaggccgctc gagcaccaca aggatgacgt tgtgcttcac aagggggagac gctccgcaac
 300
 gataggcttg actcatttca cttgaggaac ggggtcaaaa ctgtgggcgc gggcaagccc
 360
 gctccacac aagcccgctc ccacattgga tctccaatgt gggctacagc cttactgcac
 420
 attgatgatg acttcttctc gccacttctg cggcagtgcc ttggaggctc tttcccacgc
 480
 gt
 482

<210> 2224
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 2224
 Met Ser Gln Ala Tyr Arg Cys Gly Ala Ser Pro Leu Met Lys His Asn

```

      1             5             10             15
Val Ile Leu Val Val Leu Asp Gly Leu Asn Tyr Glu Val Ala Arg His
      20             25             30
Ala Met Gly His Leu Gln Ala Tyr Ile Ser Ala Gly Arg Ala Ala Leu
      35             40             45
Tyr Lys Leu Asp Cys Glu Leu Pro Ala Leu Ser Arg Pro Leu Asp Lys
      50             55             60
Cys Ile Phe Thr Gly Val Pro Pro Ile Asp Ser Gly Ile Val His Asn
      65             70             75             80
Asn Val Ser Arg Leu Ser Asn Gln Arg Ser Ile Phe His Tyr Ala Thr
      85             90             95
Asp Ala Gly Leu Thr Thr Ala Ala Ala
      100             105

```

<210> 2225

<211> 753

<212> DNA

<213> Homo sapiens

<400> 2225

```

naccgctctg atccacacgg gccactgacg tggcgttatg acagggagcg ggccgggtgcc
60
ggcgtcatcc tcgatctcat gggtcacgga gaggatctcg tccagtatct actcaagggg
120
cgattcactg aggtgtccgc cgtgtccgag acgttcatcc gtcagcgctc caagccactc
180
aaggagggca tcgcccacac aggttggggc gtctcggacg agctcggggc ggtgggcaac
240
gaggattatt gcgctgtcat cgcccgtatg gaaaacggag tgatgtgcac cctggagtcc
300
agtcgggtca gtgttgggcc gcgcgcggag tacatcgctg agatctatgg aaccgacgga
360
tcaatccggt ggaacttcga ggatctcaac catttgcagg tctgtctggg gcgaaacaat
420
cgtgccctgc agggatatgt caactgcatg gccggaccag acttcccgga gttcatgcgt
480
ttccaaccgg gagccggaac atccatgggc tttagcaga tgaaggctgt tgaggctgcg
540
aaattcgtcc gaggggtcct ggatgggcag caatatggcc catctgtcgc cgatggttgg
600
gcctcagcgg aggtcaacga tgcgatcgtt gcctcctcgc ggggaccatg cctggcatga
660
cgtgaagccg gtttcgggga gaaccacgtt cgataagtga ccgcgtcctc gcgtgtctgt
720
gaccaggcct ggcggcacaa ccaggctcgcc ggc
753

```

<210> 2226

<211> 219

<212> PRT

<213> Homo sapiens

<400> 2226

```

Xaa Ala Ser Asp Pro His Gly Pro Leu Thr Trp Arg Tyr Asp Arg Glu

```

```

      1           5           10           15
Arg Ala Gly Ala Gly Val Ile Leu Asp Leu Met Gly His Gly Glu Asp
      20
Leu Val Gln Tyr Leu Leu Lys Gly Arg Phe Thr Glu Val Ser Ala Val
      35           40           45
Ser Glu Thr Phe Ile Arg Gln Arg Pro Lys Pro Leu Lys Glu Gly Ile
      50           55           60
Gly His Thr Gly Trp Val Val Ser Asp Glu Leu Gly Pro Val Gly Asn
      65           70           75           80
Glu Asp Tyr Cys Ala Val Ile Ala Arg Met Glu Asn Gly Val Met Cys
      85           90           95
Thr Leu Glu Ser Ser Arg Val Ser Val Gly Pro Arg Ala Glu Tyr Ile
      100           105           110
Val Glu Ile Tyr Gly Thr Asp Gly Ser Ile Arg Trp Asn Phe Glu Asp
      115           120           125
Leu Asn His Leu Gln Val Cys Leu Gly Arg Asn Asn Arg Ala Leu Gln
      130           135           140
Gly Tyr Val Asn Cys Met Ala Gly Pro Asp Phe Pro Glu Phe Met Arg
      145           150           155           160
Phe Gln Pro Gly Ala Gly Thr Ser Met Gly Phe Asp Asp Met Lys Val
      165           170           175
Val Glu Ala Ala Lys Phe Val Arg Gly Val Leu Asp Gly Gln Gln Tyr
      180           185           190
Gly Pro Ser Val Ala Asp Gly Trp Ala Ser Ala Glu Val Asn Asp Ala
      195           200           205
Ile Val Ala Ser Cys Gly Gly Pro Cys Leu Ala
      210           215

```

<210> 2227

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2227

```

ggatccgaaa cggtgggagc ataaagcagc atggcgccacc tactgaagac ggtggtggct
60
ggctgttcat gtcctttcct tagcaacttg gggctcctcta aggttctacc tgggaagaga
120
gactttgtac gaacgcttcg tactcaccag gcactgtggt gtaaatcccc ggtaaagcca
180
ggaattccat ataagcagtt gacagttggg gtccccaagg agattttcca aaacgagaag
240
cgagttgcac tgtctcctgc ggggggtccag gccctgggtc agcagggtct caatgttgct
300
gtggaatcag gcgcaggcga agct
324

```

<210> 2228

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2228

```

Met Ala His Leu Leu Lys Thr Val Val Ala Gly Cys Ser Cys Pro Phe

```

```

      1           5           10           15
Leu Ser Asn Leu Gly Ser Ser Lys Val Leu Pro Gly Lys Arg Asp Phe
      20           25           30
Val Arg Thr Leu Arg Thr His Gln Ala Leu Trp Cys Lys Ser Pro Val
      35           40           45
Lys Pro Gly Ile Pro Tyr Lys Gln Leu Thr Val Gly Val Pro Lys Glu
      50           55           60
Ile Phe Gln Asn Glu Lys Arg Val Ala Leu Ser Pro Ala Gly Val Gln
      65           70           75           80
Ala Leu Val Lys Gln Gly Phe Asn Val Val Val Glu Ser Gly Ala Gly
      85           90           95
Glu Ala

```

<210> 2229

<211> 320

<212> DNA

<213> Homo sapiens

<400> 2229

```

acgcgtgaag gggccctgtg acgaggtcat ttctgtccat ggggggtcca gatggtgagg
60
cccacagaga gggaacgggc ggggggaggg gagagagaa gacagactca ggcagaaccc
120
tagctcagcc ccttctctgcg tgccctggccc tgggaggatg ccatcccccag tccctcttc
180
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<211> 94

<212> PRT

<213> Homo sapiens

<400> 2230

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      20           25           30
Pro Ala Cys Leu Ala Leu Gly Gly Cys His Pro Gln Ser Pro Leu Leu
      35           40           45
Gly Pro Ala Leu Gly Thr Arg His Arg Trp Ile Gln Cys Ile Leu Ser
      50           55           60
Pro Leu Arg Ser Cys Ala Ala Ile Ser Ser Phe Ser Gly Tyr Arg Ala
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<211> 671

<212> DNA

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<400> 2231

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<213> Homo sapiens

<400> 2232

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Gly Val Arg Val Glu Thr Gly Glu Gly Ser Glu His Leu Trp Asp Thr
35     40     45
His His Val Pro Gly Thr Glu Pro Tyr Leu Asp Leu Leu Gln Pro Ser
50     55     60
Gln Trp His Cys Glu Ala Ser Val Val Leu Gln Met Arg Lys Leu Arg
65     70     75     80
Phe Val Ala Ile Thr Asp Lys Gln Met Thr Leu Asn Gly Ala Gly His
85     90     95
Val Ile Cys His Arg Tyr Met His Arg Thr Met Gln Thr Ser Gln Ser
100    105    110
Pro Leu Ser Gln Thr Arg Leu Thr Ile Arg Asp Met Gln Thr Leu Ala
115    120    125
Gly Leu Gly Leu Phe Pro Ile Gly Asp Ser Leu Val Pro Pro Trp Pro
130    135    140
Leu Met Pro Thr Ala Val Trp Lys Ala Gly Ser Leu Leu Arg Arg Gln

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 35 40 45
 Ile Gln Ser Lys Leu Tyr Arg Ala Ala Leu Glu Thr Asp Glu Asn Leu
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 Cys Met Leu Arg Glu Ile Gly Lys His Ile Asn Met Asp Gly Thr Ile
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Ile Thr Phe Phe Val Pro Val Phe Glu Pro Leu Pro Pro Gln Tyr Phe					
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Val Ser Phe Arg His Leu Ile Leu Pro Glu Lys Tyr Pro Pro Pro Thr					
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Thr Pro Met Glu Ala Leu Ala Glu Gln Val Tyr Met Asp Trp Tyr Glu					
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Lys Phe Gln Asp Arg Leu Asn Lys Lys Val Val Leu Leu Thr Gly Glu					
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Lys Lys Pro Val Ile Val Phe Val Pro Ser Arg Lys Gln Thr Arg Leu					
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Tyr Tyr Asn Gly Lys Ile His Ala Tyr Val Asp Tyr Pro Ile Tyr Asp	1235		1240		1245
Val Leu Gln Met Val Gly His Ala Asn Arg Pro Leu Gln Asp Asp Glu	1250		1255		1260
Gly Arg Cys Val Ile Met Cys Gln Gly Ser Lys Asp Phe Phe Lys	1265		1270		1275
Lys Phe Leu Tyr Glu Pro Leu Pro Val Glu Ser His Leu Asp His Cys	1285		1290		1295
Met His Asp His Phe Asn Ala Glu Ile Val Thr Lys Thr Ile Glu Asn	1300		1305		1310
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Thr Ile Glu Leu Phe Ser Met Ser Leu Asn Ala Lys Thr Lys Val Arg	1395		1400		1405
Gly Leu Ile Glu Ile Ile Ser Asn Ala Ala Glu Tyr Glu Asn Ile Pro	1410		1415		1420
Ile Arg His His Glu Asp Asn Leu Leu Arg Gln Leu Ala Gln Lys Val	1425		1430		1435
Pro His Lys Leu Asn Asn Pro Lys Phe Asn Asp Pro His Val Lys Thr	1445		1450		1455
Asn Leu Leu Leu Gln Ala His Leu Ser Arg Met Gln Leu Ser Ala Glu	1460		1465		1470
Leu Gln Ser Asp Thr Glu Glu Ile Leu Ser Lys Ala Ile Arg Leu Ile	1475		1480		1485
Gln Ala Cys Val Asp Val Leu Ser Ser Asn Gly Trp Leu Ser Pro Ala	1490		1495		1500
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Met Glu Asp Glu Glu Arg Asn Ala Leu Leu Gln Leu Thr Asp Ser Gln	1555		1560		1565
Ile Ala Asp Val Ala Arg Phe Cys Asn Arg Tyr Pro Asn Ile Glu Leu	1570		1575		1580
Ser Tyr Glu Val Val Asp Lys Asp Ser Ile Arg Ser Gly Gly Pro Val	1585		1590		1595
Val Val Leu Val Gln Leu Glu Arg Glu Glu Glu Val Thr Gly Pro Val	1605		1610		1615
Ile Ala Pro Leu Phe Pro Gln Lys Arg Glu Glu Gly Trp Trp Val Val	1620		1625		1630
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 540
 ccctggcccg ctctgccatc ttctctgtga cctaccctc acgcgt
 586

<210> 2236
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 2236
 Met Ser Pro Lys Gln Pro Leu His Gly Val Arg Val Gln Val Glu Val
 1 5 10 15
 Glu Val Phe Arg Asp Leu Leu Phe Leu Pro His Ile Ile Gln Ser Gln
 20 25 30
 Asp Pro Lys Asp Gly Leu Asn Phe Asn Leu Glu Leu Glu Arg Gln Thr
 35 40 45
 Leu Asp Gln Asp Pro Leu Ser Lys Val Leu Ala Gly Val Ala Leu Gly
 50 55 60
 Gly Tyr Ser Val Pro Arg Leu His Pro Arg Gln Val Pro Gly Arg Gly
 65 70 75 80
 Glu Ala Gly Pro Gly Ala Gly Ala Ala Val Glu Gly Leu His Cys Ala

```

      85              90              95
Gly Pro His Leu Leu Gly Pro Pro Ala Leu Ala Glu Arg Ala Thr Met
      100              105              110
Ser Gln Leu Pro Gly Ser Ser Gly Arg Arg Cys
      115              120

```

<210> 2237
 <211> 421
 <212> DNA
 <213> Homo sapiens

```

<400> 2237
cttaggaagg cacacctgtg tccactgca gccaaagagga agcaccctctt
60
tggggcgag gagtgctggc cagcttgggg atagtccctg gaagtggctg ggagcactga
120
gggaggagct gaggtccaag cctctctcca gtgcatcacc ctggtcagga gtggggcagt
180
gtggagccag gggtctctca gccagcacct gctgcactat gggtctccagc tgtgcaagac
240
caccctgtgag aaggagtctt gttgggagca ggggtgggaa gcaactgtggg agagggtgcc
300
ttggctcggg tagcaggagc cttgatgtat cttgaagcca gggggccgac tgaggcgctt
360
gtctgaaggc ctccatgaga gggagggggc tggagggggc tgttcccaat aatagctcta
420
t
421

```

<210> 2238
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 2238
Met Glu Ala Phe Arg Gln Ala Pro Gln Ser Ala Pro Trp Leu Gln Asp
1      5      10      15
Thr Ser Arg Ser Leu Leu Pro Glu Pro Arg Thr Pro Leu Pro Gln Cys
      20      25      30
Phe Pro Thr Leu Leu Pro Thr Arg Leu Leu Thr Gly Gly Leu Ala
      35      40      45
Gln Leu Glu Pro Ile Val Gln Gln Val Leu Ala Glu Glu Pro Leu Ala
      50      55      60
Pro His Cys Pro Thr Pro Asp Gln Gly Asp Ala Leu Glu Glu Gly Leu
65      70      75      80
Asp Leu Ser Ser Ser Leu Ser Ala Pro Asp His Phe Gln Gly Leu Ser
      85      90      95
Pro Ser Trp Pro Ala Leu Leu Arg Pro Lys Arg Ser Val Trp Gly Ala
      100     105     110
Ser Ser Trp Leu Gln Trp Asp Thr Gly Val Pro Ser
      115     120

```

<210> 2239
 <211> 623

<212> DNA

<213> Homo sapiens

<400> 2239

gctagcagga ctcagaaatc tgctgttgag cacaaagcca aaaaatctct gtcccatcct
 60
 agccattcca ggccctgggccc catgggcacc ccacacaata aggctaagag tccagggtgc
 120
 aggcagccag gcagcagctc tagctcagcc cctgggcagc ccagcacagg ggttgctcga
 180
 cccacagtta gttctggccc tgtgcctagg cgccagaatg gcagctccag ctccaggacct
 240
 gagcgatcaa tcagtgggtc caagaagcca accaatgact caaatccctc taggcggaca
 300
 gtcagtggta catgtggccc tggacaacct gcaagcagct cagggtggccc tgggcgaccc
 360
 atcagtgggt cagttagttc tgcaagaccc ttgggcagct ctctgggccc tggccggcct
 420
 gtgagcagtc cacatgaact tcgacgacca gtgagtggct tgggcccccc gggggcgtct
 480
 gtcagtggcc ctgggagatc cataagtggc ccaattccag ctggacggac tgtcagtaat
 540
 tcagtcaccag gaagaccagt gagcagcttg ggacctgggc aaacagttag tagctcagggt
 600
 cccactataa agcctaagtg cac
 623

<210> 2240

<211> 207

<212> PRT

<213> Homo sapiens

<400> 2240

Ala	Ser	Arg	Thr	Gln	Lys	Ser	Ala	Val	Glu	His	Lys	Ala	Lys	Lys	Ser
1				5					10					15	
Leu	Ser	His	Pro	Ser	His	Ser	Arg	Pro	Gly	Pro	Met	Val	Thr	Pro	His
			20					25					30		
Asn	Lys	Ala	Lys	Ser	Pro	Gly	Val	Arg	Gln	Pro	Gly	Ser	Ser	Ser	Ser
		35				40					45				
Ser	Ala	Pro	Gly	Gln	Pro	Ser	Thr	Gly	Val	Ala	Arg	Pro	Thr	Val	Ser
	50					55					60				
Ser	Gly	Pro	Val	Pro	Arg	Gln	Asn	Gly	Ser	Ser	Ser	Ser	Gly	Pro	
65					70				75					80	
Glu	Arg	Ser	Ile	Ser	Gly	Ser	Lys	Lys	Pro	Thr	Asn	Asp	Ser	Asn	Pro
				85					90					95	
Ser	Arg	Arg	Thr	Val	Ser	Gly	Thr	Cys	Gly	Pro	Gly	Gln	Pro	Ala	Ser
			100				105						110		
Ser	Ser	Gly	Gly	Pro	Gly	Arg	Pro	Ile	Ser	Gly	Ser	Val	Ser	Ser	Ala
		115				120						125			
Arg	Pro	Leu	Gly	Ser	Ser	Arg	Gly	Pro	Gly	Arg	Pro	Val	Ser	Ser	Pro
		130				135					140				
His	Glu	Leu	Arg	Arg	Pro	Val	Ser	Gly	Leu	Gly	Pro	Pro	Gly	Arg	Ser
145					150					155				160	
Val	Ser	Gly	Pro	Gly	Arg	Ser	Ile	Ser	Gly	Pro	Ile	Pro	Ala	Gly	Arg

```

                165                170                175
Thr Val Ser Asn Ser Val Pro Gly Arg Pro Val Ser Ser Leu Gly Pro
                180                185                190
Gly Gln Thr Val Ser Ser Ser Gly Pro Thr Ile Lys Pro Lys Cys
                195                200                205

```

<210> 2241

<211> 656

<212> DNA

<213> Homo sapiens

<400> 2241

```

nnacgcgtga agggcagcag caacaccacg gagtgtgttc ccgtgcccac ctccgagcac
60
gtggccgaga tcgtgggcag gcaaggctgc aagattaagg ccttgagggc caagaccaac
120
acctacatta gaaccccggg aaggggagag gaaccagtgt tcattggtgac agggcgacgg
180
gaggacgtgg ccacagcccg gcgggaaatc atctcagcag cggagcactt ctccatgatc
240
cgtgcctccc gcaacaagtc aggcgcgcgc tttggtgtgg ctctgctct gcccgccag
300
gtgaccatcc gtgtgcgggt gccctaccgc gtggtggggc tgggtggtgg ccccaaaggg
360
gcaaccatca agcgcattcca gcagcaaac aacacataca ttatcacacc aagcgtgac
420
cgcgaccccg tgttcagat caccgggtgc ccaggcaacg tggagcgtgc gcgcgaggag
480
atcgagacgc acatcgcggt gcgcactggc aagatcctcg agtacaaca tgaaaacgac
540
ttcctggcgg ggagccccga cgcagcaatc gatagccgct actccgacgc ctggcggggtg
600
caccagcccc gctgcaagcc cctctccacc ttccggcaga acagcctggg ctgcag
656

```

<210> 2242

<211> 218

<212> PRT

<213> Homo sapiens

<400> 2242

```

Xaa Arg Val Lys Gly Ser Ser Asn Thr Thr Glu Cys Val Pro Val Pro
1      5      10
Thr Ser Glu His Val Ala Glu Ile Val Gly Arg Gln Gly Cys Lys Ile
20     25     30
Lys Ala Leu Arg Ala Lys Thr Asn Thr Tyr Ile Arg Thr Pro Gly Arg
35     40     45
Gly Glu Glu Pro Val Phe Met Val Thr Gly Arg Arg Glu Asp Val Ala
50     55     60
Thr Ala Arg Arg Glu Ile Ile Ser Ala Ala Glu His Phe Ser Met Ile
65     70     75     80
Arg Ala Ser Arg Asn Lys Ser Gly Ala Ala Phe Gly Val Ala Pro Ala
85     90     95
Leu Pro Gly Gln Val Thr Ile Arg Val Arg Val Pro Tyr Arg Val Val

```

```

          100              105              110
Gly Leu Val Val Gly Pro Lys Gly Ala Thr Ile Lys Arg Ile Gln Gln
      115              120              125
Gln Thr Asn Thr Tyr Ile Ile Thr Pro Ser Arg Asp Arg Asp Pro Val
      130              135              140
Phe Glu Ile Thr Gly Ala Pro Gly Asn Val Glu Arg Ala Arg Glu Glu
      145              150              155              160
Ile Glu Thr His Ile Ala Val Arg Thr Gly Lys Ile Leu Glu Tyr Asn
      165              170              175
Asn Glu Asn Asp Phe Leu Ala Gly Ser Pro Asp Ala Ala Ile Asp Ser
      180              185              190
Arg Tyr Ser Asp Ala Trp Arg Val His Gln Pro Gly Cys Lys Pro Leu
      195              200              205
Ser Thr Phe Arg Gln Asn Ser Leu Gly Cys
      210              215

```

<210> 2243

<211> 384

<212> DNA

<213> Homo sapiens

<400> 2243

```

gaattcagca tttaaattgct actcgttggc atgcaatttg ctgtcatgaa aacgactgtg
60
gatttcatttc ctggttaagaa tcttctgact tattgagctg catgtcagaa gcaaaagca
120
aaaaaaccaa atatgtacat aaacagtggt tatcattcct taaaagagaa ggaaaataaa
180
tccctaaata atgtggactg gaacacagaa atccaaggct ggccgcacgg gtccctggctg
240
ggatggcatc cggggagctg ctgctgggga cgtgcttgcc ggcacaggtc aggggagccg
300
ggttctgcct cctccttgcc cactctcttt gcgcctctcc tgtgctgcgc tgtcttgttt
360
tacctcccat cctgggcct tgga
384

```

<210> 2244

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2244

```

Met Gly Gly Lys Thr Arg Gln Ala Ser Thr Gly Arg Ala Gln Arg Glu
  1              5              10              15
Trp Ala Arg Arg Arg Gln Asn Pro Ala Pro Leu Thr Cys Ala Gly Lys
      20              25              30
His Val Pro Ser Ser Ser Pro Asp Ala Ile Pro Ala Arg Thr Arg
      35              40              45
Ala Ala Ser Leu Gly Phe Leu Cys Ser Ser Pro His Tyr Leu Gly Ile
      50              55              60
Tyr Phe Pro Ser Leu Leu Arg Asn Asp Asn Thr Val Leu Cys Thr Tyr
      65              70              75              80
Leu Val Phe Leu Leu Phe Ala Ser Asp Met Gln Leu Asn Lys Ser Glu

```

85 90 95
 Asp Ser Tyr Gln Glu Met Asn Pro Gln Ser Phe Ser
 100 105

<210> 2245
 <211> 632
 <212> DNA
 <213> Homo sapiens

<400> 2245
 acgcgtgcga ttaccgtcaa ggctggtgtg gtgagcgcgtg atctgcacga gcggacgtct
 60
 tcgagagaag aggtcggacg cgagaggctc aactatggtc acaccttggc ccacgtatt
 120
 gagggccaca agcatttcac gtggcgtcat ggcgaggctg acgcggtggg catggtgttt
 180
 gcggccgaac tgtgcaccg gtacctggga ctgtccgatg aggtcgttgc gcgcacccgc
 240
 actatcctgt ctgagatcgg attgcctgtt acctgtgacg agattaagtg ggcagatctg
 300
 cgcaagacga tgaacgtgga caagaaaacc agggtagacc cgcagaccgg gcgtcaagt
 360
 ttgcggtttg tcggtattca caaaccgggt caggtcgccca tgatcgtcga cctgacgag
 420
 gccgcttttag ccgagtgeta cgaccgggtg tccgcacggt aaaaacgttc ggaaatgaac
 480
 atgtggctgc gggtcagtcg gcattcaggc ctccgtgacg ccgtcgacc caagtgatgt
 540
 gaogattcgg gaaatatctt gttgggcaact cttgagcctc gcctgattcc ccatacccca
 600
 cttaagttca gtatcgacgg catgaatccg ga
 632

<210> 2246
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 2246
 Thr Arg Ala Ile Thr Val Lys Ala Gly Val Val Ser Ala Asp Leu His
 1 5 10 15
 Glu Arg Thr Ser Ser Arg Glu Glu Val Gly Arg Glu Arg Leu Asn Tyr
 20 25 30
 Gly His Thr Leu Ala His Ala Ile Glu Ala His Lys His Phe Thr Trp
 35 40 45
 Arg His Gly Glu Ala Asp Ala Val Gly Met Val Phe Ala Ala Glu Leu
 50 55 60
 Ser His Arg Tyr Leu Gly Leu Ser Asp Glu Val Val Ala Arg Thr Arg
 65 70 75 80
 Thr Ile Leu Ser Glu Ile Gly Leu Pro Val Thr Cys Asp Glu Ile Lys
 85 90 95
 Trp Ala Asp Leu Arg Lys Thr Met Asn Val Asp Lys Lys Thr Arg Val
 100 105 110
 Asp Pro Gln Thr Gly Arg Gln Val Leu Arg Phe Val Gly Ile His Lys

```

          115              120              125
Pro Gly Gln Val Ala Met Ile Val Asp Pro Asp Glu Ala Ala Leu Ala
   130              135              140
Glu Cys Tyr Asp Arg Cys Ser Ala Arg
145              150

```

```

<210> 2247
<211> 324
<212> DNA
<213> Homo sapiens

```

```

<400> 2247
gggcgttcgc ctccagggtt ctccccgaca ctggatgccac acctgcccag gggcagaagg
60
gaggttgggc gtggggagtg cggggtacag tcagagtgtc caggacagtt tggagcagtg
120
cctcttaate ttggcgcac agcacctggg agctttaaat agacccccac gccttgggcg
180
ccccaccgc tgacccccc gatctcagct ctgcctttcc cgctctcttg ctgggttgca
240
taagccagcg attcccaacc cggctgtac ctggaagcta cccaggagc ttctggagaa
300
tgtgccgtgt gagccatccc cctg
324

```

```

<210> 2248
<211> 105
<212> PRT
<213> Homo sapiens

```

```

<400> 2248
Met Ala His Thr Ala His Ser Pro Glu Ala Pro Gly Val Ala Ser Arg
   1           5           10           15
Tyr Ser Arg Gly Trp Glu Ser Leu Ala Tyr Ala Thr Gln Gln Arg Gly
   20           25           30
Gly Lys Gly Arg Ala Glu Ile Gly Trp Val Ser Gly Gly Gly Ala Gln
   35           40           45
Gly Val Gly Val Tyr Leu Lys Leu Pro Gly Ala Val Arg Pro Arg Leu
   50           55           60
Arg Gly Thr Ala Pro Asn Cys Pro Gly Asn Ser Asp Cys Thr Arg His
   65           70           75           80
Ser Pro Arg Pro Thr Ser Leu Leu Pro Leu Gly Arg Leu Ala Ser Ser
   85           90           95
Val Gly Glu Asn Pro Gly Gly Glu Arg
   100           105

```

```

<210> 2249
<211> 394
<212> DNA
<213> Homo sapiens

```

```

<400> 2249
gaaaaccgga taacagggtg tatacaagcc tctgagttct gggagcaaca accagctcaa
60

```

```

ccgcgaagg aaagtgaagaa agcaattaag ttgggaaccg cgggggttttc ccattccac
120
ggtggaaacc gcggccagtg aattgaaatc cgcttcctta aggcgaatg ggccttaaa
180
aggcaaggtc aaccgccgc cagtgtgatg gaatttgcaa gaattcggtt tagcaccctc
240
ccggcttttc tcccgaccgc gtgcagggtg ggctgcgctg ggctggggag gaactgggag
300
ctgggggctc atgtcctgta taaaggggct gcagggggcg tgtctcccc cagaagactg
360
gccacatggg gacaggcctc ctgggggcag atct
394

```

<210> 2250

<211> 104

<212> PRT

<213> Homo sapiens

<400> 2250

```

Met Ser Pro Gln Leu Pro Val Pro Pro Arg Pro Ser Ala Ala His Pro
  1           5           10           15
Ala Arg Gly Arg Glu Lys Ser Arg Glu Gly Ala Lys Pro Asn Ser Cys
      20           25           30
Lys Phe His His Thr Gly Gly Arg Leu Thr Leu Pro Phe Lys Gly Pro
      35           40           45
Phe Arg Leu Lys Glu Ala Asp Phe Asn Ser Leu Ala Ala Val Ser Thr
      50           55           60
Val Gly Met Gly Lys Pro Arg Gly Ser Gln Leu Asn Cys Phe Leu Thr
      65           70           75           80
Phe Pro Cys Gly Leu Ser Trp Leu Leu Leu Pro Glu Leu Arg Gly Leu
      85           90           95
Tyr Thr Pro Cys Tyr Pro Val Phe
      100

```

<210> 2251

<211> 654

<212> DNA

<213> Homo sapiens

<400> 2251

```

acgcgtactt attcgccacc atgattatga ccagtgtttc cagtcggttc agttgttgca
60
gtggaatagt caggttaaat ttaatgtgac cgtttatcgc aatctgccga ccactcgca
120
ttcaatcatg acttcgtgat aaaagattga gtgtgaggtt ataacgccga agcggtaaaa
180
attttaattt ttgcgcgtga ggggttgacc aagcgaagcg cggtaggttt tctgcttagg
240
agtttaatca tgtttcagac ttttatttct cgccataatt caaacttttt tcttgataag
300
ctggttctca cttctgttac tccagcttct tcggcacctg ttttacagac acctaaagct
360
acatcgtaaa cgttatatatt tgatagtttg acggttaatg ctggtaatgg tggttttctt
420

```

cattgcattc agatggatac atctgtcaac gccgctaate aggttgtttc tgttggtgct
 480
 gatattgctt ttgatgccga ccctaaattt ttgcctgtt tgggtcgctt tgagctcttc
 540
 tcgggtccga ctaccctccc gactgcctat gatgtttatc ctttggatgg tcgccatgat
 600
 ggtggttatt ataccgtcaa ggactgtgtg actattgacg tccttctctg tacg
 654

<210> 2252

<211> 135

<212> PRT

<213> Homo sapiens

<400> 2252

Met	Phe	Gln	Thr	Phe	Ile	Ser	Arg	His	Asn	Ser	Asn	Phe	Phe	Ser	Asp
1				5					10					15	
Lys	Leu	Val	Leu	Thr	Ser	Val	Thr	Pro	Ala	Ser	Ser	Ala	Pro	Val	Leu
			20					25					30		
Gln	Thr	Pro	Lys	Ala	Thr	Ser	Ser	Thr	Leu	Tyr	Phe	Asp	Ser	Leu	Thr
		35						40				45			
Val	Asn	Ala	Gly	Asn	Gly	Gly	Phe	Leu	His	Cys	Ile	Gln	Met	Asp	Thr
	50				55					60					
Ser	Val	Asn	Ala	Ala	Asn	Gln	Val	Val	Ser	Val	Gly	Ala	Asp	Ile	Ala
65					70					75				80	
Phe	Asp	Ala	Asp	Pro	Lys	Phe	Phe	Ala	Cys	Leu	Val	Arg	Phe	Glu	Ser
			85					90						95	
Ser	Ser	Val	Pro	Thr	Thr	Leu	Pro	Thr	Ala	Tyr	Asp	Val	Tyr	Pro	Leu
			100					105					110		
Asp	Gly	Arg	His	Asp	Gly	Gly	Tyr	Tyr	Thr	Val	Lys	Asp	Cys	Val	Thr
	115						120					125			
Ile	Asp	Val	Leu	Pro	Arg	Thr									
	130					135									

<210> 2253

<211> 327

<212> DNA

<213> Homo sapiens

<400> 2253

ggatcctgct gggcctcttt tacgtgatgt tgaccagacc gctggtgcgc attattcgcg
 60
 cactgagcac cagcaagcag gcccgcttgg attgccacc ggtgcacgaa aacgatgaaa
 120
 tcggcgtatt ggtcaacgtc gcccaaccagc aattcgacaa tatggaaacc gaaatcgagc
 180
 agcgccgccca cgccgaggac gcgctcaccg aatacctggg ccaactggaa gatatcgctc
 240
 ccgcacgcac cctggagctc aaggccagca accaacgctt gagccaatcc aacgatgagc
 300
 tggaagcggc aaagttgacc gccttggg
 327

<210> 2254

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2254

```

Met Leu Thr Gln Pro Leu Val Arg Ile Ile Arg Ala Leu Ser Thr Ser
 1              5              10              15
Lys Gln Ala Arg Leu Asp Cys Pro Pro Gly His Glu Asn Asp Glu Ile
      20              25              30
Gly Val Leu Val Asn Val Ala Asn Gln Gln Phe Asp Asn Met Glu Thr
      35              40              45
Glu Ile Glu Gln Arg Arg His Ala Glu Asp Arg Leu Thr Glu Tyr Leu
      50              55              60
Gly Gln Leu Glu Asp Ile Val Ser Ala Arg Thr Leu Glu Leu Lys Ala
      65              70              75              80
Ser Asn Gln Arg Leu Ser Gln Ser Asn Asp Glu Leu Glu Ala Ala Lys
      85              90              95

Leu Thr Ala Leu
      100

```

<210> 2255

<211> 357

<212> DNA

<213> Homo sapiens

<400> 2255

```

nngctagcac atgagaagtg tgaagtttat actttgcttg ggcgatcacg ccgttttcca
60
aatatggctc atgcaacttc tggccaaagg ggtcacattg agcgtgctgc tatcaatgct
120
cctgtacagg gcagtgccagc tgaatgttgc atgtgtgcaa tgccttgagat agacaggaat
180
actcgtctta aggagcttgg ttggacgcta ctcttgccag tgcattgatga agtgatactg
240
gaagggccct cagagtctgc ggagtnggcc aagtcctatg ttgttgagtg catgtctaag
300
cccttctatg gcaccaatat cctgagggtc gaccttgctg ttgatgccaa gtgtgca
357

```

<210> 2256

<211> 119

<212> PRT

<213> Homo sapiens

<400> 2256

```

Xaa Leu Ala His Glu Lys Cys Glu Val Tyr Thr Leu Leu Gly Arg Ser
 1              5              10              15
Arg Arg Phe Pro Asn Met Ala His Ala Thr Ser Gly Gln Arg Gly His
      20              25              30
Ile Glu Arg Ala Ala Ile Asn Ala Pro Val Gln Gly Ser Ala Ala Asp
      35              40              45
Val Ala Met Cys Ala Met Leu Glu Ile Asp Arg Asn Thr Arg Leu Lys
      50              55              60
Glu Leu Gly Trp Thr Leu Leu Leu Gln Val His Asp Glu Val Ile Leu

```



```

65              70              75              80
Glu Gly Pro Ser Glu Ser Ala Glu Xaa Ala Lys Ser Ile Val Val Glu
              85              90              95
Cys Met Ser Lys Pro Phe Tyr Gly Thr Asn Ile Leu Arg Val Asp Leu
              100              105              110
Ala Val Asp Ala Lys Cys Ala
              115

```

<210> 2257
 <211> 626
 <212> DNA
 <213> Homo sapiens

```

<400> 2257
nnaatgacaa aaaatatgaa ccaaaatagt gacagtggca gtacaaataa ctataaaagc
60
ctgaaaccta aattagaaaa tctgagttct ttaccaccag attctgacag aacatcagaa
120
gtatatctac atgaagaatt acagcaggac atgcaaaagt ttaagaatga ggtcaacaca
180
ttagaagaag agttcctggc ttggaagaaa gaaaatgttc aacttcataa agaggttgaa
240
gaagaaatgg agaagcacag aagtaaatagc acagaattat caggaaccct aactgatggt
300
actactgttg gcaatgatga tgatggacta aatcagcaga ttcctaggaa ggaaaatgaa
360
gagcatgaca ggcctgcaga taaaacagct aatgaaaaga acaagggtcaa aaaccaaata
420
tatcctgagg ctgactttgc tgactcaatg gagccatctg aaatagcctc agaggattgt
480
gaattgtctc actctgttta tgagaatttt atgttgctga ttgaaacaat tagaatggag
540
tataaaggta ggaccactgc ataaatgcaa ggccttttga tgtatcctgc agtaaatgtg
600
gtatacattg ctgagaactg acgcgt
626

```

<210> 2258
 <211> 187
 <212> PRT
 <213> Homo sapiens

```

<400> 2258
Xaa Met Thr Lys Asn Met Asn Gln Asn Ser Asp Ser Gly Ser Thr Asn
1              5              10              15
Asn Tyr Lys Ser Leu Lys Pro Lys Leu Glu Asn Leu Ser Ser Leu Pro
20              25              30
Pro Asp Ser Asp Arg Thr Ser Glu Val Tyr Leu His Glu Glu Leu Gln
35              40              45
Gln Asp Met Gln Lys Phe Lys Asn Glu Val Asn Thr Leu Glu Glu Glu
50              55              60
Phe Leu Ala Leu Lys Lys Glu Asn Val Gln Leu His Lys Glu Val Glu
65              70              75              80
Glu Glu Met Glu Lys His Arg Ser Asn Ser Thr Glu Leu Ser Gly Thr

```


	85		90		95										
Val	Val	Asp	Arg	Pro	Glu	Tyr	Val	Val	Pro	Glu	Phe	Phe	Asp	Glu	
	100						105					110			
Arg	Val	Thr	Arg	Lys	Cys	Leu	Pro	Leu	Glu	Asn	Phe	Lys	Asn	Asp	Leu
	115						120					125			
Pro	Leu	Asp	Glu	Tyr	Asn	Gly	Phe	Ile	Ile	Val	Thr	Arg			
	130					135					140				

<210> 2261

<211> 660

<212> DNA

<213> Homo sapiens

<400> 2261

```

ngctagctgc tgctcctgag gatcggccgc agaatttgc tgccgatctg tccgggttgc
60
ttgagcccaa gcgcgaggtc gatgtgtccg gcgaccgcgc gcgttgccgt gggagcatag
120
tgtcgggtgca cgctgaccga gaggtccgtg cggagagtac tcccgatgat atttgcgggc
180
agctcgatgc cgtggccgcc atgatggccc ttgtctatgg gtcgaatgtg actattcccg
240
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480
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<210> 2262

<211> 139

<212> PRT

<213> Homo sapiens

<400> 2262

```

Met Pro Gly Gly Ser Ser Thr Ser Phe Thr Glu Arg Cys Ser Ile Gly
1      5      10      15
Pro Asn Gly Cys Pro Cys Gly Gln Pro Leu Tyr Leu Val Met Gly Arg
20     25     30
Asn Pro Met Ser Ser Arg Asn Gly Phe Gln Ala Thr Asp Leu Ala Leu
35     40     45
Ile Ala Val Phe Ala Ala Leu Ile Ala Val Leu Ala Val Ile Pro Pro
50     55     60
Met Phe Met Val Gly Ala Val Pro Phe Ala Leu Gln Met Val Ala Val
65     70     75     80
Met Leu Ala Pro Met Val Leu Gly Ser Ile Arg Gly Gly Cys Ala Val

```

```

      85              90              95
Gly Leu Tyr Ile Leu Val Gly Ala Leu Gly Leu Pro Val Phe Ser Gly
      100              105              110
Gly Ser Ser Gly Ile Gly Val Leu Val Gly Pro Thr Gly Gly Tyr Leu
      115              120              125
Trp Gly Trp Leu Ile Gly Ala Phe Val Ala Gly
      130              135

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<210> 2263

<211> 491

<212> DNA

<213> Homo sapiens

<400> 2263

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nacgcgttcc cggtcgaccg aggcaaagcg aaaagtaagc aggggtgccc tagtccccgt
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120
gagggcaccc ggtctcgac cggcgcaatg ggcaccttca aacctggggc tgccgcattg
180
gctatttcac gtgggggttcc gggtatcccg attgcttttag taggagcatg ggcggctatg
240
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300
cctatggacc ctgttcccg cgagatcgcc caccaattct ccgaacggat tcgtcgccag
360
gtcattgagt tgcacgacca aaccgcccgc gcctacggca tgccaaccct tgacgaatac
420
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480
tcgacgtgca c
491

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<210> 2264

<211> 163

<212> PRT

<213> Homo sapiens

<400> 2264

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Xaa Ala Phe Pro Val Asp Arg Gly Lys Gly Lys Ser Lys Gln Gly Ala
1      5      10      15
Arg Ser Pro Arg Ser His Arg Gly Met Ala Gly Ser Leu Leu Thr Asp
      20      25      30
Gly Val Pro Leu Leu Ile Phe Pro Glu Gly Thr Arg Ser Arg Thr Gly
      35      40      45
Ala Met Gly Thr Phe Lys Pro Gly Ala Ala Ala Leu Ala Ile Ser Arg
      50      55      60
Gly Val Pro Val Ile Pro Ile Ala Leu Val Gly Ala Trp Ala Ala Met
65      70      75      80
Pro Ser Glu Gln Ala Arg Leu Pro Lys Gly Arg Pro Leu Val His Val
      85      90      95
Ala Ile Gly His Pro Met Asp Pro Val Pro Gly Glu Ile Ala His Gln
      100      105      110
Phe Ser Glu Arg Ile Arg Arg Gln Val Ile Glu Leu His Asp Gln Thr

```

```

      115              120              125
Ala Arg Ala Tyr Gly Met Pro Thr Leu Asp Glu Tyr Gly Arg His Arg
      130              135              140
Ala Leu Ser Gln Ala Ser Glu Ser Gly Asp Thr Ala Ser Thr Asn His
      145              150              155              160
Ser Thr Cys

```

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<210> 2265
<211> 328
<212> DNA
<213> Homo sapiens

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<400> 2265
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gtcaacacgg cagacacatg ctggcagaaa cctgctgga gttgccctg agcattgatg
120
cataccaccc gagaggagga gaggggtggtg ggagaaatca gatcagagtt caaaatgcac
180
cggaagggtc cggaaatgta agactgcacc ttgcaggaac tgtcaatgcc actaccaata
240
tcaactcatt acgtcaagca cttgagagca gctgcgaaca caattctctg actcctaacc
300
tttagcacgt gactggggacc actggaca
328

```

```

<210> 2266
<211> 100
<212> PRT
<213> Homo sapiens

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```

<400> 2266
Met Gly Ile Gly Gln His Gly Trp Ile Tyr Cys Ile Thr Cys Leu Pro
1          5          10          15
Ser Gly Lys Ser Gln His Gly Arg His Met Leu Ala Glu Thr Leu Leu
20         25         30
Glu Leu Pro Leu Ser Ile Asp Ala Tyr His Pro Arg Gly Gly Glu Gly
35         40         45
Gly Gly Arg Asn Gln Ile Arg Val Gln Asn Ala Pro Glu Gly Leu Gly
50         55         60
Asn Val Arg Leu His Leu Ala Gly Thr Val Asn Ala Thr Thr Asn Ile
65         70         75         80
Thr His Leu Arg Gln Ala Leu Glu Ser Ser Cys Glu His Asn Ser Leu
85         90         95
Thr Pro Asn Leu
100

```

```

<210> 2267
<211> 370
<212> DNA
<213> Homo sapiens

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<400> 2267

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agatctatgc aggttagcgct ggtctccggg gggtaagttg tccactccct gtcagatggc
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 agaccatgga gggctaagtc aggctgggaa ggctaggcag agtctccaga aacaggtcac
 120
 cgagggagacc accactgaat tgcactctcg ctggggagtt aagccatatt cccctaagac
 180
 agcagtgacc ggagtggcca atctgtacag ggacaggctc aaggccacag caactcaggg
 240
 gacagagatg gtgaagcagg catgtcctaa agcctccctt cttaaccctg accttgaagg
 300
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 360
 gtcaacgcgt
 370

<210> 2268

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2268

Met	Ala	Asp	His	Gly	Gly	Leu	Met	Gln	Ala	Gly	Lys	Ala	Arg	Gln	Ser
1				5					10				15		
Ser	Gln	Lys	Gln	Val	Thr	Glu	Gly	Ala	Thr	Glu	Leu	His	Ser	Arg	
			20					25				30			
Trp	Gly	Val	Lys	Pro	Tyr	Pro	Pro	Lys	Thr	Ala	Val	Thr	Gly	Val	Ala
			35					40				45			
Asn	Leu	Tyr	Arg	Asp	Arg	Leu	Lys	Ala	Thr	Ala	Thr	Gln	Gly	Thr	Glu
			50				55				60				
Met	Val	Lys	Gln	Ala	Cys	Pro	Lys	Ala	Ser	Leu	Leu	Asn	Pro	Asp	Leu
					70				75					80	
Glu	Gly	Gln	Glu	Thr	Ser	His	Leu	Arg	Met	Leu					
			85						90						

<210> 2269

<211> 507

<212> DNA

<213> Homo sapiens

<400> 2269

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 120
 gacaaacgctc tgcttgacaa atacggagcc ccgaccgccg aggcctatgt ggagtcggca
 180
 ctgtgggagg ccagcctctt tgagcaatac ggattccggg atttcaaaat ctcggtgaag
 240
 caccacgacc cggctgtcat gatccgtgcc tatgaacagc tcgcccgaat atcgagattat
 300
 ccccttcatt tgggcgttac tgaggctggg ccggccttcc aaggcaccat caagtggcg
 360
 gtggccttcg ggcattctct tgccgagggg atcggcgata ccatacgctg ctctctgtcg
 420

gctgatccgg tcgaggaagt caaggtgggt atcaagatcc tggagtcgct caacctacgt
 480
 cctcgaggtc tagagatcgt ctctctgc
 507

<210> 2270
 <211> 169
 <212> PRT
 <213> Homo sapiens

<400> 2270
 Leu Ser Asp Arg Val Asn Pro Gly Asn Ile Arg Lys Phe Asp Asp Gln
 1 5 10 15
 Ile Glu Ser Ile Cys Lys Ala Ala Thr Glu His Gly Thr Ser Ile Arg
 20 25 30
 Ile Gly Val Asn Ala Gly Ser Leu Asp Lys Arg Leu Leu Asp Lys Tyr
 35 40 45
 Gly Ala Pro Thr Ala Glu Ala Met Val Glu Ser Ala Leu Trp Glu Ala
 50 55 60
 Ser Leu Phe Glu Gln Tyr Gly Phe Arg Asp Phe Lys Ile Ser Val Lys
 65 70 75 80
 His His Asp Pro Val Val Met Ile Arg Ala Tyr Glu Gln Leu Ala Ala
 85 90 95
 Lys Cys Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Ala
 100 105 110
 Phe Gln Gly Thr Ile Lys Ser Ala Val Ala Phe Gly His Leu Leu Ala
 115 120 125
 Glu Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
 130 135 140
 Glu Glu Val Lys Val Gly Ile Lys Ile Leu Glu Ser Leu Asn Leu Arg
 145 150 155 160
 Pro Arg Gly Leu Glu Ile Val Ser Cys
 165

<210> 2271
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 2271
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 60
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 120
 gaaggcatgg cgccgttgac ctccgacgcg gtggcgcggt tggccactta cagcgcacgg
 180
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 240
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 300
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 360
 atgctcgctg gggctcatct gatcgacacc gccggtgcgg ccgtggggcaa atgcaacggg
 420

ctgacggtgc tgggaagtcg cgattcggcg ttcggcgtgc cggcgcgat ttcgccacg
 480
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 540
 atccactcca agggcgtgat gatccttacc ggt
 573

<210> 2272

<211> 191

<212> PRT

<213> Homo sapiens

<400> 2272

Xaa	Ala	Asp	Pro	Asp	Phe	Gln	Glu	Met	Leu	Arg	Ala	Leu	Val	Asp	Phe
1				5					10					15	
Asp	Glu	Asp	Ile	Pro	Met	Val	Asp	Glu	Ser	Leu	Glu	Gln	Phe	Ala	Gln
			20					25					30		
Leu	Leu	Lys	Thr	Arg	Thr	Ser	Glu	Gly	Met	Ala	Pro	Leu	Thr	Ser	
		35					40				45				
Asp	Ala	Val	Ala	Arg	Leu	Ala	Thr	Tyr	Ser	Ala	Arg	Leu	Ala	Asp	His
		50				55					60				
Gln	Gly	Arg	Val	Ser	Ala	Arg	Ile	Gly	Asp	Leu	Phe	Gln	Leu	Val	Ser
65					70				75					80	
Glu	Ala	Asp	Phe	Ile	Arg	His	Leu	Ala	Gly	Asp	Glu	Met	Thr	Asp	Ala
			85						90					95	
Gly	His	Ile	Glu	Arg	Ala	Leu	Lys	Ala	Lys	Ala	Thr	Arg	Thr	Gly	Arg
			100					105					110		
Val	Ser	Ala	Arg	Ile	Leu	Asp	Asp	Met	Leu	Ala	Gly	Val	Ile	Leu	Ile
			115				120					125			
Asp	Thr	Ala	Gly	Ala	Ala	Val	Gly	Lys	Cys	Asn	Gly	Leu	Thr	Val	Leu
			130			135					140				
Glu	Val	Gly	Asp	Ser	Ala	Phe	Gly	Val	Pro	Ala	Arg	Ile	Ser	Ala	Thr
145					150					155				160	
Val	Tyr	Pro	Gly	Gly	Ser	Gly	Ile	Val	Asp	Ile	Glu	Arg	Glu	Val	Asn
				165					170					175	
Leu	Gly	Gln	Pro	Ile	His	Ser	Lys	Gly	Val	Met	Ile	Leu	Thr	Gly	
			180					185					190		

<210> 2273

<211> 4355

<212> DNA

<213> Homo sapiens

<400> 2273

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 120
 gagaggagg aggaagtgat cacctgtttt gagaggcct cctggatcgc tcaggtgttc
 180
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 300

aacctgaaga aggggaacat cgtgaagggc atgagagagc tccgggaggt gctgcggact
360
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420
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660
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780
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960
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<210> 2274

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2274

Ser Phe Gln His Ala Ser Gly Phe Leu Gly Glu His Ser Pro Gly Gly
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 Gln Arg Ser Cys Arg Gly Gly Leu Ser Leu Glu Arg Leu Pro Asn Ser
 20 25 30
 Ile Ala Ser Arg Phe Arg Leu Thr Glu Arg Glu Glu Glu Val Ile Thr
 35 40 45
 Cys Phe Glu Arg Ala Ser Trp Ile Ala Gln Val Phe Leu Gln Glu Leu
 50 55 60
 Glu Lys Thr Thr Asn Asn Ser Thr Ser Arg His Leu Lys Gly Cys His
 65 70 75 80
 Pro Leu Asp Tyr Glu Leu Thr Tyr Phe Leu Glu Ala Ala Leu Gln Ser
 85 90 95
 Ala Tyr Val Lys Asn Leu Lys Lys Gly Asn Ile Val Lys Gly Met Arg
 100 105 110
 Glu Leu Arg Glu Val Leu Arg Thr Val Glu Thr Lys Ala Thr Gln Asn
 115 120 125
 Phe Lys Val Met Ala Ala Lys His Leu Ala Gly Val Leu Leu His Ser
 130 135 140
 Leu Ser Gly Val Leu Leu Glu Pro Pro Val Pro Pro Ser Ala

145

150

155

<210> 2275

<211> 608

<212> DNA

<213> Homo sapiens

<400> 2275

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 120
 aaggagaaca ggagacctca aaaggaagaa ccagggtgtg cccaacctt ttttccaaac
 180
 caaagtcttg gtttacttac acccactgct atgacacctc ctgttctaac cacagccgaa
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 300
 atttcaagca caatcagttt tcattcaaga actcttaatc tgacagatgt gattgaagaa
 360
 ctagcccaag caagtactca gactttgaag agcacaattg cttctgaaac aactttgtcc
 420
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 480
 ccattcttga gcagcagtg c tactctaata ccagttccca tctccctccc ctttactcag
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 608

<210> 2276

<211> 167

<212> PRT

<213> Homo sapiens

<400> 2276

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Gly	Cys	Ala	Pro	Thr	Phe	Phe	Pro	Asn	Gln	Ser	Ser	Gly	Phe	Thr	Thr
			20					25					30		
Pro	Thr	Ala	Met	Thr	Pro	Pro	Val	Leu	Thr	Thr	Ala	Glu	Thr	Ser	Val
			35				40					45			
Lys	Pro	Ser	Val	Ser	Ala	Phe	Thr	His	Ser	Pro	Pro	Glu	Asn	Thr	Thr
			50			55				60					
Gly	Ile	Ser	Ser	Thr	Ile	Ser	Phe	His	Ser	Arg	Thr	Leu	Asn	Leu	Thr
			65			70			75					80	
Asp	Val	Ile	Glu	Glu	Leu	Ala	Gln	Ala	Ser	Thr	Gln	Thr	Leu	Lys	Ser
			85					90						95	
Thr	Ile	Ala	Ser	Glu	Thr	Thr	Leu	Ser	Ser	Lys	Ser	His	Gln	Ser	Thr
			100				105						110		
Thr	Thr	Arg	Lys	Ala	Ile	Ile	Arg	His	Ser	Thr	Ile	Pro	Pro	Phe	Leu
			115				120					125			
Ser	Ser	Ser	Ala	Thr	Leu	Ile	Pro	Val	Pro	Ile	Ser	Pro	Pro	Phe	Thr

```

      130              135              140
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Thr Asn Thr Val Val Lys Leu
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<210> 2277
<211> 640
<212> DNA
<213> Homo sapiens

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540
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640

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<210> 2278
<211> 95
<212> PRT
<213> Homo sapiens

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<400> 2278
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Gly Arg Ser Ser Pro Gly Thr Ala Gln Pro Gly Pro Xaa Thr Lys Ser
20      25      30
Cys Cys Pro Pro Trp Leu Ser Ser Pro Pro Ala Ala Cys Leu Pro Ser
35      40      45
Ser Leu Leu Ser Pro Tyr Pro Val Leu Pro Ser Pro Ser Cys Lys Val
50      55      60
His Ala Thr Pro Gln Glu Glu Pro Gln Arg Leu Ser Ser Asp Pro Thr
65      70      75      80
Leu Ser Ala Pro Thr Leu Pro Pro His Gln Ile Leu Ser Thr Pro
85      90      95

```

<210> 2279

<211> 331

<212> DNA

<213> Homo sapiens

<400> 2279

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```

<210> 2280

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2280

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Met Ile Val Arg Leu Trp Ala Thr Val His Lys Asp Gly Pro Cys Leu
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Arg Val Arg Arg Thr Leu Pro Asp Gln Gly Asp Ala Gln Gly Pro Arg
20        25        30
Glu Cys Met Glu Ser Glu Gly Thr Gly Pro Thr His Ser Pro Ser Ser
35        40        45
Pro Ala Val Leu Phe Ser Phe Leu His Cys Ala Phe Val Ser Phe Leu
50        55        60
Gly Thr Ser Phe Thr Pro Ala Cys Ile Ser Ser Leu Ser His Gly Ser
65        70        75        80
Pro Leu Ser Trp Ser Ser Gly Ala Val Pro Ile
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```

<210> 2281

<211> 409

<212> DNA

<213> Homo sapiens

<400> 2281

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180
gataatgaag ccaggctctg aatgggatgg ctctacccca agtgaggact ccgagggtac
240
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300

```

gcctgacttg tggatagatg ctaagaagcc cttcagtttg aaagcagatg gtgagaatcc
 360
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 409

<210> 2282
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 2282
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 20 25 30
 Pro Ser Glu Asp Ser Arg Gly Thr Phe Val Pro Asp Ile Leu His Gly
 35 40 45
 Asn Phe Gln Glu Gly Gly Gln Leu Ala Ser Ala Ala Pro Asp Leu Trp
 50 55 60
 Ile Asp Ala Lys Lys Pro Phe Ser Leu Lys Ala Asp Gly Glu Asn Pro
 65 70 75 80
 Asp Ile Leu Thr His Cys Glu His Asp Tyr Gly Glu Thr Thr Thr Arg
 85 90 95

<210> 2283
 <211> 404
 <212> DNA
 <213> Homo sapiens

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 120
 ccgacaattt ctagttaaatt ccgacgaaag ttatttgtaa aatactctgc aacctctttt
 180
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 240
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 300
 cgacttccag ctaaagcgca ggcgtcccat gccacttcct ctccgaagat gcgtaaagtt
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 404

<210> 2284
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 2284
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 1 5 10 15
 His Leu Leu Val Val Phe Phe Leu Val Gly Ala Val Pro Thr Ile Ser

				20						25						30	
Ser	Lys	Phe	Arg	Arg	Lys	Phe	Ile	Val	Lys	Tyr	Ser	Ala	Thr	Ser	Phe		
				35						40						45	
Leu	Leu	Cys	His	Leu	Gly	Gly	Gly	Cys	Asn	Phe	Pro	His	His	Cys	Arg		
				50						55						60	
Val	Leu	Arg	Asn	Arg	Leu	Gln	Pro	Cys	His	Arg	Ser	Ser	Gln	Leu	His		
				65						70						75	
Gln	Ala	Phe	Gly	Arg	Ala	Val	Ile	Arg	Leu	Pro	Ala	Lys	Ala	Gln	Ala		
				85						90						95	
Ser	His	Ala	Thr	Ser	Ser	Pro	Lys	Met	Arg	Lys	Val	Arg	Thr	Arg	Lys		
				100						105						110	
Gln	Gly	Ala	Val	Glu	Arg	Ser	Ser	Ala	Pro								
				115						120							

<210> 2285

<211> 6505

<212> DNA

<213> Homo sapiens

<400> 2285

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<210> 2286

<211> 1784

<212> PRT

<213> Homo sapiens

<400> 2286

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 35 40 45
 Ile Val His Pro Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr
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 Glu Leu Trp Pro Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg
 65 70 75 80
 Asp Ala Pro Ala Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg
 85 90 95
 Phe Asn Leu Thr Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser
 100 105 110
 Glu Thr Arg Arg Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His
 115 120 125
 Thr Pro Ala Cys His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu
 130 135 140
 Gly Gly Leu Ala Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe
 145 150 155 160
 Gln Leu Ser Asn Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro
 165 170 175
 Ala Arg Pro Gly His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala
 180 185 190
 Pro Glu Arg Leu Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys

1677

625 630 635 640
 Glu Tyr Phe Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro
 645 650 655
 Cys Tyr Gln Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys
 660 665 670
 Lys Asn Val Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp
 675 680 685
 Arg Cys Gly Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser
 690 695 700
 Gly Thr Phe Xaa Arg Arg Pro Arg Val Xaa Gly Tyr Val Asp Val Gly
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 Ala Ala Asn Phe Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe
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 Leu Asn Gly Gly Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala
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 Gly Thr Thr Phe Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr
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 785 790 795 800
 Arg Gly Pro Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr
 805 810 815
 Leu His Gly Arg Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr
 820 825 830
 Glu Pro Gly Ser Glu Pro Gly Pro Pro Ala Ala Ser Thr Ser Val
 835 840 845
 Ser Pro Ser Leu Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly
 850 855 860
 Gly Trp Gly Gln Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu
 865 870 875 880
 Val Leu Met Gly Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser
 885 890 895
 Asn Pro Gly Val His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly
 900 905 910
 His Asp Glu Val Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp
 915 920 925
 Thr Lys Cys Thr Val Thr Cys Gly Arg Gly Val Gln Arg Gln Asn Val
 930 935 940
 Tyr Cys Leu Glu Arg Gln Ala Gly Pro Val Asp Glu Glu His Cys Asp
 945 950 955 960
 Pro Leu Gly Arg Pro Asp Asp Gln Gln Arg Lys Cys Ser Glu Gln Pro
 965 970 975
 Cys Pro Ala Arg Trp Trp Ala Gly Glu Trp Gln Leu Cys Ser Ser Ser
 980 985 990
 Cys Gly Pro Gly Gly Leu Ser Arg Arg Ala Val Leu Cys Ile Arg Ser
 995 1000 1005
 Val Gly Leu Asp Glu Gln Ser Ala Leu Glu Pro Pro Ala Cys Glu His
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 Leu Pro Arg Pro Pro Thr Glu Thr Pro Cys Asn Arg His Val Pro Cys
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 1090 1095 1100
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 Pro His His Leu Ala Pro Arg Pro Ser Pro Ala Ser Ser Pro Lys Pro
 1125 1130 1135
 Gly Thr Met Gly Asn Ala Ile Glu Glu Glu Ala Pro Glu Leu Asp Leu
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 Pro Gly Pro Val Phe Val Asp Asp Phe Tyr Tyr Asp Tyr Asn Phe Ile
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 Asp Leu Ala Gly Thr Gly Asp Arg Thr Pro Pro His Ser His Pro
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 Ala Lys Glu Glu Gly Val Leu Gly Pro Trp Ser Pro Ser Pro Trp Pro
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 Ser Gln Ala Gly Arg Ser Pro Pro Pro Ser Glu Gln Thr Pro Gly
 1235 1240 1245
 Asn Pro Leu Ile Asn Phe Leu Pro Glu Glu Asp Thr Pro Ile Gly Ala
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 Pro Asp Leu Gly Leu Pro Ser Leu Ser Trp Pro Arg Val Ser Thr Asp
 1265 1270 1275 1280
 Gly Leu Gln Thr Pro Ala Thr Pro Glu Ser Gln Asn Asp Phe Pro Val
 1285 1290 1295
 Gly Lys Asp Ser Gln Ser Gln Leu Pro Pro Pro Trp Arg Asp Arg Thr
 1300 1305 1310
 Asn Glu Val Phe Lys Asp Asp Glu Glu Pro Lys Gly Arg Gly Ala Pro
 1315 1320 1325
 His Leu Pro Pro Arg Pro Ser Ser Thr Leu Pro Pro Leu Ser Pro Val
 1330 1335 1340
 Gly Ser Thr His Ser Ser Pro Ser Pro Asp Val Ala Glu Leu Trp Thr
 1345 1350 1355 1360
 Gly Gly Thr Val Ala Trp Glu Pro Ala Leu Glu Gly Gly Leu Gly Pro
 1365 1370 1375
 Val Asp Ser Glu Leu Trp Pro Thr Val Gly Val Ala Ser Leu Leu Pro
 1380 1385 1390
 Pro Pro Ile Ala Pro Leu Pro Glu Met Lys Val Arg Asp Ser Ser Leu
 1395 1400 1405
 Glu Pro Gly Thr Pro Ser Phe Pro Ala Pro Gly Pro Gly Ser Trp Asp
 1410 1415 1420
 Leu Gln Thr Val Ala Val Trp Gly Thr Phe Leu Pro Thr Thr Leu Thr
 1425 1430 1435 1440
 Gly Leu Gly His Met Pro Glu Pro Ala Leu Asn Pro Gly Pro Lys Gly
 1445 1450 1455
 Gln Pro Glu Ser Leu Ser Pro Glu Val Pro Leu Ser Ser Arg Leu Leu
 1460 1465 1470
 Ser Thr Pro Ala Trp Asp Ser Pro Ala Asn Ser His Arg Val Pro Glu
 1475 1480 1485
 Thr Gln Pro Leu Ala Pro Ser Leu Ala Glu Ala Gly Pro Pro Ala Asp

1490 1495 1500
 Pro Leu Val Val Arg Asn Ala Ser Trp Gln Ala Gly Asn Trp Ser Glu
 1505 1510 1515 1520
 Cys Ser Thr Thr Cys Gly Leu Gly Ala Val Trp Arg Pro Val Arg Cys
 1525 1530 1535
 Ser Ser Gly Arg Asp Glu Asp Cys Ala Pro Ala Gly Arg Pro Gln Pro
 1540 1545 1550
 Ala Arg Arg Cys His Leu Arg Pro Cys Ala Thr Trp His Ser Gly Asn
 1555 1560 1565
 Trp Ser Lys Cys Ser Arg Ser Cys Gly Gly Ser Ser Val Arg Asp
 1570 1575 1580
 Val Gln Cys Val Asp Thr Arg Asp Leu Arg Pro Leu Arg Pro Phe His
 1585 1590 1595 1600
 Cys Gln Pro Gly Pro Ala Lys Pro Pro Ala His Arg Pro Cys Gly Ala
 1605 1610 1615
 Gln Pro Cys Leu Ser Trp Tyr Thr Ser Ser Trp Arg Glu Cys Ser Glu
 1620 1625 1630
 Ala Cys Gly Gly Gly Glu Gln Arg Leu Val Thr Cys Pro Glu Pro
 1635 1640 1645
 Gly Leu Cys Glu Glu Ala Leu Arg Pro Asn Thr Thr Arg Pro Cys Asn
 1650 1655 1660
 Thr His Pro Cys Thr Gln Trp Val Val Gly Pro Trp Gly Gln Cys Ser
 1665 1670 1675 1680
 Ala Pro Cys Gly Gly Val Gln Arg Arg Leu Val Lys Cys Val Asn
 1685 1690 1695
 Thr Gln Thr Gly Leu Pro Glu Glu Asp Ser Asp Gln Cys Gly His Glu
 1700 1705 1710
 Ala Trp Pro Glu Ser Ser Arg Pro Cys Gly Thr Glu Asp Cys Glu Pro
 1715 1720 1725
 Val Glu Pro Pro Arg Cys Glu Arg Asp Arg Leu Ser Phe Gly Phe Cys
 1730 1735 1740
 Glu Thr Leu Arg Leu Leu Gly Arg Cys Gln Leu Pro Thr Ile Arg Thr
 1745 1750 1755 1760
 Gln Cys Cys Arg Ser Cys Ser Pro Pro Ser His Gly Ala Pro Ser Arg
 1765 1770 1775
 Gly His Gln Arg Val Ala Arg Arg
 1780

<210> 2287

<211> 750

<212> DNA

<213> Homo sapiens

<400> 2287

tgacacaggt tatttctctt tggtaaata tcttacaagt cttttttaaa tcttcactt
 60
 tggcctataa aagtatcatc atccccattt tacagaatgg gaaagtaagg cgtggggagg
 120
 ttgaggacat ttgtacagag tcaggttaact ggaggaactg gactacaacc ctgctcagt
 180
 cagccagtgt gactgagcgc ctctgagag ccaggtggat tctgccctca aggatccatg
 240
 ctctgggcaa gaaaccacc catcagcagg tggcttctgc tgagcccaa caggcacaca
 300

gaggggtcca tgggagccca gaggggagca tctgaccagg ctcaggggaa ggaatgtgtc
 360
 cagcagagtc acagaggagc agtatgagtt agccaggtag gggacattcc aggcagggga
 420
 gcagcaggac aaaagcatag aggttagcact gccagtgcc agttccaaaa taagagggtg
 480
 actgctacag ggtccatata ggaaaataat gggaaataca tttggacagg aggtggggtc
 540
 tgtaacaaa gactttaatt ccagggttaag gaatctggat gttaaaaaa cattagctgc
 600
 cattttaca gtgctacttc ccaggctctg tgcctttctg ggagccttga aggtttgtga
 660
 gctggaagga gatattagga acaaaacgat gcatgaggat agctcaggta aaggttattg
 720
 ataagtaaga atgcctggca ccaaacgcgt
 750

<210> 2288

<211> 142

<212> PRT

<213> Homo sapiens

<400> 2288

Met	Ala	Ala	Asn	Val	Val	Leu	Thr	Ser	Arg	Phe	Leu	Asn	Leu	Glu	Leu
1			5						10					15	
Lys	Ser	Phe	Val	Thr	Asp	Pro	Thr	Ser	Cys	Pro	Asn	Val	Phe	Pro	Ile
			20						25				30		
Ile	Phe	Leu	Tyr	Gly	Pro	Cys	Ser	Ser	Gln	Pro	Leu	Ile	Leu	Glu	Leu
		35						40				45			
Gly	Thr	Gly	Ser	Ala	Thr	Ser	Met	Leu	Leu	Ser	Cys	Cys	Ser	Pro	Ala
		50				55					60				
Trp	Asn	Val	Pro	Tyr	Leu	Ala	Asn	Ser	Tyr	Cys	Ser	Ser	Val	Thr	Leu
					70					75				80	
Leu	Asp	Thr	Phe	Leu	Pro	Leu	Ser	Leu	Val	Arg	Cys	Ser	Pro	Leu	Gly
				85					90					95	
Ser	His	Gly	Pro	Leu	Cys	Val	Pro	Val	Val	Ala	Gln	Gln	Lys	Pro	Pro
			100					105					110		
Ala	Asp	Gly	Trp	Val	Ser	Cys	Pro	Glu	His	Gly	Ser	Leu	Arg	Ala	Glu
		115				120						125			
Ser	Thr	Trp	Leu	Ser	Gly	Gly	Ala	Gln	Ser	His	Trp	Leu	His		
		130				135						140			

<210> 2289

<211> 381

<212> DNA

<213> Homo sapiens

<400> 2289

caggacgcgg cctcggcggg gcccgggccg aacggctgcg gacacctggg cgccgaggag
 60
 ccgagcgcgg ccgcctccgg catggatcat tgctgacgg tggagcgga gctggagag
 120
 gtgctgcaca agttctcggg ctacgggcag ctgtgcgagc gcggcctgga ggagctcatc
 180

gactacaccg gcggtctcaa gcaccagatc ctgcagagcc acgccaaga tgctgaatta
 240
 tcaggggacac ttctactgt ttgacacag ggctgtaaaa gaataanaag gggatactgg
 300
 ttcaaaaatt ggcctccgac cacaagaca tccacagcag tggttctcgg gttggaaaag
 360
 ccattgatga ggattcactt t
 381

<210> 2290
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 2290
 Met Asp His Cys Val Thr Val Glu Arg Glu Leu Glu Lys Val Leu His
 1 5 10 15
 Lys Phe Ser Gly Tyr Gly Gln Leu Cys Glu Arg Gly Leu Glu Glu Leu
 20 25 30
 Ile Asp Tyr Thr Gly Gly Leu Lys His Gln Ile Leu Gln Ser His Gly
 35 40 45
 Gln Asp Ala Glu Leu Ser Gly Thr Leu Ser Leu Val Leu Thr Gln Gly
 50 55 60
 Cys Lys Arg Ile Xaa Arg Gly Tyr Trp Phe Lys Asn Trp Pro Pro Thr
 65 70 75 80
 Thr Lys Thr Ser Thr Ala Val Phe Leu Gly Leu Glu Lys Pro Leu Met
 85 90 95
 Arg Ile His Phe
 100

<210> 2291
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 2291
 gcattgctcta ccgcaaaagtc ggggtccccac cgattaaaaa tgcccggggtc gaggacagcc
 60
 ttccggcagca ccgactcatt atcggcaccg acctagtcaa ttgccaccac ctgcttatgc
 120
 aagtgggtoga tagaagcccc agccggctta agccagtctc ggaaaaaccac cacatatcgc
 180
 acatgttctgt tgtgacgatg cagctgagcc attgaatoga cggtcagcgc catgaacgcc
 240
 cgatgctcgt tgacggtaag actcgcgcgac ccagcaacgt cggcggttgt cgtgccctca
 300
 tcggtgtgaat ggcgacgagc gacgatgacg tcatgtccgc cggcaaaaga ggctgcggaa
 360
 gcctcgcgta attcttgggg accgaggtcc tcggcgcgccc ggtctgaccc caccgccttg
 420
 aacttggcgt taaggaccga cctcagctga gcctccccctg acgggttaga caggtattcc
 480
 tccgtccagt cccgcgctgc ccgaggcaag ctcaccccc agttgagctg ccaataccgc
 540

cacgacagga tctcgaaaag attggggacg cgt
573

<210> 2292
<211> 140
<212> PRT
<213> Homo sapiens

<400> 2292
Met Ser Leu Pro Arg Ala Ala Arg Asp Trp Gln Glu Glu Tyr Leu Ser
1 5 10 15
Asn Pro Ser Gly Glu Ala His Val Arg Ser Val Leu Asn Ala Lys Phe
20 25 30
Lys Ala Val Gly Ser Asp Arg Arg Ala Glu Asp Leu Gly Pro Gln Glu
35 40 45
Leu Arg Glu Ala Ser Ala Ala Phe Phe Ala Gly Gly His Asp Val Ile
50 55 60
Val Ala Arg Arg His Tyr Thr Asp Glu Gly Thr Thr Thr Ala Asp Val
65 70 75 80
Ala Gly Ser Ala Ser Leu Thr Val Asn Glu His Arg Ala Phe Met Ala
85 90 95
Leu Thr Val Asp Ser Met Ala Gln Leu His Arg His Asn Glu His Val
100 105 110
Arg Tyr Val Val Val Phe Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser
115 120 125
Ile Asp His Leu His Lys Gln Val Val Ala Ile Asp
130 135 140

<210> 2293
<211> 358
<212> DNA
<213> Homo sapiens

<400> 2293
acgcgtgaag gaatggaagc tgctctcgtc ggtgcacaca agactggcgg gtgccattg
60
gtgaacactg tcgctaagaa ctggttgaac cggtcaaca cgccggatat gaaacccact
120
gaggagatca agcggcagtt ccaaggtctg cattggttgg gacgtaagta tgggctcaac
180
cacggagagt tctatcttga cgacgagcag tgggccacgc tcatggccgg gtcctctttc
240
gaggcgaaac cgcgcattaa gagcaacttt gattccgagg gcgctgttgt ggatccggat
300
tccgattcac ttgctggggc tgatcgagat gcccgaggtg ctccggatgc atgccttc
358

<210> 2294
<211> 115
<212> PRT
<213> Homo sapiens

<400> 2294
Met Glu Ala Ala Leu Val Gly Ala His Lys Thr Gly Gly Cys Pro Leu

1	5	10	15
Val Asn Thr	Val Ala Lys Asn Trp	Leu Asn Arg	Leu Asn Thr Pro Asp
	20	25	30
Met Lys Pro Thr	Glu Glu Ile Lys Arg	Gln Phe	Gln Gly Leu His Trp
	35	40	45
Leu Gly Arg Lys	Tyr Gly Leu Asn His	Gly Glu Phe	Tyr Leu Asp Asp
	50	55	60
Glu Gln Trp Ala	Thr Leu Met Ala Gly	Ser Ser Phe	Glu Ala Asn Pro
	65	70	75
Arg Ile Lys Ser	Asn Phe Asp Ser	Glu Gly Ala	Val Val Asp Pro Asp
	85	90	95
Ser Asp Ser Leu	Ala Gly Ala Asp	Arg Asp Ala	Arg Gly Ala Ser Asp
	100	105	110
Ala Cys Leu			
	115		

<210> 2295

<211> 546

<212> DNA

<213> Homo sapiens

<400> 2295

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ggcaccgatc cgagtgggtg tgccgggatt aggnccgcatc tanaaacatt ctccgccctt
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ggggcggtatg gctgctcggt cattaccgca ctggtagcgc aaaatacgcg cggcgtgcag
120
tcgggtgatc gtatcgaacc ggattttgtc ggtgcacaac tggactctgt gttcagcgat
180
gtccgcattg attccaccaa aatcggcatg ctggcagagg cggatatcgt ggaagcggtc
240
gcggagcgcc tcaaacatta tcgcgttaaa aacgtgttac ttgatacggg gatgctggcg
300
aaaagtggcg atccgctgct atctctctgt gctgtcgaaa ctctgcgaaa acaccttctg
360
ccacacgtcg cgctgatcac gccaaatttg ccggaggcgg cggcgctgct ggatgcgcct
420
catgcccgtg ccgagcacga gatgaaagag caggggscgc cacttctggc gcttggtgct
480
gaggcagtcg tgatgaaagg cggccatctt gacgatctg agagcccgga ctggctcttc
540
acgcgt
546

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<210> 2296

<211> 182

<212> PRT

<213> Homo sapiens

<400> 2296

Gly Thr Asp Pro	Ser Gly Gly Ala	Gly Ile Arg Xaa	Asp Leu Xaa Thr
1	5	10	15
Phe Ser Ala Leu	Gly Ala Tyr Gly	Cys Ser Val Ile	Thr Ala Leu Val
	20	25	30
Ala Gln Asn Thr	Arg Gly Val Gln	Ser Val Tyr Arg	Ile Glu Pro Asp

```

          35              40              45
Phe Val Gly Ala Gln Leu Asp Ser Val Phe Ser Asp Val Arg Ile Asp
 50              55              60
Ser Thr Lys Ile Gly Met Leu Ala Glu Ala Asp Ile Val Glu Ala Val
 65              70              75              80
Ala Glu Arg Leu Lys His Tyr Arg Val Lys Asn Val Val Leu Asp Thr
          85              90              95
Val Met Leu Ala Lys Ser Gly Asp Pro Leu Leu Ser Pro Ala Ala Val
          100              105              110
Glu Thr Leu Arg Lys His Leu Leu Pro His Val Ala Leu Ile Thr Pro
          115              120              125
Asn Leu Pro Glu Ala Ala Ala Leu Leu Asp Ala Pro His Ala Arg Thr
          130              135              140
Glu His Glu Met Lys Glu Gln Gly Arg Ala Leu Leu Ala Leu Gly Cys
          145              150              155              160
Glu Ala Val Leu Met Lys Gly Gly His Leu Asp Asp Pro Glu Ser Pro
          165              170              175
Asp Trp Leu Phe Thr Arg
          180

```

<210> 2297

<211> 414

<212> DNA

<213> Homo sapiens

<400> 2297

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gggaattccg ggcccttccc cccaagcccg ggtaattttt tgtattttta aaaaaaaagg
 60
gaatttttccc acgttggggg ggggggggttc ggactttttc ccccaaaaac cccccccccc
 120
caccceccca aaggccgaaa agcaggggcca aaaccccccg gacccccccc gggggggggca
 180
aaaggaaaaa cccctttttt tttttttttt tttatcac atgagggtct ctggttaata
 240
aatgttgaga tgtaggggta ggtgagatta aacaggttct tttttcatg atttctcgga
 300
gtctttatga tgctccacac cagtacttct caaagctgac tgtgtatata aaacactggg
 360
gatctgaccc acatgtaaag tctgatttct ttggtctggg gcaggcctga aatn
 414

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<210> 2298

<211> 67

<212> PRT

<213> Homo sapiens

<400> 2298

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Lys Lys Arg Glu Phe Ser His Val Gly Gly Gly Gly Phe Gly Leu Phe
 1              5              10              15
Pro Pro Lys Thr Pro Pro Pro His Pro Pro Lys Gly Arg Lys Ala Gly
          20              25              30
Pro Lys Pro Pro Gly Pro Pro Gly Gly Ala Lys Gly Lys Thr Pro
          35              40              45
Phe Phe Phe Phe Phe Phe Tyr Thr His Glu Gly Leu Trp Leu Ile Asn

```

50 55 60

Val Glu Met

65

<210> 2299

<211> 987

<212> DNA

<213> Homo sapiens

<400> 2299

ngagatgtct aagttatttt ttttttcccc gaaggcaa at ggctggcg tg gaagcacaac

60

ccgctttcac ttttcgaatt tgtgcttagc tcttttcttg tacctgcga ctctgacac

120

acatgctgtg atgtgtgccg agggaggaat tggtcagcta cacaacctgg atcttaccac

180

agttttgata tgactgaggc tctccaatgg gccagatata actggcgacg gctgatcaga

240

ggtgcaacca gggatgatga ttcagggccca tacaactatt cctcgtgtgt cgctgtggg

300

cgcaagtctc ctccagatccc taaactgtca ggaaggcacc ggattgttgt tccccacac

360

cagcccttca aggatgagta tgagaagttc tccggagcct atgtgaacaa tcgaatacga

420

acaacaaagt acacacttct gaattttgtg ccaagaaatt tatttgaaca atttcacaga

480

gctgccaatt tatatttctc gttcctagtt gtccctgaact gggtagccttt ggtagaagcc

540

ttccaaaagg aaatcaccat gttgcctctg gtgggtgtcc ttacaattat cgcaattaaa

600

gatggcctgg aagattatcg gaaatacaaa attgacaaac agatcaataa tttataaact

660

aaagtttata gtaggaaaga gaaaaaatac attgaccgat gctggaaaga cgttactgtt

720

ggggacttta ttcgcctctc ctgcaacgag gtcatccctg cagacatggt actactcttt

780

tccactgac cagatggaat ctgtcacatt gagacttctg gtcttgatgg agagagcaat

840

ttaaaacaga ggcaggtggg tcggggatat gcagaacagg actctgaagt tgatcctgag

900

aagttttcca gtaggataga atgtgaaagc ccaacaatg acctcagcag attccgaggc

960

ttcctagaac attccaacaa agaacgc

987

<210> 2300

<211> 266

<212> PRT

<213> Homo sapiens

<400> 2300

Met Thr Glu Ala Leu Gln Trp Ala Arg Tyr His Trp Arg Arg Leu Ile

1 5 10 15

Arg Gly Ala Thr Arg Asp Asp Asp Ser Gly Pro Tyr Asn Tyr Ser Ser

			20					25				30			
Leu	Leu	Ala	Cys	Gly	Arg	Lys	Ser	Ser	Gln	Ile	Pro	Lys	Leu	Ser	Gly
		35					40					45			
Arg	His	Arg	Ile	Val	Val	Pro	His	Ile	Gln	Pro	Phe	Lys	Asp	Glu	Tyr
	50					55					60				
Glu	Lys	Phe	Ser	Gly	Ala	Tyr	Val	Asn	Asn	Arg	Ile	Arg	Thr	Thr	Lys
65					70					75					80
Tyr	Thr	Leu	Leu	Asn	Phe	Val	Pro	Arg	Asn	Leu	Phe	Glu	Gln	Phe	His
				85					90					95	
Arg	Ala	Ala	Asn	Leu	Tyr	Phe	Leu	Phe	Leu	Val	Val	Leu	Asn	Trp	Val
			100					105					110		
Pro	Leu	Val	Glu	Ala	Phe	Gln	Lys	Glu	Ile	Thr	Met	Leu	Pro	Leu	Val
		115					120					125			
Val	Val	Leu	Thr	Ile	Ile	Ala	Ile	Lys	Asp	Gly	Leu	Glu	Asp	Tyr	Arg
	130					135					140				
Lys	Tyr	Lys	Ile	Asp	Lys	Gln	Ile	Asn	Asn	Leu	Ile	Thr	Lys	Val	Tyr
145					150					155					160
Ser	Arg	Lys	Glu	Lys	Lys	Tyr	Ile	Asp	Arg	Cys	Trp	Lys	Asp	Val	Thr
				165					170					175	
Val	Gly	Asp	Phe	Ile	Arg	Leu	Ser	Cys	Asn	Glu	Val	Ile	Pro	Ala	Asp
		180						185					190		
Met	Val	Leu	Leu	Phe	Ser	Thr	Asp	Pro	Asp	Gly	Ile	Cys	His	Ile	Glu
	195						200					205			
Thr	Ser	Gly	Leu	Asp	Gly	Glu	Ser	Asn	Leu	Lys	Gln	Arg	Gln	Val	Val
	210					215					220				
Arg	Gly	Tyr	Ala	Glu	Gln	Asp	Ser	Glu	Val	Asp	Pro	Glu	Lys	Phe	Ser
225					230					235					240
Ser	Arg	Ile	Glu	Cys	Glu	Ser	Pro	Asn	Asn	Asp	Leu	Ser	Arg	Phe	Arg
				245					250					255	
Gly	Phe	Leu	Glu	His	Ser	Asn	Lys	Glu	Arg						
		260						265							

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<210> 2301
<211> 390
<212> DNA
<213> Homo sapiens
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<400> 2301
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nncgccacct ctcccgcgna ttccctgaa gcctgcgata acactatgga aatcgctgag
120
nncggttgcca cgttgaattc aacacaaacg caanactaca tgcccgattt cccaccccg
180
gaggggggaga atgaggaatc ctggttcgtc aaagaagttg aacgcggttt gcactaccga
240
ttccccgagg gcattcccgga tgacgtacgc aagcaggcag attatgaagt agggattatt
300
accagatggg gattccccgg ctactctctg gtggtcgcgg attttatcaa ctgggcgaag
360
ataaacggaa ttcgagtggg ccccgggcgt
390
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<210> 2302

<211> 130

<212> PRT

<213> Homo sapiens

<400> 2302

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Tyr Pro Lys Arg Phe Lys Phe Asp Ala Asp Glu Phe Tyr Leu Lys Ser
 1           5           10           15
Ser Glu Glu Met Xaa Ala Thr Ser Ser Ala Xaa Phe Pro Glu Ala Cys
 20           25           30
Asp Asn Thr Met Glu Ile Ala Glu Xaa Val Ala Thr Leu Asn Ser Thr
 35           40           45
Gln Thr Gln Xaa Tyr Met Pro Asp Phe Pro Thr Pro Glu Gly Glu Asn
 50           55           60
Glu Glu Ser Trp Phe Val Lys Glu Val Glu Arg Gly Leu His Tyr Arg
 65           70           75           80
Phe Pro Glu Gly Ile Pro Asp Asp Val Arg Lys Gln Ala Asp Tyr Glu
 85           90           95
Val Gly Ile Ile Thr Gln Met Gly Phe Pro Gly Tyr Phe Leu Val Val
100           105           110
Ala Asp Phe Ile Asn Trp Ala Lys Asn Asn Gly Ile Arg Val Gly Pro
115           120           125
Gly Arg
130

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<210> 2303

<211> 638

<212> DNA

<213> Homo sapiens

<400> 2303

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nnggatccag gctgcccctg tgtgtctcct tcagtcttcg ttagtgcct gctgctgtct
60
gcacctgtgt ttggctacct gggcgaccga catagccgca aggctaccat gagcttcggt
120
atcttgtgtt ggtagcaggc tggecctctt agctccttca tctccccccg gtattcttgg
180
ctcttcttcc tgtccccggg catcgaggcg actggctcgg ccagctactc caccatcgcg
240
cccaccgtcc tggcgacact ctctgtgagg gaccagcgca cccgcgtgct ggctgtcttc
300
tacatcttta tccccgttgg aagtggctcg ggctacgtgc tggggctcgg tgtgacgatg
360
ctgactggga actggcgctg ggcctccga gtcatgccct gcctggaggc cgtggccttg
420
atcctgctta tcttgtgtgt tccagaccca cccgggggag ctgccgagac acagggggag
480
ggggccgtgg gaggtctcag aagcagctgg tgtgaggacg tcagatacct ggggaaaaac
540
tggagttttt tgtggtcgac cctcggagtg accgccatgg cctttgtgac tggagccctg
600
gggttctggg cccccaagtt tctgctcgag gcaacgct
638

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<210> 2304

<211> 212
 <212> PRT
 <213> Homo sapiens

<400> 2304
 Xaa Asp Pro Gly Cys Pro Cys Val Ser Pro Ser Val Phe Val Ser Cys
 1 5 10 15
 Leu Leu Leu Ser Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg His Ser
 20 25 30
 Arg Lys Ala Thr Met Ser Phe Gly Ile Leu Leu Trp Ser Gly Ala Gly
 35 40 45
 Leu Ser Ser Ser Phe Ile Ser Pro Arg Tyr Ser Trp Leu Phe Phe Leu
 50 55 60
 Ser Arg Gly Ile Glu Gly Thr Gly Ser Ala Ser Tyr Ser Thr Ile Ala
 65 70 75 80
 Pro Thr Val Leu Gly Asp Leu Phe Val Arg Asp Gln Arg Thr Arg Val
 85 90 95
 Leu Ala Val Phe Tyr Ile Phe Ile Pro Val Gly Ser Gly Leu Gly Tyr
 100 105 110
 Val Leu Gly Ser Ala Val Thr Met Leu Thr Gly Asn Trp Arg Trp Ala
 115 120 125
 Leu Arg Val Met Pro Cys Leu Glu Ala Val Ala Leu Ile Leu Leu Ile
 130 135 140
 Leu Leu Val Pro Asp Pro Pro Arg Gly Ala Ala Glu Thr Gln Gly Glu
 145 150 155 160
 Gly Ala Val Gly Gly Phe Arg Ser Ser Trp Cys Glu Asp Val Arg Tyr
 165 170 175
 Leu Gly Lys Asn Trp Ser Phe Val Trp Ser Thr Leu Gly Val Thr Ala
 180 185 190
 Met Ala Phe Val Thr Gly Ala Leu Gly Phe Trp Ala Pro Lys Phe Leu
 195 200 205
 Leu Glu Ala Arg
 210

<210> 2305
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 2305
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 60
 tcggaccagc acacttttgac cgctcgtggtc gcctcgtgac atgggggtaac gcgaacctgc
 120
 tcgctcctgt tcttgacctc ttccgtgccc ccattgacaa cgatcgggca agttcactgg
 180
 cccgcaacgc tattgggtgac gcagcactcg cagctggtct cgaccgactc gtccacacca
 240
 cggcgtcggt gcgcgacgag ggcgatgagt tggctcgtct tactcgcagc gctgctgccg
 300
 ccgcacgcaa ttccatgacg acaacgtgga gttggcgcg
 340

<210> 2306

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 2306
 Met Glu Leu Arg Ala Ala Ala Ala Leu Arg Val Thr Thr Thr Asn
 1 5 10 15
 Ser Ser Pro Ser Ser Arg Thr Asp Ala Val Val Trp Thr Ser Arg Ser
 20 25 30
 Arg Pro Ala Ala Ser Ala Ala Ser Pro Ile Ala Leu Arg Ala Ser Glu
 35 40 45
 Leu Ala Arg Ser Leu Ser Met Gly Ala Arg Lys Arg Ser Arg Thr Gly
 50 55 60
 Ala Thr Arg Phe Ala Leu Pro His Val Thr Arg Arg Pro Arg Arg Ser
 65 70 75 80
 Lys Cys Ala Gly Pro Arg Leu Gln Pro Val Pro Ser Arg Cys Asp Cys
 85 90 95
 Asp Asp Ala Gly Arg
 100

<210> 2307
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 2307
 ngcttctcag ctgaaggggg agataaagct ctacataaga tgggtccagg tgggggcaaa
 60
 gccaaaggcac tgggtggggc tggcagtgagg agcaagggct cagcaggtgg cggaagcaag
 120
 cgacgggtga gcagcgaaga cagctccctg gagccagacc tggccgagat gagcctggat
 180
 gacagcagcc tggccctggg cgcagaggcc aggaccttcg ggggattccc tgagagccct
 240
 ccacccctgtc ctctccacgg tggctcccga ggcccttcca ctttcccttc tgagccccca
 300
 gatacttatg aagaagatgg tgatgagagt ggcaatgggc ttcccaaaac caaagaggca
 360

<210> 2308
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 2308
 Xaa Phe Ser Ala Glu Gly Gly Asp Lys Ala Leu His Lys Met Gly Pro
 1 5 10 15
 Gly Gly Gly Lys Ala Lys Ala Leu Gly Gly Ala Gly Ser Gly Ser Lys
 20 25 30
 Gly Ser Ala Gly Gly Gly Ser Lys Arg Arg Leu Ser Ser Glu Asp Ser
 35 40 45
 Ser Leu Glu Pro Asp Leu Ala Glu Met Ser Leu Asp Ser Ser Leu
 50 55 60
 Ala Leu Gly Ala Glu Ala Arg Thr Phe Gly Gly Phe Pro Glu Ser Pro

```

65              70              75              80
Pro Pro Cys Pro Leu His Gly Gly Ser Arg Gly Pro Ser Thr Phe Leu
              85              90              95
Pro Glu Pro Pro Asp Thr Tyr Glu Glu Asp Gly Asp Glu Ser Gly Asn
              100              105              110
Gly Leu Pro Pro Lys Thr Lys Glu Ala
              115              120

```

<210> 2309
 <211> 395
 <212> DNA
 <213> Homo sapiens

```

<400> 2309
ggatccctac aaatggggcc ctgctctgag cacattccca tgagggtctgc ctgccctgtg
60
cactctctgc cctggggccgc ggggctctgac tgggttccca cctctctcta cccactgggg
120
tcttttcag caggcacagg gattcctcat gggggaggca gagccacccc gtctgtcttc
180
ggtgacggcc tgagctgtgc acggcctccc ctgccctcct gttctcaggc cccccagggt
240
ccatccagcc ccagcgtgtg gcgttctggc tcttccttgg agtctcctcc cagaccacgc
300
gactccactc acactgtgcc tagcggactg tgtggttgat gcagccggct cacttgagtg
360
tgttgtgtta tgcccacaac aggccttgccg tcacc
395

```

<210> 2310
 <211> 108
 <212> PRT
 <213> Homo sapiens

```

<400> 2310
Met Gly Pro Cys Ser Glu His Ile Pro Met Arg Ala Ala Cys Pro Val
1      5      10      15
His Ser Leu Pro Trp Ala Ala Gly Pro Asp Trp Val Pro Thr Ser Ser
20      25      30
Tyr Pro Leu Gly Ser Phe Pro Ala Gly Thr Gly Ile Pro His Gly Gly
35      40      45
Gly Arg Ala His Pro Ser Val Leu Gly Asp Gly Leu Ser Cys Ala Arg
50      55      60
Pro Pro Leu Pro Ser Cys Ser Gln Ala Pro Gln Gly Pro Ser Ser Pro
65      70      75      80
Ser Val Trp Arg Ser Gly Ser Ser Leu Glu Ser Pro Pro Arg Pro Arg
85      90      95
Asp Ser Thr His Thr Val Pro Ser Gly Leu Cys Gly
100      105

```

<210> 2311
 <211> 378
 <212> DNA
 <213> Homo sapiens

```

<400> 2311
gtgcacgccc agatgctgcc gcaagacaag cagcgtgtcg tcggcgagtt gaagcgccag
60
ggcttctcag tgatcaaggt cggcgatggc atcaatgatt gcgacgctct cgccgcggcg
120
gatgtcggca gtcccatggg cggcagcgcg gacgtggctc tcgaaacggc cgatgctgcc
180
gtccttcacg gacgggtggg ggacgtcttc gcgatgatcg ccctatcgaa gcgaaccatg
240
gccaacattc gacagaacat cgcgatcgcg atcgggctaa aggcggtgtt ccttgaacg
300
accgtcgctg gcatacggg gctttggcct gcaatcctcg ccgatacggg gaccacggag
360
cttgtgacca tgaacgcg
378

```

```

<210> 2312
<211> 126
<212> PRT
<213> Homo sapiens

```

```

<400> 2312
Val His Ala Glu Met Leu Pro Gln Asp Lys Gln Arg Val Val Gly Glu
1      5      10      15
Leu Lys Arg Gln Gly Phe Ser Val Ile Lys Val Gly Asp Gly Ile Asn
20     25     30
Asp Cys Asp Ala Leu Ala Ala Ala Asp Val Gly Ser Pro Met Gly Gly
35     40     45
Ser Ala Asp Val Ala Leu Glu Thr Ala Asp Ala Ala Val Leu His Gly
50     55     60
Arg Val Gly Asp Val Phe Ala Met Ile Ala Leu Ser Lys Arg Thr Met
65     70     75     80
Ala Asn Ile Arg Gln Asn Ile Ala Ile Ala Ile Gly Leu Lys Ala Val
85     90     95
Phe Leu Val Thr Thr Val Val Gly Ile Thr Gly Leu Trp Pro Ala Ile
100    105    110
Leu Ala Asp Thr Gly Thr Thr Glu Leu Val Thr Met Asn Ala
115    120    125

```

```

<210> 2313
<211> 669
<212> DNA
<213> Homo sapiens

```

```

<400> 2313
ctagtcgcat ggtctcgctg gtctttagtg gagcataccg acacatcggt gactcaaagc
60
atccgaatca tggtctgtcc tggttggcct ggaaccatta acgtacgcct caccatcgcc
120
ttaagcgacg ccggtctagc tgtcgaagtc accgcgcgca atgtcggtag gacagcgggg
180
ccgcttgatg acgcagcaca cccctatctc tgtctgggtg gcaccatcga cgactggaga
240

```

gtcgacgccc cgtttacctc gtggttacag gtcgatgac ggctgctacc aatgcagatg
 300
 cgcgagatgg acagcatcca cgcgctgaac ggtctcacgg gcggacagcg caccttcgat
 360
 accgcttaca ccgtagaagg aggcggaac cgtcggatcg cccgcattggc gtatccgggt
 420
 ctcaacgggtg aaacgagcca cgaattgtgg ggcgacgccc cgatgagctg ggtgcaagtc
 480
 tacactccag acgaccgcca cagtctggcc atcgagccaa tgacctgcgg cccagatgca
 540
 tttaatgagg gcccgaccca cggtagcgtc attcgactgg agcccggtaa tgacgtcaca
 600
 ctgcactggg gcacgccta acccgcgga gctcgaaagg acaaggacgg gaaggcagga
 660
 ttcacgcgt
 669

<210> 2314

<211> 206

<212> PRT

<213> Homo sapiens

<400> 2314

Leu Val Ala Trp Ser Arg Trp Ser Leu Val Glu His Thr Asp Thr Ser
 1 5 10 15
 Val Thr Gln Thr Ile Arg Ile Met Ala Arg Pro Gly Trp Pro Gly Thr
 20 25 30
 Ile Asn Val Arg Leu Thr His Arg Leu Ser Asp Ala Gly Leu Ala Val
 35 40 45
 Glu Val Thr Ala Arg Asn Val Gly Thr Thr Ala Gly Pro Leu Gly Tyr
 50 55 60
 Ala Ala His Pro Tyr Leu Cys Leu Gly Gly Thr Ile Asp Asp Trp Thr
 65 70 75 80
 Val Asp Ala Pro Phe Thr Ser Trp Leu Gln Val Asp Asp Arg Leu Leu
 85 90 95
 Pro Met Gln Met Arg Glu Met Asp Ser Ile His Ala Leu Asn Gly Leu
 100 105 110
 Thr Gly Gly Gln Arg Thr Phe Asp Thr Ala Tyr Thr Val Lys Gly Gly
 115 120 125
 Arg Asn Arg Arg Ile Ala Arg Met Ala Tyr Pro Gly Leu Asn Gly Glu
 130 135 140
 Thr Ser His Glu Leu Trp Gly Asp Ala Ala Met Ser Trp Val Gln Val
 145 150 155 160
 Tyr Thr Pro Asp Asp Arg His Ser Leu Ala Ile Glu Pro Met Thr Cys
 165 170 175
 Gly Pro Asp Ala Phe Asn Glu Gly Pro Thr His Gly Asp Val Ile Arg
 180 185 190
 Leu Glu Pro Gly Asn Asp Val Thr Leu His Trp Gly Ile Ala
 195 200 205

<210> 2315

<211> 546

<212> DNA

<213> Homo sapiens

<400> 2315
 nacgcgtccc tcacgatac cgagcccggg atgggaaaac ggggtgtatcg cgttgaggcc
 60
 acccaaggcc gaccaattcg catcgataag gcggtcgctt atcacacttc tcgcggcggtg
 120
 ccggtacatg aactgtttga ccgagtgcgc cgcagcttag accgagtgcg tgaacagggg
 180
 cacaacgtct actacgacga acagcgtgca tggcttgacg attactgggc aacggctgat
 240
 gttgaggtcg aggggtgcccc gaccggtatt cagcaggctg tcagggtggaa ccttttccag
 300
 attgctcagg catcagcccg tgcagatcaa cttggcattc cggcaaaggg tgtaaccggg
 360
 tcaggctatg aaggccacta cttttgggac actgagggtt atgtcatccc gatgttgacc
 420
 tacactcatc caagaatcgc tgagaatcgc ctgagattcc ggggtgaatac ctttccgcaa
 480
 gctcgacgcc gggctaagga attgtctgaa cgaggcgccc ttttcccggt gcgaacaatc
 540
 accgggt
 546

<210> 2316

<211> 182

<212> PRT

<213> Homo sapiens

<400> 2316

Xaa	Ala	Ser	Leu	Ile	Asp	Thr	Glu	Pro	Gly	Met	Gly	Lys	Arg	Val	Tyr
1			5						10					15	
Arg	Val	Glu	Ala	Thr	Gln	Gly	Arg	Pro	Ile	Arg	Ile	Asp	Lys	Ala	Val
		20					25						30		
Ala	Tyr	His	Thr	Ser	Arg	Gly	Val	Pro	Val	His	Glu	Leu	Phe	Asp	Arg
		35				40						45			
Val	Arg	Arg	Ser	Leu	Asp	Arg	Val	Arg	Glu	Gln	Gly	His	Asn	Val	Tyr
		50				55					60				
Tyr	Asp	Glu	Gln	Arg	Ala	Trp	Leu	Asp	Asp	Tyr	Trp	Ala	Thr	Ala	Asp
65				70					75					80	
Val	Glu	Val	Glu	Gly	Ala	Pro	Thr	Gly	Ile	Gln	Gln	Ala	Val	Arg	Trp
				85					90					95	
Asn	Leu	Phe	Gln	Ile	Ala	Gln	Ala	Ser	Ala	Arg	Ala	Asp	Gln	Leu	Gly
		100						105					110		
Ile	Pro	Ala	Lys	Gly	Val	Thr	Gly	Ser	Gly	Tyr	Glu	Gly	His	Tyr	Phe
		115				120						125			
Trp	Asp	Thr	Glu	Val	Tyr	Val	Ile	Pro	Met	Leu	Thr	Tyr	Thr	His	Pro
		130				135					140				
Arg	Ile	Ala	Glu	Asn	Ala	Leu	Arg	Phe	Arg	Val	Asn	Thr	Leu	Pro	Gln
145				150					155					160	
Ala	Arg	Arg	Arg	Ala	Lys	Glu	Leu	Ser	Glu	Arg	Gly	Ala	Leu	Phe	Pro
				165					170					175	
Trp	Arg	Thr	Ile	Thr	Gly										
				180											

<210> 2317

<211> 496

<212> DNA

<213> Homo sapiens

<400> 2317

gccccggggc tcgggaacgg tcaactgacct gcagcaggca atggcgggtcg cggtttaatc
 60
 aggggttctgc acggagtttt ggatagtcgg tccagtcgcc actggcaagg cgcgaccagg
 120
 cagctgctga cgctgctgtg atgccaggga gatcggagac gattcgtggg tgcattctgcc
 180
 ggggtcagttc gatcagcgcg gtcgttcgag cgcttcctga acgcagcccc tgcctggcgca
 240
 gacgtcggct gagtgggcct ggtgtgagat gcaaccccggt attcctgccca ggaaagagcc
 300
 atccctcggg tcggtgtctc gatgtgtcag cgagctcggc gatcgcattc ccgaggacct
 360
 cgggcagttc gattggctcg gctccgatgg tgagcttccc cggtcgtgat gtcacgtcga
 420
 cctgctcacg ggtgagcgcg acgatgagag tgaggtggag gccgtagagg agcacgagca
 480
 acccagcggc acgcgt
 496

<210> 2318

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2318

Met	Pro	Arg	Arg	Ser	Glu	Thr	Ile	Arg	Gly	Cys	Ile	Cys	Arg	Val	Ser
1				5					10				15		
Ser	Ile	Ser	Ala	Val	Val	Arg	Ala	Leu	Pro	Glu	Arg	Ser	Pro	Cys	Trp
			20					25					30		
Arg	Arg	Arg	Arg	Leu	Ser	Gly	Pro	Gly	Val	Arg	Cys	Asn	Pro	Gly	Phe
			35				40					45			
Leu	Pro	Gly	Lys	Ser	His	Pro	Ser	Gly	Arg	Cys	Leu	Asp	Val	Ser	Ala
			50			55				60					
Ser	Ser	Ala	Ile	Ala	Phe	Pro	Arg	Thr	Ser	Gly	Ser	Ser	Ile	Gly	Ser
65					70				75					80	
Ala	Pro	Met	Val	Ser	Phe	Pro	Gly	Arg	Asp	Val	Thr	Ser	Thr	Cys	Ser
			85					90						95	
Arg	Val	Ser	Ala	Thr	Met	Arg	Val	Arg	Trp	Arg	Pro				
			100					105							

<210> 2319

<211> 1748

<212> DNA

<213> Homo sapiens

<400> 2319

ntgatcaagt ctcgggtctct ggattataacc ttgttctctc gaacttggat ctttctctgct
 60

gaatatactc aattccaaaa ttatgtgaaa gaattgaaga aaaaacggaa gcagaaaaact
120
tttatagtga aaccagctaa tgggtgcaatg ggtcatggga ttcttttgat aagaaatggg
180
gacaaacttc catctcagga tcatttgatt gttcaagaat acattgaaaa gcctttccta
240
atggaaggtt acaagtttga cttacgaatt tatattctgg ttacatcgtg tgatccacta
300
aaaatatctt tctaccatga tgggcttctg cgaatgggta cagagaagta cattccacct
360
aatgagtcca atttgaccca gttatacatg catctgacaa actactccgt gaacaagcat
420
aatgagcatt ttgaacggga tgaaactgag aacaaaggca gcaaactgtc catcaaattg
480
tttacagaat tccttcaagc aaatcaacat gatgttgcta agttttggag tgatatttca
540
gaattggttg taaagaccct gattgtagca gaacctcatg tctctgcatgc ctatcgaatg
600
tgtagacctg gtcaacctcc aggaagcgaa agtgtctgct ttgaagtctc gggatttgat
660
atthttgttg atagaaaaact aaagccatgg cttctggaga ttaaccgagc cccaagcttt
720
ggaactgac agaaaaataga ctatgatgta aaaaggggag tgctgctaaa tgcgttgaa
780
ctactaaaca taaggaccag tgacaaaaga agaaacttgg ccaacaaaaa agctgagggt
840
caaaggaggc tctatggtca aaattcaatt aaaaggctct taccaggctc ctcagactgg
900
gaacagcaga gacaccagtt ggagaggcgg aaagaagagt tgaaagagag actcgctcaa
960
gtacgaaagc agatctcacg agaagaacat gaaaatcgac atatggggaa ttatagacga
1020
atthtacctc ctgaagataa agcattactt gaaaagtatg aaaatttgtt agctgttgcc
1080
tttcagacct tcctttcagg aagagcagct tcattccagc gagagttgaa taatcctttg
1140
aaaaggatga aggaagaaga tattttggat cttctggagc aatgtgaaat tgatgatgaa
1200
aagttgatgg gaaaaactac caagactcga ggaccaaagc ctctgtgttc tatgcctgag
1260
agtactgaga taatgaaaag accaaagtac tgcagcagtg acagcagtta tgatagtagc
1320
agcagctctt cagaatctga cgaaaatgaa aaagaagagt accaaaaataa gaaaagagaa
1380
aagcaagtta catataatct taaaccctcc aacctacta aattaattca acaaccagc
1440
tccataagac gttcagtcag ctgccctcgg tccatctctg ctcaatcacc ttccagtggg
1500
gacaccgcc cattttctgc tcaacaaatg atatctgtgt cacggccaac ttctgcatct
1560
cgggtcacatt ccttaaaacc gggccttcct cctacatgag gcatctgcct cacagtaatg
1620
atgctgctc taccaactct caagtgaagt agtctttgag gcaactgaaa acaaaagaac
1680

aagaagatga tctaacaagt cagaccttat ttgttctcaa agacatgaag atccgggtttc
 1740
 caggaaag
 1748

<210> 2320

<211> 532

<212> PRT

<213> Homo sapiens

<400> 2320

Xaa	Ile	Lys	Ser	Arg	Ser	Leu	Asp	Tyr	Thr	Phe	Val	Pro	Arg	Thr	Trp
1			5						10					15	
Ile	Phe	Pro	Ala	Glu	Tyr	Thr	Gln	Phe	Gln	Asn	Tyr	Val	Lys	Glu	Leu
			20				25						30		
Lys	Lys	Lys	Arg	Lys	Gln	Lys	Thr	Phe	Ile	Val	Lys	Pro	Ala	Asn	Gly
		35					40					45			
Ala	Met	Gly	His	Gly	Ile	Ser	Leu	Ile	Arg	Asn	Gly	Asp	Lys	Leu	Pro
	50					55					60				
Ser	Gln	Asp	His	Leu	Ile	Val	Gln	Glu	Tyr	Ile	Glu	Lys	Pro	Phe	Leu
	65			70						75				80	
Met	Glu	Gly	Tyr	Lys	Phe	Asp	Leu	Arg	Ile	Tyr	Ile	Leu	Val	Thr	Ser
				85					90					95	
Cys	Asp	Pro	Leu	Lys	Ile	Phe	Leu	Tyr	His	Asp	Gly	Leu	Val	Arg	Met
		100						105					110		
Gly	Thr	Glu	Lys	Tyr	Ile	Pro	Pro	Asn	Glu	Ser	Asn	Leu	Thr	Gln	Leu
		115					120					125			
Tyr	Met	His	Leu	Thr	Asn	Tyr	Ser	Val	Asn	Lys	His	Asn	Glu	His	Phe
	130					135					140				
Glu	Arg	Asp	Glu	Thr	Glu	Asn	Lys	Gly	Ser	Lys	Arg	Ser	Ile	Lys	Trp
	145				150					155				160	
Phe	Thr	Glu	Phe	Leu	Gln	Ala	Asn	Gln	His	Asp	Val	Ala	Lys	Phe	Trp
			165						170					175	
Ser	Asp	Ile	Ser	Glu	Leu	Val	Val	Lys	Thr	Leu	Ile	Val	Ala	Glu	Pro
		180						185					190		
His	Val	Leu	His	Ala	Tyr	Arg	Met	Cys	Arg	Pro	Gly	Gln	Pro	Pro	Gly
		195					200					205			
Ser	Glu	Ser	Val	Cys	Phe	Glu	Val	Leu	Gly	Phe	Asp	Ile	Leu	Leu	Asp
	210				215					220					
Arg	Lys	Leu	Lys	Pro	Trp	Leu	Leu	Glu	Ile	Asn	Arg	Ala	Pro	Ser	Phe
	225				230					235				240	
Gly	Thr	Asp	Gln	Lys	Ile	Asp	Tyr	Asp	Val	Lys	Arg	Gly	Val	Leu	Leu
			245						250					255	
Asn	Ala	Leu	Lys	Leu	Leu	Asn	Ile	Arg	Thr	Ser	Asp	Lys	Arg	Arg	Asn
		260					265						270		
Leu	Ala	Lys	Gln	Lys	Ala	Glu	Ala	Gln	Arg	Arg	Leu	Tyr	Gly	Gln	Asn
	275					280						285			
Ser	Ile	Lys	Arg	Leu	Leu	Pro	Gly	Ser	Ser	Asp	Trp	Glu	Gln	Gln	Arg
	290					295				300					
His	Gln	Leu	Glu	Arg	Arg	Lys	Glu	Glu	Leu	Lys	Glu	Arg	Leu	Ala	Gln
	305				310					315				320	
Val	Arg	Lys	Gln	Ile	Ser	Arg	Glu	Glu	His	Glu	Asn	Arg	His	Met	Gly
			325						330					335	
Asn	Tyr	Arg	Arg	Ile	Tyr	Pro	Pro	Glu	Asp	Lys	Ala	Leu	Leu	Glu	Lys

```

          340              345              350
Tyr Glu Asn Leu Leu Ala Val Ala Phe Gln Thr Phe Leu Ser Gly Arg
      355              360              365
Ala Ala Ser Phe Gln Arg Glu Leu Asn Asn Pro Leu Lys Arg Met Lys
      370              375              380
Glu Glu Asp Ile Leu Asp Leu Leu Glu Gln Cys Glu Ile Asp Asp Glu
      385              390              395              400
Lys Leu Met Gly Lys Thr Thr Lys Thr Arg Gly Pro Lys Pro Leu Cys
      405              410              415
Ser Met Pro Glu Ser Thr Glu Ile Met Lys Arg Pro Lys Tyr Cys Ser
      420              425              430
Ser Asp Ser Ser Tyr Asp Ser Ser Ser Ser Ser Ser Glu Ser Asp Glu
      435              440              445
Asn Glu Lys Glu Glu Tyr Gln Asn Lys Lys Arg Glu Lys Gln Val Thr
      450              455              460
Tyr Asn Leu Lys Pro Ser Asn His Tyr Lys Leu Ile Gln Gln Pro Ser
      465              470              475              480
Ser Ile Arg Arg Ser Val Ser Cys Pro Arg Ser Ile Ser Ala Gln Ser
      485              490              495
Pro Ser Ser Gly Asp Thr Arg Pro Phe Ser Ala Gln Gln Met Ile Ser
      500              505              510
Val Ser Arg Pro Thr Ser Ala Ser Arg Ser His Ser Leu Asn Pro Gly
      515              520              525
Leu Pro Pro Thr
      530

```

<210> 2321

<211> 433

<212> DNA

<213> Homo sapiens

<400> 2321

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caattgtgtg gacgtgtcta tgtgtgtttc taattctata ctatcttgaa aatgggtcag
60
cgttctagaa atacagccac ataatttttt ttgttttgaa aaactgtcga gcaaatgcac
120
acaggtcata atggcaggta acagaccatt tattgaagtg ctgaaacaaa tagaaaaaaa
180
agtccaggac accatcacag agcagtactt ccctgtgtgag atactctcag ctaagtaaga
240
attgagtgtg acaacaataa aacaaatacc catagggttt tcaaacagta acaaccgcgt
300
cagggttagc agcattttcta gaccttgatg gttaaagtat gttctcaacc tttgctttca
360
gacactggat cactgcttaa gtagecctta tcttttcccc ctaatttttg ttgaagatgc
420
cagaggtgga gtg
433

```

<210> 2322

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2322

```

Met Leu Leu Thr      Leu Ser Gly Leu Leu Leu Phe Glu Lys Pro Met Gly
 1              5              10              15
Ile Cys Phe Ile Val Val Ser Leu Asn Ser Tyr Leu Ala Glu Ser Ile
              20              25              30
Ser Gln Gly Lys Tyr Cys Ser Val Met Val Ser Trp Thr Leu Phe Ser
              35              40              45
Ile Cys Phe Ser Thr Ser Ile Asn Gly Leu Leu Pro Ala Ile Met Thr
              50              55              60
Cys Met His Leu Leu Ser Ser Phe Ser Lys Gln Lys Lys Leu Cys Gly
65              70              75              80
Cys Ile Ser Arg Thr Leu Asn His Phe Gln Asp Ser Ile Glu Leu Glu
              85              90              95
Thr His Ile Asp Thr Ser Thr Gln Leu
              100              105

```

<210> 2323

<211> 532

<212> DNA

<213> Homo sapiens

<400> 2323

```

acgcgtcaaa actggcaaa ctggcggctt agggggaggg gcaagtggac ttggaggccc
60
tcctccactg tgcacccctt tggaaaaaaa gcggaggggg catcaagtaa aagtttcttg
120
ccaggcagag ccagctcggc ggcctcccg acatagctgg ggtagcagg ggttgcttct
180
ctgccggcca cagcgtctc caggagccag ccggggagag ctgagccaag gccgaaggag
240
ccgcctgcgg gcttagccgc cccctcccg ccgttgccc cagagcggac gctgggacgc
300
ccggggtctg gcagctctgc gcccggttag gagcgggcgg gcgagcatta gcctgcgtcc
360
tgagagaagg gcgcagcgcc gcagttgagg ccgaagcagc cctcgcgagg cgtaggatac
420
ctgtcagtga gcgccggat tgcacggccc ccgggtagt cctgccggcg agggggcggga
480
gctcgggtga ctggccatc cccatcccg gccaggccc ggaggcggcg cg
532

```

<210> 2324

<211> 51

<212> PRT

<213> Homo sapiens

<400> 2324

```

Thr Arg Gln Asn Trp Gln Ser Trp Arg Leu Arg Gly Arg Gly Lys Trp
 1              5              10              15
Thr Trp Arg Pro Ser Ser Thr Val His Pro Leu Gly Lys Lys Ala Glu
              20              25              30
Gly Ala Ser Ser Lys Ser Phe Leu Pro Gly Arg Ala Ser Ser Ala Ala
              35              40              45
Pro Arg Thr

```

50

<210> 2325

<211> 459

<212> DNA

<213> Homo sapiens

<400> 2325

nnacgcgtgc aggaccgcat gagcgccatc tgggagagag gagtgggtgg aggaagatg
 60
 gatgagaacc gttttgtggc cggtaccagt tccaacgcag ctaagcttct gaacctgtat
 120
 ccccgaagg gccgcattat tcccgagacc gatgctgatg tgggtggtgtg ggaccagaa
 180
 gccacaaaga ccattctcagc cagcacgcag gtccaggag gagacttcaa cctgtatgag
 240
 aacatgcgct gccacggcgt gccactggtc accatcagcc gggggcgcgt cgtgtatgag
 300
 aacggcgtct tcatgtgcgc cgagggcacc ggcaagttct gtcccttgag gtccttccca
 360
 gacatgtct acaagaagct ggtccagaga gagaagactt taaaggttag aggagtggcc
 420
 cgactcctt acctggggga tgcgctgtt gtcgtgcac
 459

<210> 2326

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2326

Xaa	Arg	Val	Gln	Asp	Arg	Met	Ser	Ala	Ile	Trp	Glu	Arg	Gly	Val	Val
1				5					10					15	
Gly	Gly	Lys	Met	Asp	Glu	Asn	Arg	Phe	Val	Ala	Val	Thr	Ser	Ser	Asn
			20					25					30		
Ala	Ala	Lys	Leu	Leu	Asn	Leu	Tyr	Pro	Arg	Lys	Gly	Arg	Ile	Ile	Pro
		35				40					45				
Gly	Ala	Asp	Ala	Asp	Val	Val	Val	Trp	Asp	Pro	Glu	Ala	Thr	Lys	Thr
		50				55				60					
Ile	Ser	Ala	Ser	Thr	Gln	Val	Gln	Gly	Gly	Asp	Phe	Asn	Leu	Tyr	Glu
				70					75					80	
Asn	Met	Arg	Cys	His	Gly	Val	Pro	Leu	Val	Thr	Ile	Ser	Arg	Gly	Arg
				85				90						95	
Val	Val	Tyr	Glu	Asn	Gly	Val	Phe	Met	Cys	Ala	Glu	Gly	Thr	Gly	Lys
			100					105					110		
Phe	Cys	Pro	Leu	Arg	Ser	Phe	Pro	Asp	Thr	Val	Tyr	Lys	Lys	Leu	Val
			115				120					125			
Gln	Arg	Glu	Lys	Thr	Leu	Lys	Val	Arg	Gly	Val	Ala	Arg	Thr	Pro	Tyr
			130			135					140				
Leu	Gly	Asp	Val	Ala	Val	Val	Val	His							
145						150									

<210> 2327

<211> 599

<212> DNA

<213> Homo sapiens

<400> 2327

gaattccaga agatcaagta ttcttacgat gccctggaga agaagcagtt tctccccgtg
 60
 gcctttctctg tgggaacgc cttctcatat tatcagagca acagaggcct ccaggaagac
 120
 tcagagatcc gagcagctga gaagaaattt gggagcaaca aggccgagat ggtgggtgcct
 180
 gactttctcg agcttttcaa ggagagagcc acagccccct tctttgtatt tcagggtgttc
 240
 tgtgtggggc tctgggtgcct ggatgagtac tgggtactaca gcgtctttac gctatccatg
 300
 ctggtggcgt tcgaggcctc gctgggtcag cagcagatgc ggaacatgct ggagatccgg
 360
 aagatgggca acaagcccca catgatccag gtctaccgaa gccgcaagtg gaggcccat
 420
 gccagtgatg agatcgtacc aggggacatc gtctccatcg gtgaggccgg gttccgctca
 480
 gtcccagtg gagccccagc ctcagggcct ctggccaacc ctctcgcctc tgcctcgcag
 540
 gccgctcccc acaggagaac ctggtgccat gtgacgtgct tctgctgcga ggccgctgc
 599

<210> 2328

<211> 199

<212> PRT

<213> Homo sapiens

<400> 2328

Glu Phe Gln Lys Ile Lys Tyr Ser Tyr Asp Ala Leu Glu Lys Lys Gln
 1 5 10 15
 Phe Leu Pro Val Ala Phe Pro Val Gly Asn Ala Phe Ser Tyr Tyr Gln
 20 25 30
 Ser Asn Arg Gly Phe Gln Glu Asp Ser Glu Ile Arg Ala Ala Glu Lys
 35 40 45
 Lys Phe Gly Ser Asn Lys Ala Glu Met Val Val Pro Asp Phe Ser Glu
 50 55 60
 Leu Phe Lys Glu Arg Ala Thr Ala Pro Phe Phe Val Phe Gln Val Phe
 65 70 75 80
 Cys Val Gly Leu Trp Cys Leu Asp Glu Tyr Trp Tyr Tyr Ser Val Phe
 85 90 95
 Thr Leu Ser Met Leu Val Ala Phe Glu Ala Ser Leu Val Gln Gln
 100 105 110
 Met Arg Asn Met Ser Glu Ile Arg Lys Met Gly Asn Lys Pro His Met
 115 120 125
 Ile Gln Val Tyr Arg Ser Arg Lys Trp Arg Pro Ile Ala Ser Asp Glu
 130 135 140
 Ile Val Pro Gly Asp Ile Val Ser Ile Gly Glu Ala Gly Phe Arg Ser
 145 150 155 160
 Val Pro Val Gly Ala Pro Ala Ser Gly Pro Leu Ala Asn Pro Pro Ala
 165 170 175
 Ser Ala Leu Gln Ala Ala Pro His Arg Arg Thr Trp Cys His Val Thr

```

                180                185                190
Cys Phe Cys Cys Glu Ala Ala
      195

<210> 2329
<211> 392
<212> DNA
<213> Homo sapiens

<400> 2329
acgcgttcca tgaatgctgg tgcggctgcc gcgattgcta tgtacgcctg gacgacgcag
60
tgggtgtccaa agccacgcac tagctgatcg gggagaaccg tcaccttcta ggctcgtgtc
120
atgagcacgcg aaccactga ggaaccactc cgactagtgt tggcattcaa tccagtgcct
180
agtgcctccc gggttgtcca tcatcatgcg acgagatttc gcctggcggt gcaggccttc
240
attgtcgtcg tcattggtgg tttgttgtgg gcgttgacgg ccgacgcctt ccagttatcg
300
acgggtgatgt ggatgctcgg ggcattgggtg gtgctattcc tcgtgctttt cgtcatccag
360
aatctgcggc tgcacgccgc tcgcaaggat cc
392

<210> 2330
<211> 90
<212> PRT
<213> Homo sapiens

<400> 2330
Met Ser Thr Gln Pro Thr Glu Glu Pro Leu Arg Leu Val Val Ala Phe
1      5      10      15
Asn Pro Val Pro Ser Ala Ser Arg Val Ala His His His Ala Thr Arg
20     25     30
Phe Arg Leu Ala Val Gln Ala Phe Ile Val Val Val Ile Gly Gly Leu
35     40     45
Leu Trp Ala Leu Thr Ala Asp Ala Phe Gln Leu Ser Thr Val Met Trp
50     55     60
Met Leu Gly Ala Trp Val Val Leu Phe Leu Val Leu Phe Val Ile Gln
65     70     75     80
Asn Leu Arg Leu His Ala Ala Arg Lys Asp
      85      90

<210> 2331
<211> 2813
<212> DNA
<213> Homo sapiens

<400> 2331
nnggagcaag agagttatta aaagtgggtg gaagacttcc tgggtgcagga ggctcactcc
60
gatttaaggt gcccgagtcc acgctgatgg actgccgtag acaactgaaa gacagtaagc
120

```

aaattttatc tattacaaag aacttttaaag ttgagaatat tggacctctt cctataactg
180
tttcgtctct gaaaattaat ggggtataact gccaaaggta tggattcgag gtgctggatt
240
gggattcagt ttccccgga cccaaacaca tcccgcgata tcagcattgt gttcactcca
300
gactttacct cctcctgggt aattcgggac ctaagtcttg taaccgcagc ggacctagaa
360
tttcgcttca ctctcaatgt gactctccct catcacctgt tgccttgtg tgcagacgtg
420
gttccaggac ccagctggga ggagtcattt tggaggctca cggctcttct tgtcagtttg
480
tccctgttgg gtgtgatatt aatagccttc caacaagcac agtacattct catggaattc
540
atgaaaacaa gacagaggca aaatgctagc tcctcttcac agcaaaacaa tggctcctatg
600
gatgtaata cccccatto ttacaaaagc aattgcaaga actttctcga tacatatggc
660
ccctctgata aaggcagggg gaagaactgc cttccagtga acactcccca aagcaggatc
720
cagaatgctg caaagaggag cccagccacc tatgggtcatt ctcaagaaga gcacaatgc
780
tcagtgtatt acagtaaaaca caaaaccagc acagctgcgg ccagcagcac cagcacgact
840
actgaggaaa aacagacttc acccctgggc agctcactgc ctgctgctaa agaggacatt
900
tgcaactgat ccatgctgga gaactggatc agcctcagat atgcaagtgg cataaatgtc
960
aacctgcaga agaatttaac ccttcccaaa aacttactga ataaagaaga aaacacactg
1020
aaaaaacaca ttgttttcag taatccttct tcagaatgta gtatgaagga ggaatacag
1080
acatgtatgt ttcttaagga aactgacatt aaaacttcag agaacacagc tgagttcaag
1140
gaacgggagc tctgtccact gaagacctcc aagaaactac ctgaaaacca tttaccaaga
1200
aactcacctc agtaccacca gccagacttg ccagaaattt ccaggaaaaa taatgggaat
1260
aaccagcaag tacctgtcaa gaatgaagta gatcattgtg aaaatttgaa gaaggtggac
1320
acaaagcctt cttcagaaaa gaagattcac aaaacatcta gagaagacat gttttctgag
1380
aaacaggaca tacctttcgt agagcaagaa gatecttata ggaagaaaaa gcttcaggag
1440
aaaagagaa gaaatttaca aaatttaaat tggagtaaaa gtcgaacatg tagaaagaac
1500
aagaaaaagg gtgtgtctcc agtctcaagg cctcctgaac agagtgatct aaagcttgtg
1560
tgcaagtact ttgagaggtc tgagctgagc agtgacatca atgtaagaag ctgggtgata
1620
caggaaagca ctaggagggt ttgtaaagca gatgccgaaa ttgcaagcag tttacctgct
1680
gccagagag aggcaggta ctaccagaag cctgagaaga aatgtgtgga caagttctgc
1740

tccgattcca gctctgactg tgggagctcc tctggcagcg tgcgtgccag ccggggcagc
 1800
 tgggggagct ggagcagcac cagcagctcc gacggggata agaagcccat ggtggacgccc
 1860
 cagcacttcc tgcgggcccg agacagtgtt tcacaaaatg attttccctc tgaagctccc
 1920
 atctccttga atctttctca taacatctgc aatcccatga ccgtgaatag tctcccacaa
 1980
 tacgcagagc cttcctgtcc cagccttccct gccggggcca caggtgttga agaagataaa
 2040
 ggtctttact cacctggaga cctgtggccc actccgccag tgtgtgtgac aagcagctta
 2100
 aactgcaccc tggagaacgg cgtgccttgt gtgattcagg agtcggcccc gggtcataat
 2160
 agtttcattg attggagtgc aacatgcgaa ggccagtttt ccagcgcata ctgtccattg
 2220
 gaattgaacg attacaatgc ctttcagaa gaaaacatga actatgccaa tggcttcccc
 2280
 tgtcctgcag atgttcagac agactttatt gatcacaact ctcagtctac ctggaacacc
 2340
 ccacccaaca tgcctgtctg ctggggacat gccagtttca tcagctctcc gccctacctc
 2400
 acaagcaccg gaagcttgct tccaatgtct ggactttttg gttccatctg gggcccgcaa
 2460
 agcgatgtgt atgaaaattg ctgccccatc aacccccacca cggaacattc gacccacatg
 2520
 gaaaaccaag cggctgtgtg caaggaatac taccgggggt tcaaccggtt tcgcgcctat
 2580
 atgaacctgg acatatggac taccacagcg aataggaatg caaatttccc actgtctaga
 2640
 gactcgagtt actgtgggaa tgtgtgaaaa taattggatt tttaaacaat gtgaataaag
 2700
 aggcttgtgt tttgattact agtgtaaaat gggtatttag atagattatg acattgggtg
 2760
 atatttggc acttttatat gaaaataaat tttttaatga aaaaaaaaaa aaa
 2813

<210> 2332

<211> 789

<212> PRT

<213> Homo sapiens

<400> 2332

Pro Asp Phe Thr Ser Ser Trp Val Ile Arg Asp Leu Ser Leu Val Thr
 1 5 10 15
 Ala Ala Asp Leu Glu Phe Arg Phe Thr Leu Asn Val Thr Leu Pro His
 20 25 30
 His Leu Leu Pro Leu Cys Ala Asp Val Val Pro Gly Pro Ser Trp Glu
 35 40 45
 Glu Ser Phe Trp Arg Leu Thr Val Phe Phe Val Ser Leu Ser Leu Leu
 50 55 60
 Gly Val Ile Leu Ile Ala Phe Gln Gln Ala Gln Tyr Ile Leu Met Glu
 65 70 75 80
 Phe Met Lys Thr Arg Gln Arg Gln Asn Ala Ser Ser Ser Ser Gln Gln

[illegible]

```

      515                      520                      525
Asp Ser Val Ser Gln Asn Asp Phe Pro Ser Glu Ala Pro Ile Ser Leu
  530                      535                      540
Asn Leu Ser His Asn Ile Cys Asn Pro Met Thr Val Asn Ser Leu Pro
  545                      550                      555                      560
Gln Tyr Ala Glu Pro Ser Cys Pro Ser Leu Pro Ala Gly Pro Thr Gly
      565                      570                      575
Val Glu Glu Asp Lys Gly Leu Tyr Ser Pro Gly Asp Leu Trp Pro Thr
      580                      585                      590
Pro Pro Val Cys Val Thr Ser Ser Leu Asn Cys Thr Leu Glu Asn Gly
      595                      600                      605
Val Pro Cys Val Ile Gln Glu Ser Ala Pro Val His Asn Ser Phe Ile
      610                      615                      620
Asp Trp Ser Ala Thr Cys Glu Gly Gln Phe Ser Ser Ala Tyr Cys Pro
      625                      630                      635                      640
Leu Glu Leu Asn Asp Tyr Asn Ala Phe Pro Glu Glu Asn Met Asn Tyr
      645                      650                      655
Ala Asn Gly Phe Pro Cys Pro Ala Asp Val Gln Thr Asp Phe Ile Asp
      660                      665                      670
His Asn Ser Gln Ser Thr Trp Asn Thr Pro Pro Asn Met Pro Ala Ala
      675                      680                      685
Trp Gly His Ala Ser Phe Ile Ser Ser Pro Pro Tyr Leu Thr Ser Thr
      690                      695                      700
Arg Ser Leu Ser Pro Met Ser Gly Leu Phe Gly Ser Ile Trp Ala Pro
      705                      710                      715                      720
Gln Ser Asp Val Tyr Glu Asn Cys Cys Pro Ile Asn Pro Thr Thr Glu
      725                      730                      735
His Ser Thr His Met Glu Asn Gln Ala Val Val Cys Lys Glu Tyr Tyr
      740                      745                      750
Pro Gly Phe Asn Pro Phe Arg Ala Tyr Met Asn Leu Asp Ile Trp Thr
      755                      760                      765
Thr Thr Ala Asn Arg Asn Ala Asn Phe Pro Leu Ser Arg Asp Ser Ser
      770                      775                      780
Tyr Cys Gly Asn Val
785

```

<210> 2333

<211> 501

<212> DNA

<213> Homo sapiens

<400> 2333

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cgatgattg gtgtgggaca aatactattc aacaagagta cctaatacat tgtttaaggc
60
gaagtaataa atatgaatgg ggtgtatcat ataatgaaca acgaatatcc atatagtcca
120
gacgaagtgc ttcacaaagc aaaatcatat ttgtcagcag atgaatatga gtatgtttta
180
aaaagctatc atattgctta tgaagcacat aaaggtcagt tccgaaaaaa cggattacca
240
tacattatgc atcctataca agttgcaggt attttaacag aaatgcgatt agacggacgc
300
acgattgtcg caggtttttt gcatgatgta attgaagata caccgtatac atttgaagat
360

```

gtaaaagaaa tgttcaatga agaagttgct cgaattgttg atgggtgtgac gaagcttaaa
 420
 aaaataaaat accgctcaaa agaagaacaa caagctgaaa atcatcgcaa gttatttatt
 480
 gcgattgcca aagatgtacg c
 501

<210> 2334
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 2334
 Met Asn Gly Val Tyr His Ile Met Asn Asn Glu Tyr Pro Tyr Ser Ala
 1 5 10 15
 Asp Glu Val Leu His Lys Ala Lys Ser Tyr Leu Ser Ala Asp Glu Tyr
 20 25 30
 Glu Tyr Val Leu Lys Ser Tyr His Ile Ala Tyr Glu Ala His Lys Gly
 35 40 45
 Gln Phe Arg Lys Asn Gly Leu Pro Tyr Ile Met His Pro Ile Gln Val
 50 55 60
 Ala Gly Ile Leu Thr Glu Met Arg Leu Asp Gly Pro Thr Ile Val Ala
 65 70 75 80
 Gly Phe Leu His Asp Val Ile Glu Asp Thr Pro Tyr Thr Phe Glu Asp
 85 90 95
 Val Lys Glu Met Phe Asn Glu Glu Val Ala Arg Ile Val Asp Gly Val
 100 105 110
 Thr Lys Leu Lys Lys Ile Lys Tyr Arg Ser Lys Glu Glu Gln Gln Ala
 115 120 125
 Glu Asn His Arg Lys Leu Phe Ile Ala Ile Ala Lys Asp Val Arg
 130 135 140

<210> 2335
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 2335
 ggatcctgag cgtggggact tctttgcact ccacagaacc ctccattgta cctctacttt
 60
 tctctgcaga tggaccacac agcattcccc tgtgggtgct gcagggaggg ctgtgagaac
 120
 cccatgggcc gtgtggaatt taatcaggca agagttcaga cccatttcat ccacacactc
 180
 acccgctgc agttggaaca ggaggctgag agcttttaggg agctggaggc cctgtccca
 240
 ggcagccccc ccagccctgg tgaggaggcc ctggtcccta ctttcccaat ggccaaggcc
 300
 cccatgaaca atgagctggg agacaacagc tgcagcagcg acatgactga ttcttccaca
 360
 gcattcttcat cagcatcggg cactagt
 387

<210> 2336

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2336

```

Met Asp His Thr Ala Phe Pro Cys Gly Cys Cys Arg Glu Gly Cys Glu
 1           5           10           15
Asn Pro Met Gly Arg Val Glu Phe Asn Gln Ala Arg Val Gln Thr His
           20           25           30
Phe Ile His Thr Leu Thr Arg Leu Gln Leu Glu Gln Glu Ala Glu Ser
 35           40           45
Phe Arg Glu Leu Glu Ala Pro Ala Gln Gly Ser Pro Pro Ser Pro Gly
 50           55           60
Glu Glu Ala Leu Val Pro Thr Phe Pro Leu Ala Lys Pro Pro Met Asn
65           70           75           80
Asn Glu Leu Gly Asp Asn Ser Cys Ser Ser Asp Met Thr Asp Ser Ser
           85           90           95
Thr Ala Ser Ser Ser Ala Ser Gly Thr Ser
100           105

```

<210> 2337

<211> 359

<212> DNA

<213> Homo sapiens

<400> 2337

```

ngagaagagg aggagtcac gccagggggc gccatctcca ggctcgcca agccgctggg
60
accatgtgca gctcaagaat ggctccggc ccatcggcct cggggcaggg gaagggcagc
120
ttctctgcac cagcttcct gctgggctcc agggcccca ggctgaggcc gggggccca
180
gggtcaatgc caggcaccct gctattgagg aacctatcca ggaggaagga ctcgggcaga
240
cctgcgggat cctcgtctc ccacgggtcc tcattggcaga agcagaagga gctggagtcg
300
ctgaggtccg tgggcaggcg ggctggggcc aacgtggggg caccgacctc ctcaaagct
359

```

<210> 2338

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2338

```

Met Cys Ser Ser Arg Met Ala Ser Gly Pro Ser Ala Ser Gly Gln Gly
 1           5           10           15
Lys Gly Ser Phe Ser Ala Pro Ala Ser Leu Leu Gly Ser Arg Ala His
           20           25           30
Arg Leu Arg Pro Gly Ala Gln Gly Ser Met Pro Gly Thr Leu Leu Leu
 35           40           45
Arg Asn Leu Ser Arg Arg Lys Asp Ser Gly Arg Pro Ala Gly Ser Ser
 50           55           60
Ser Ser His Gly Ser Ser Trp Gln Lys Gln Lys Glu Leu Glu Ser Leu

```

```

65              70              75              80
Arg Ser Val Gly Arg Arg Ala Gly Pro Asn Val Gly Ser Pro Thr Ser
              85              90              95
Ser Lys

```

```

<210> 2339
<211> 439
<212> DNA
<213> Homo sapiens

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```

<400> 2339
acgcgtggcg tcagtcagg cagacttggg aggtcgccta caccgtcaac tcggttgcca
60
ccctgtcctc caccttcgtc gtgcgagtcg tcagtgctct gtggtttggt ccctccgggc
120
actgggtccc gtggggtctg taatgctggg gcgctcggcg cgatgtgccca gttccttggt
180
gagttactcc tctacactgg tgtgaacaag accggagaat tcccccccat attctcgttt
240
cccgtcgcgc ccgcacgtca ttgggactgg cttttacgcg gtagtggttg ccgtactctg
300
gttgctctgc ggcacggctg gcagggggat catgtcatga gtccgacggt gagcgagcgg
360
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420
ttgtcggggg gcgggtgctg
439

```

```

<210> 2340
<211> 92
<212> PRT
<213> Homo sapiens

```

```

<400> 2340
Met Cys Gln Phe Leu Gly Glu Leu Leu Tyr Thr Gly Val Asn Lys
1              5              10              15
Thr Gly Glu Phe Pro Pro Ile Phe Ser Phe Pro Ala Arg Pro Ala Arg
20              25              30
His Trp Asp Trp Leu Leu Arg Gly Ser Gly Cys Arg Thr Leu Val Ala
35              40              45
Leu Arg His Gly Arg Gln Gly Asp His Val Met Ser Pro Thr Val Ser
50              55              60
Glu Arg Arg Leu Ser Ala Pro Met Arg Arg Gly Ile Val Ala Leu Cys
65              70              75              80
Val Ala Met Ala Phe Val Leu Ser Gly Cys Gly Ala
              85              90

```

```

<210> 2341
<211> 411
<212> DNA
<213> Homo sapiens

```

```

<400> 2341

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gccccaacctc ccctccatcc tgcccaagat ggatcttgct gagcctccct ggcatatgcc
60
tctgcaggag gagccagagg aggtcacgga ggaggaggag gaaagggaag aagaggagag
120
ggagaaggaa gcagaggagg aggaggaaga ggaagagctg ctctgtgtgag cgggtcccca
180
ggagccaccg cacaggccca tgcctcttca cctagcacca gcagcagcac cagcagccag
240
agtctctggg ccaccggca caggcaggag gattctggag accaggccac atcaggcnat
300
ggaagtggag agcagtgtga aaccacacct gtcagtgcc tcagtcacc caagtacagt
360
ggccccgggg gttcagaact atagccagga gtctgggggc actgagtggc n
411

<210> 2342

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2342

Ala	Ser	Leu	Ala	Tyr	Ala	Ser	Ala	Gly	Gly	Ala	Arg	Gly	Gly	His	Gly
1				5					10					15	
Gly	Gly	Gly	Gly	Lys	Gly	Arg	Arg	Gly	Glu	Gly	Glu	Gly	Ser	Arg	Gly
			20					25					30		
Gly	Gly	Gly	Arg	Gly	Arg	Ala	Ala	Pro	Val	Ser	Gly	Ser	Pro	Gly	Ala
			35				40					45			
Thr	Ala	Gln	Ala	His	Ala	Pro	Ser	Pro	Ser	Thr	Ser	Ser	Ser	Thr	Ser
	50					55				60					
Ser	Gln	Ser	Pro	Gly	Ala	Thr	Arg	His	Arg	Gln	Glu	Asp	Ser	Gly	Asp
				70						75				80	
Gln	Ala	Thr	Ser	Gly	Xaa	Gly	Ser	Gly	Glu	Gln	Cys	Glu	Thr	His	Leu
				85					90					95	
Val	Ser	Ala	Leu	Ser	His	Pro	Lys	Tyr	Ser	Gly	Pro	Gly	Gly	Ser	Glu
			100					105						110	

Leu

<210> 2343

<211> 522

<212> DNA

<213> Homo sapiens

<400> 2343

ggccccgaga agatgctgat gccttcacag tttcccaacc agggccagca gggattctct
60
ggaggccagg gaccctacca agccatgtcc caggacatgg gcaataccga agacatgttc
120
agccctgatc agagctcaat gcccatgagc aacgtgggca ccaccggct cagccacatg
180
cctctgcccc ctgcgtccaa tctctctggg accgtgcatt cagcccaaaa cggggggcta
240
ggcaggcgcc cttcggacct caccatcagt attaatcaga tgggctcacc gggcatgggg
300

cacttgaagt cgccaccct tagccagggt cactcaccctc tggtcacctc gccctctgcc
 360
 aaacctcaagt caccacagac tccctcacag atgggtgcctc tgccttctgc caaccgcga
 420
 ggacctctca agtcgcccc ggtcctcggc tctccctca gtgtccgttc acccaatggc
 480
 tcgcccagca ggctcaagtc tcttccatg gcggtgcctt ct
 522

<210> 2344
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 2344
 Gly Pro Gln Lys Met Leu Met Pro Ser Gln Phe Pro Asn Gln Gly Gln
 1 5 10 15
 Gln Gly Phe Ser Gly Gly Gln Gly Pro Tyr Gln Ala Met Ser Gln Asp
 20 25 30
 Met Gly Asn Thr Gln Asp Met Phe Ser Pro Asp Gln Ser Ser Met Pro
 35 40 45
 Met Ser Asn Val Gly Thr Thr Arg Leu Ser His Met Pro Leu Pro Pro
 50 55 60
 Ala Ser Asn Pro Pro Gly Thr Val His Ser Ala Pro Asn Arg Gly Leu
 65 70 75 80
 Gly Arg Arg Pro Ser Asp Leu Thr Ile Ser Ile Asn Gln Met Gly Ser
 85 90 95
 Pro Gly Met Gly His Leu Lys Ser Pro Thr Leu Ser Gln Val His Ser
 100 105 110
 Pro Leu Val Thr Ser Pro Ser Ala Asn Leu Lys Ser Pro Gln Thr Pro
 115 120 125
 Ser Gln Met Val Pro Leu Pro Ser Ala Asn Pro Pro Gly Pro Leu Lys
 130 135 140
 Ser Pro Gln Val Leu Gly Ser Ser Leu Ser Val Arg Ser Pro Thr Gly
 145 150 155 160
 Ser Pro Ser Arg Leu Lys Ser Pro Ser Met Ala Val Pro Ser
 165 170

<210> 2345
 <211> 561
 <212> DNA
 <213> Homo sapiens

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 35 40 45
 Phe Arg Leu Phe Leu Arg Phe Trp Cys Leu Leu Ala Cys Ala Pro
 50 55 60
 Ala Ser Pro Ala Leu Ser Glu Ser Leu Ala Leu Ser Asp Val Ser Asp
 65 70 75 80
 Ser Gln Phe Cys Ser Arg Arg Ser Asp Ser Leu Ser Thr Ile Ala Ile
 85 90 95
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 100 105 110
 Leu Ser Asn Pro Glu Tyr Lys Asp Thr Pro Met Asp Ile Ala Gln Leu
 115 120 125
 Pro His Leu Pro Glu Lys Thr Ser Glu Ser Ser Glu Thr Ser Asp Ser
 130 135 140
 Glu Ser Asp Ser Lys Asp Thr Ser Gly Ile Thr Glu Asp Asn Glu Asn
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 Ser Lys Xaa Pro Thr Arg Arg Gly Thr Ser Pro Arg Thr Ala Lys Thr
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<210> 2348

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2348

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Leu	Lys	Gly	Glu	Tyr	Ser	Arg	Asn	Val	Gly	Pro	Asn	Ile	Asp	Ala	Trp
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Ser	Asp	Phe	Gln	Pro	Leu	Gly	Val	Val	Ala	Gly	Ile	Thr	Pro	Phe	Asn
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Phe	Pro	Ala	Met	Val	Pro	Leu	Trp	Met	Tyr	Pro	Leu	Ala	Ile	Val	Cys
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Leu	Leu	Ile	Ala	Gln	Leu	Leu	Gln	Glu	Ala	Gly	Leu	Pro	Lys	Gly	Val
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<211> 139
 <212> PRT
 <213> Homo sapiens

<400> 2350

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 Leu Ala Phe Leu Asp Asp Ile Ile Ala His Asn His Ile Lys Trp Ile
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 Gly Asn Thr Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala
 50 55 60
 Arg Ile Asn Gly Ile Gly Ala Met Val Thr Thr Phe Gly Val Gly Glu
 65 70 75 80
 Leu Ser Ala Val Asn Gly Ile Ala Gly Ser Tyr Ala Glu Arg Val Pro
 85 90 95
 Val Ile Ala Ile Thr Gly Ala Pro Thr Arg Ala Val Glu Gln Glu Gly
 100 105 110
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 Lys Met Phe Glu Pro Ile Thr Thr Ala Gln Ala
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 <212> DNA
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<400> 2351

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<213> Homo sapiens

<400> 2352

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Asp Gln Tyr Asp Arg Phe Val Arg Gly Asn Thr Val Leu Ala Gln Pro
      35           40           45
Asn Asp Ala Gly Met Ile Arg Ile Asp Asp Asn Leu Gly Ile Ala Leu
      50           55           60
Ser Leu Asp Ala Asn Gly Arg Gln Thr Thr Leu Asn Pro Tyr Leu Gly
65           70           75           80
Ala Gln Leu Ala Leu Cys Glu Ala Tyr Arg Asn Val Ala Val Ser Gly
      85           90           95
Ala Thr Pro Val Ala Val Thr Asp Cys Leu Asn Tyr Gly Ser Pro Tyr
      100          105          110
Asp Pro Asp Val Met Trp Gln Phe Asp Glu Thr Ile Leu Gly Leu Val
      115          120          125
Asp Gly Cys Arg Glu Leu Gly Val Pro Val Thr Gly Gly Asn Val Ser
      130          135          140
Leu His Asn Arg Thr Gly Asp Glu Ser Ile Arg Pro Thr Pro Leu Val
145          150          155          160
Gly Val Leu Gly Val Ile Asp Asp Val His Arg Arg Ile Pro Ser Ala
      165          170          175
Phe Ala His Asp Gly Asp Ala Val Leu Leu Leu Gly Thr Thr Lys Cys
      180          185          190
Glu Phe Gly Gly Ser Val Tyr Glu Asp Val Ile His Ala Gly His Leu
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<210> 2353

<211> 422

<212> DNA

<213> Homo sapiens

<400> 2353

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 Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu Met Leu Lys Met Thr
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 Glu Glu Asp Phe Glu Lys Val Ile Lys Ile Asn Leu Thr Gly Ala Phe
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 Asn Met Thr Gln Ala Val Leu Lys Gln Met Ile Lys Ala Arg Glu Gly
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 Ala Ile Ile Asn Met Ser Ser Val Val Gly Leu Met Gly Asn Ile Gly
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<211> 1000

<212> PRT

<213> Homo sapiens

<400> 2356

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35          40          45
Glu Trp Cys Phe Gly Leu Val Ile Phe Ala Gly Pro Asp Thr Lys Leu
50          55          60
Met Gln Asn Ser Gly Arg Thr Lys Phe Lys Arg Thr Ser Ile Asp Arg
65          70          75          80
Leu Met Asn Thr Leu Val Leu Trp Ile Phe Gly Phe Leu Val Cys Met
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Gly Val Ile Leu Ala Ile Gly Asn Ala Ile Trp Glu His Glu Val Gly
100          105          110
Met Arg Phe Gln Val Tyr Leu Pro Trp Asp Glu Ala Val Asp Ser Ala
115          120          125
Phe Phe Ser Gly Phe Leu Ser Phe Trp Ser Tyr Ile Ile Ile Leu Asn
130          135          140
Thr Val Val Pro Ile Ser Leu Tyr Val Ser Val Glu Val Ile Arg Leu
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245          250          255
Phe Trp Asp Pro Ser Leu Leu Glu Ala Val Lys Ile Gly Asp Pro His
260          265          270
Thr His Glu Phe Phe Arg Leu Leu Ser Leu Cys His Thr Val Met Ser
275          280          285
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290          295          300
Glu Gly Ala Leu Val Thr Ala Ala Arg Asn Phe Gly Phe Val Phe Arg
305          310          315          320
Ser Arg Thr Pro Lys Thr Ile Thr Val His Glu Met Gly Thr Ala Ile
325          330          335
Thr Tyr Gln Leu Leu Ala Ile Leu Asp Phe Asn Asn Ile Arg Lys Arg
340          345          350
Met Ser Val Ile Val Arg Asn Pro Glu Gly Lys Ile Arg Leu Tyr Cys
355          360          365
Lys Gly Ala Asp Thr Ile Leu Leu Asp Arg Leu His His Ser Thr Gln
370          375          380
Glu Leu Leu Asn Thr Thr Met Asp His Leu Asn Glu Tyr Ala Gly Glu
385          390          395          400
Gly Leu Arg Thr Leu Val Leu Ala Tyr Lys Asp Leu Asp Glu Glu Tyr
405          410          415
Tyr Glu Glu Trp Ala Glu Arg Arg Leu Gln Ala Ser Leu Ala Gln Asp

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 Val Leu Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Gly Tyr Ser
 485 490 495
 Cys Lys Met Leu Thr Asp Asp Met Thr Glu Val Phe Ile Val Thr Gly
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 His Thr Val Leu Glu Val Arg Glu Glu Xaa Gln Glu Ser Pro Gly Glu
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 Asp Asp Gly Leu Ile Xaa Arg Ser Val Gly Asn Gly Phe Thr Tyr Gln
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 Asp Lys Leu Ser Ser Ser Lys Leu Thr Ser Val Leu Glu Ala Val Ala
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 Ala Val Ile Cys Cys Arg Val Thr Pro Leu Gln Lys Ala Gln Val Val
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 Gly Ala Asn Asp Val Ser Met Ile Lys Thr Ala His Ile Gly Val Gly
 625 630 635 640
 Ile Ser Gly Gln Glu Gly Ile Gln Ala Val Leu Ala Ser Asp Tyr Ser
 645 650 655
 Phe Ser Gln Phe Lys Phe Leu Gln Arg Leu Leu Leu Val His Gly Arg
 660 665 670
 Trp Ser Tyr Leu Arg Met Cys Lys Phe Leu Cys Tyr Phe Tyr Lys
 675 680 685
 Asn Phe Ala Phe Thr Met Val His Phe Trp Phe Gly Phe Phe Cys Gly
 690 695 700
 Phe Ser Ala Gln Thr Val Tyr Asp Gln Tyr Phe Ile Thr Leu Tyr Asn
 705 710 715 720
 Ile Val Tyr Thr Ser Leu Pro Val Leu Ala Met Gly Val Phe Asp Gln
 725 730 735
 Asp Val Pro Glu Gln Arg Ser Met Glu Tyr Pro Lys Leu Tyr Glu Pro
 740 745 750
 Gly Gln Leu Asn Leu Leu Phe Asn Lys Arg Glu Phe Phe Ile Cys Ile
 755 760 765
 Ala Gln Gly Ile Tyr Thr Ser Val Leu Met Phe Phe Ile Pro Tyr Gly
 770 775 780
 Val Phe Ala Asp Ala Thr Arg Asp Asp Gly Thr Gln Leu Ala Asp Tyr
 785 790 795 800
 Gln Ser Phe Ala Val Thr Val Ala Thr Ser Leu Val Ile Val Val Ser
 805 810 815
 Val Gln Ile Gly Leu Asp Thr Gly Tyr Trp Thr Ala Ile Asn His Phe
 820 825 830
 Phe Ile Trp Gly Ser Leu Ala Val Tyr Phe Ala Ile Leu Phe Ala Met
 835 840 845
 His Ser Asn Gly Leu Phe Asp Met Phe Pro Asn Gln Phe Arg Phe Val

```

      850              855              860
Gly Asn Ala Gln Asn Thr Leu Ala Gln Pro Thr Val Trp Leu Thr Ile
865              870              875              880
Val Leu Thr Thr Val Val Cys Ile Met Pro Val Val Ala Phe Arg Phe
      885              890              895
Leu Arg Leu Asn Leu Lys Pro Asp Leu Ser Asp Thr Val Arg Tyr Thr
      900              905              910
Gln Leu Val Arg Lys Lys Gln Lys Ala Gln His Arg Cys Met Arg Arg
      915              920              925
Val Gly Arg Thr Gly Ser Arg Arg Ser Gly Tyr Ala Phe Ser His Gln
      930              935              940
Glu Gly Phe Gly Glu Leu Ile Met Ser Gly Lys Asn Met Arg Leu Ser
895              950              955              960
Ser Leu Ala Leu Ser Ser Phe Thr Thr Arg Ser Ser Ser Trp Ile
      965              970              975
Glu Ser Leu Arg Arg Lys Lys Ser Asp Ser Ala Ser Ser Pro Ser Gly
      980              985              990
Gly Ala Asp Lys Pro Leu Lys Gly
      995              1000

```

<210> 2357

<211> 408

<212> DNA

<213> Homo sapiens

<400> 2357

```

naccgcttac gttgctggag gtcaatgcgt catgccgata catcatcaga tccgcactgt
60
ggcgaccatc cttgccacca ttaccattgc cgccctagtg ctcacgggct gtaatacggc
120
ggtgcgccaa acggtgaaga cgaggtttcc cgcaagctca tcaccgtgtg ggggtgtgag
180
ccacaaaacc cactcctgcc agccgacacc aatgaaaccg gcggcacgaa agtcatcacc
240
gccttggttc cggcctgggt gtattacgac gccgacggca aaaccataaa tgatgtggcc
300
aaatccattg acttcgatgg cgaccgcacc tacacggtga cgctgcggaa aaccagattc
360
gccgacggta ctgaggtgaa ggcccataat tttgtgaaa ctgccgca
408

```

<210> 2358

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2358

```

Tyr Gly Gly Ala Pro Asn Gly Glu Asp Glu Val Ser Arg Lys Leu Ile
1              5              10              15
Thr Val Trp Gly Ala Glu Pro Gln Asn Pro Leu Leu Pro Ala Asp Thr
      20              25              30
Asn Glu Thr Gly Gly Thr Lys Val Ile Thr Ala Leu Phe Ala Gly Leu
      35              40              45
Val Tyr Tyr Asp Ala Asp Gly Lys Thr His Asn Asp Val Ala Lys Ser

```

```

      50              55              60
Ile Asp Phe Asp Gly Asp Arg Thr Tyr Thr Val Thr Leu Arg Lys Thr
65              70              75              80
Arg Phe Ala Asp Gly Thr Glu Val Lys Ala His Asn Phe Val Lys Ala
      85              90              95
Ala Ala

```

<210> 2359
 <211> 324
 <212> DNA
 <213> Homo sapiens

```

<400> 2359
aacctgaaca tgttgggatt gagagagccc gaggtgtatg ggtcggaac attggcgcgac
60
gttgagcaga cgtgtcgtga gtacggcgaa gaacttgggc ttgtaattga gtttcagcaa
120
accaatcacg aaggggcaaat gattgaatgg attcaccacg cccgtagaag gattgcgggg
180
attgtgatca atccaggagc atggacccat acatcggcag ccataccaga tgcgttgatt
240
gcagccgagg taccggtgat tgaggttcac atctcaaagt tccacaggcg tgaagatttc
300
aggcattttt cctacgtgtc acgc
324

```

<210> 2360
 <211> 108
 <212> PRT
 <213> Homo sapiens

```

<400> 2360
Asn Leu Asn Met Leu Gly Leu Arg Glu Pro Glu Val Tyr Gly Ser Glu
1      5      10      15
Thr Leu Ala Asp Val Glu Gln Thr Cys Arg Glu Tyr Gly Glu Glu Leu
      20      25      30
Gly Leu Val Ile Glu Phe Gln Gln Thr Asn His Glu Gly Gln Met Ile
      35      40      45
Glu Trp Ile His His Ala Arg Arg Arg Ile Ala Gly Ile Val Ile Asn
      50      55      60
Pro Gly Ala Trp Thr His Thr Ser Ala Ala Ile His Asp Ala Leu Ile
65      70      75      80
Ala Ala Glu Val Pro Val Ile Glu Val His Ile Ser Asn Val His Arg
      85      90      95
Arg Glu Asp Phe Arg His Phe Ser Tyr Val Ser Arg
      100      105

```

<210> 2361
 <211> 398
 <212> DNA
 <213> Homo sapiens

<400> 2361

tccggatggg actccaacct acttgggggt actgggggtg cagaaagaac gcggccctgt
 60
 gtcagggacc ggtatggaag cctcagtagg gctggagccc catcatgccc ctcccgagca
 120
 gatcaacaca gaccagctgg tcaaggggga cctccatccc tgccctgtcc tcacggagct
 180
 gtagggagag tcccaaaggc aggtggtggg gctggggcct ccaacagctg ggtcctctca
 240
 tatcacttaa ggcccaacag cacacagtct cccaagtgtg ccaggtgcca caacacggcc
 300
 atccccgtct cacagctcca ccccgctgc ctgctgcca ccatctccac aaacatatgc
 360
 tgcagctcca caccgggaa acaccacatg ctcgcttt
 398

<210> 2362

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2362

Met Pro Leu Pro Ser Arg Ser Thr Gln Thr Ser Trp Ser Arg Gly Thr
 1 5 10 15
 Ser Ile Pro Ala Leu Ser Ser Arg Ser Cys Arg Glu Ser Pro Lys Gly
 20 25 30
 Arg Trp Trp Gly Trp Gly Leu Gln Gln Leu Gly Pro Leu Ile Ser Leu
 35 40 45
 Lys Ala Gln Gln His Thr Val Ser Gln Val Cys Gln Val Pro Gln His
 50 55 60
 Gly His Pro Ala Leu Thr Ala Pro Pro Arg Leu Pro Ala Cys His His
 65 70 75 80
 Leu His Lys His Met Leu Gln Leu His Thr Arg Glu Thr Pro His Ala
 85 90 95
 Arg Phe

<210> 2363

<211> 833

<212> DNA

<213> Homo sapiens

<400> 2363

nngactctct tagctcccaa cgcaaaagcg tttaaagatg cagctcagaa gcatcaccag
 60
 cagcacaagg ggaggtccca agaaccagaa cttacatcac tgctcccgag ttcagagggt
 120
 tcctttccca ccttctcaga actttctggt tccatggcct cctctgccac ctctgccacc
 180
 tcccctgatg tgctggcctc cgtttccatc gcttctcat ggcgttcttc cgcccggtgt
 240
 tccaagccca ctgcangtcg aagcaaacgt gattgcgtta ccatcagaa ggtggcacag
 300
 ggactggcag cgggtccatc tgggagctcg tgtgctcagc ctccagatgc aggcctcccc
 360

ggccccctgct gtgggtgctag gtccccagat gagagatcac ggtcatgaag atcagcccc
 420
 aaggcagccc ctccnttcc agcctgggct ctggcggtgt ctagggtgctc acttccatgg
 480
 ctggcctgct cacagagccc tacctcagcc tgtggtaagc gcacctgctc ggccctgggtg
 540
 ctctatgatg agccaccagt cagttctgca gatgtgtccc cgagctcctg ccgagggacg
 600
 aaacacgggt gccctgctcc tagtgctgtg gcacgccacg ctccacacct gccatctgce
 660
 ctccaccac ctgctcccc aggggctccg cctcgtgact cacgctcagg caagtctccg
 720
 ggcgcgaaaca gctggctgat ggtgacatgc tgcagcctgg tcacatcaga aaccatgagg
 780
 gtggatctcc ggaggtcatc gatgtggaca gactgccaca gcccttcacg cgt
 833

<210> 2364

<211> 135

<212> PRT

<213> Homo sapiens

<400> 2364

Xaa	Thr	Pro	Leu	Ala	Pro	Asn	Ala	Lys	Ala	Phe	Lys	Asp	Ala	Ala	Gln
1				5					10				15		
Lys	His	His	Gln	Gln	His	Lys	Gly	Arg	Ser	Gln	Glu	Pro	Glu	Leu	Thr
			20					25				30			
Ser	Leu	Pro	Pro	Ser	Ser	Glu	Val	Ser	Phe	Pro	Thr	Phe	Ser	Glu	Leu
		35					40					45			
Ser	Val	Ser	Met	Ala	Ser	Ser	Ala	Thr	Ser	Ala	Thr	Ser	Pro	Asp	Val
		50				55					60				
Leu	Ala	Ser	Val	Ser	Ile	Ala	Ser	Ser	Trp	Arg	Ser	Ser	Ala	Arg	Cys
65					70					75				80	
Ser	Lys	Pro	Thr	Ala	Xaa	Arg	Ser	Lys	Arg	Asp	Cys	Val	Thr	Thr	Gln
				85				90						95	
Lys	Val	Ala	Gln	Gly	Leu	Ala	Ala	Val	Pro	Ser	Gly	Ser	Leu	Cys	Ala
			100					105					110		
Gln	Pro	Pro	Ser	Ala	Gly	Phe	Pro	Gly	Pro	Cys	Cys	Gly	Ala	Arg	Ser
		115					120					125			
Pro	Asp	Glu	Arg	Ser	Arg	Ser									
		130				135									

<210> 2365

<211> 429

<212> DNA

<213> Homo sapiens

<400> 2365

accggtgccc agtccccacg gctcgtccag acctacgttg agaaacttcg acgagacagt
 60
 ctccgtcagt tcgccaaca acctctgaac gaagtcaaga ttctccggca ctggagccaa
 120
 ggtgcttgcc ctggcatgaa cgccccagg gaggtcgacg ccgtcgggat tctcacaccg
 180

atggtgatgg gactcggttt ccaaccacgg ttccatgtga ccagacagct tctggttggc
 240
 cccgagctcg atgcctcgtc cgcgacacag accatcgagc cacctcatgt cctccgccgt
 300
 caccggggctg cggtcggccc acacctcttc ctcaccggcg taggcaaatc ccgcttcacc
 360
 atagagctca aggtgattga gaccacaccg cgccatgacg cgcgtcagga aatcaagagt
 420
 ggaacgcgt
 429

<210> 2366
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 2366
 Met Ala Arg Cys Gly Leu Asn His Leu Glu Leu Tyr Gly Glu Ala Gly
 1 5 10 15
 Phe Ala Tyr Arg Gly Glu Glu Glu Val Trp Ala Asp Arg Ser Pro Val
 20 25 30
 Thr Ala Glu Asp Met Arg Trp Leu Asp Gly Leu Cys Arg Gly Arg Gly
 35 40 45
 Ile Glu Leu Gly Ala Asn Gln Asn Cys Leu Gly His Met Glu Pro Trp
 50 55 60
 Leu Glu Thr Glu Ser His His His Arg Cys Glu Asn Pro Asp Gly Val
 65 70 75 80
 Asp Leu Pro Trp Gly Val His Ala Arg Ala Ser Thr Leu Ala Pro Val
 85 90 95
 Pro Glu Asn Leu Asp Phe Val Gln Arg Leu Leu Gly Glu Leu Thr Glu
 100 105 110
 Thr Val Ser Ser Lys Phe Leu Asn Val Gly Leu Asp Glu Pro Trp Glu
 115 120 125
 Leu Gly Thr Gly
 130

<210> 2367
 <211> 474
 <212> DNA
 <213> Homo sapiens

<400> 2367
 ngtgcacggg agaagacgtg cgcgcagttc ggccgaacct atccgggttc ggccggcagc
 60
 ggggggtcacg agctcacga cgcgcgcgcg ttcgcctcgt ggggcgtcga tttcgtcaaa
 120
 tacgatcggt gctccggtga ctccgcgcac gacgaccagg tcgcctcgtt caccgcgatg
 180
 cgtgacgcaa tccgatccac cggacgcccc atggtgtaca gcatcaaccc caacagcgaa
 240
 tcgcccggatc ggtccggagc ccaattcgat tggggcggtg tggcaaccat gacacgtacc
 300
 accaacgaca tctcgcggt gtggaccact cggccggccg gtgccgatgc gacaccggca
 360

tcgggggtatc agggggatccg cgacatcatc gacgccgtgg ccccgatcgg cgcacggggt
 420
 gcgacggcgag cttcgtcgac atggacatgc tcgtcgtcgg tgctcgcaac gcgt
 474

<210> 2368

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2368

Xaa Ala Arg Glu Lys Thr Cys Ala Gln Phe Gly Gly Thr Tyr Pro Gly
 1 5 10 15
 Ser Ala Gly Ser Gly His Glu Leu Thr Asp Ala Arg Ala Phe Ala
 20 25 30
 Ser Trp Gly Val Asp Phe Val Lys Tyr Asp Arg Cys Ser Gly Asp Ser
 35 40 45
 Ala His Asp Asp Gln Val Ala Ser Phe Thr Ala Met Arg Asp Ala Ile
 50 55 60
 Arg Ser Thr Gly Arg Pro Met Val Tyr Ser Ile Asn Pro Asn Ser Glu
 65 70 75 80
 Ser Pro Asp Arg Ser Gly Ala Gln Phe Asp Trp Gly Gly Val Ala Thr
 85 90 95
 Met Thr Arg Thr Thr Asn Asp Ile Ser Pro Val Trp Thr Thr Arg Pro
 100 105 110
 Ala Gly Ala Asp Ala Thr Pro Ala Ser Gly Tyr Gln Gly Ile Arg Asp
 115 120 125
 Ile Ile Asp Ala Val Ala Pro Ile Gly Ala Arg Val Ala Thr Ala Ala
 130 135 140
 Ser Ser Thr Trp Thr Cys Ser Ser Ser Val Ser Ala Thr Arg
 145 150 155

<210> 2369

<211> 408

<212> DNA

<213> Homo sapiens

<400> 2369

ctgaatggca ggcaggcaga ggccaccaga gccagccccc cgagaagccc tgctgagcca
 60
 aagggggagcg ccctgggacc taaccacagag ccccatctca ccttcccccg ttcttttcaaa
 120
 gtgcctcccc caacccagct caggacttcg tccatcccag ttcaggaagc acaagaggct
 180
 ccgaaaagga agagggggcc accaagaagg ctcccagccg actcccactg cctcccagct
 240
 tccacatccg ccccgctcc caggtctacc cagacagggc ccccgagcnc agactgccct
 300
 ggggagctca aggccacagc accagccagc ccaaggett ggcagtccca gtcccaagca
 360
 gatgaacgag ctgggactcc gcctecagcc cctccccctgc cccctcct
 408

<210> 2370

<211> 136

<212> PRT

<213> Homo sapiens

<400> 2370

```

Leu Asn Gly Arg Gln Ala Glu Ala Thr Arg Ala Ser Pro Pro Arg Ser
 1           5           10           15
Pro Ala Glu Pro Lys Gly Ser Ala Leu Gly Pro Asn Pro Glu Pro His
           20           25           30
Leu Thr Phe Pro Arg Ser Phe Lys Val Pro Pro Pro Thr Pro Val Arg
 35           40           45
Thr Ser Ser Ile Pro Val Gln Glu Ala Gln Glu Ala Pro Glu Arg Lys
 50           55           60
Arg Gly Pro Pro Arg Arg Leu Pro Ala Asp Ser His Cys Leu Pro Ala
 65           70           75           80
Ser Thr Ser Ala Pro Pro Arg Ser Thr Gln Thr Gly Pro Pro Ser
           85           90           95
Xaa Asp Cys Pro Gly Glu Leu Lys Ala Thr Ala Pro Ala Ser Pro Arg
           100          105          110
Leu Gly Gln Ser Gln Ser Gln Ala Asp Glu Arg Ala Gly Thr Pro Pro
           115          120          125
Pro Ala Pro Pro Leu Pro Pro Pro
           130           135

```

<210> 2371

<211> 327

<212> DNA

<213> Homo sapiens

<400> 2371

```

gaattcgggtg tgcgatgcga gcctgcagcc tgggagcaga gacaaggagc aaaggcggtg
 60
agagggttgc cagggcacc cagttacagct ggagctgcag gggacccatc cctcgagaga
 120
ggcaggcact agtcatgagg caagagatgc ctcagaagag gatgtctggcc gcagggcaca
 180
gcagagaggg agatagccc gggcactcct caggaccggg cctcagggga cagcaaacaa
 240
gattcctgat agacgcgccc aggtcatgcc ttttcagtgg tgtgagccag gttctggcgt
 300
caggcgggcc aaggtttca tgcagcn
 327

```

<210> 2372

<211> 104

<212> PRT

<213> Homo sapiens

<400> 2372

```

Met Arg Ala Cys Ser Leu Gly Ala Glu Thr Arg Ser Lys Gly Gly Glu
 1           5           10           15
Arg Val Ala Arg Ala Pro Ser Tyr Ser Trp Ser Cys Arg Gly Pro Ile
           20           25           30
Pro Arg Glu Arg Gln Ala Leu Val Met Arg Gln Glu Met Pro Gln Lys

```



```

          35              40              45
Arg Met Leu Ala Ala Gly His Ser Arg Glu Gly Asp Ser Pro Gly His
  50              55              60
Ser Ser Gly Pro Gly Leu Arg Gly Gln Gln Thr Arg Phe Leu Ile Asp
  65              70              75              80
Ala Pro Arg Ser Cys Leu Phe Ser Gly Val Ser Gln Val Leu Ala Ser
          85              90              95
Gly Gly Pro Arg Phe Ser Cys Ser
          100

```

<210> 2373

<211> 591

<212> DNA

<213> Homo sapiens

<400> 2373

```

gaattctgac attcaggaag tcaattgcag aaggtttaac caagttgatt ctgttttacc
  60
aaatcctgtc tattctgaaa agcggccaat gccagactca tctcatgatg tgaaagtctt
 120
cacttcaaa acatcagctg ttgatagatg ccaggcagta ttgaatactc agctttctatc
 180
agaaaaatgtt accaaagtgt agcaaaaattc accagcagtt tgtgaaacaa tttctgttcc
 240
caagtccatg tccactgagg aatataaatc aaaaattcaa aatgaaaata tgctacttct
 300
cgctttgtct tcacaggcac gtaagactca gaagacagta ttaaagatg ctaatcaaac
 360
tattcaggat tctaaaccag acagtgttga aatgaatcca aatacccaaa tgactggtaa
 420
ccaactgaat ttgaagaaca tggaaactcc aagtacttct aatgtaagt gagggtttt
 480
ggacaactcc ttttgcagt gacaagaatc ctcaacaaaa ggaatgcctg ctaaaagtga
 540
cagtagctgt tccatggaag tgctagcaac ctgtctttcc ctgtggaaaa a
 591

```

<210> 2374

<211> 167

<212> PRT

<213> Homo sapiens

<400> 2374

```

Met Pro Asp Ser Ser His Asp Val Lys Val Leu Thr Ser Lys Thr Ser
  1              5              10              15
Ala Val Glu Met Thr Gln Ala Val Leu Asn Thr Gln Leu Ser Ser Glu
          20              25              30
Asn Val Thr Lys Val Glu Gln Asn Ser Pro Ala Val Cys Glu Thr Ile
          35              40              45
Ser Val Pro Lys Ser Met Ser Thr Glu Glu Tyr Lys Ser Lys Ile Gln
          50              55              60
Asn Glu Asn Met Leu Leu Leu Ala Leu Leu Ser Gln Ala Arg Lys Thr
  65              70              75              80
Gln Lys Thr Val Leu Lys Asp Ala Asn Gln Thr Ile Gln Asp Ser Lys

```

```

      85              90              95
Pro Asp Ser Cys Glu Met Asn Pro Asn Thr Gln Met Thr Gly Asn Gln
      100              105              110
Leu Asn Leu Lys Asn Met Glu Thr Pro Ser Thr Ser Asn Val Ser Gly
      115              120              125
Arg Val Leu Asp Asn Ser Phe Cys Ser Gly Gln Glu Ser Ser Thr Lys
      130              135              140
Gly Met Pro Ala Lys Ser Asp Ser Ser Cys Ser Met Glu Val Leu Ala
      145              150              155              160
Thr Cys Leu Ser Leu Trp Lys
      165

```

<210> 2375

<211> 535

<212> DNA

<213> Homo sapiens

<400> 2375

```

ntggccatgt cggtgctcag cagcggcacc ctggacagtt accttgagcg tcacaaacaa
60
ctggacgcga tgccgatgct gcactttctt gccctcgacg aagaaaaccc cgccagcatc
120
tataactgcc tgcgcgcgcg cgggggcaat gcccaacgcg tacgcggggc gatcaccggc
180
gacatgtggg aaaacctcaa cgccacctgg ctggaaatgc gcagcatcgc cgccgggggc
240
ctggcccggc atggcatcag ccacttctgt gactgggtca agcagcgctc gcacctgttc
300
cgcgggggcaa cctcggggcac catcatgcgc aacgacgctt accggtttat tcgcctgggc
360
acgtttgtcg agcgcgcgga caacacctg cgctgtctgg atgcgcgcta cgaatgttt
420
ggtgaggagt cggaagaggt cagcgacctg tcggcacgcg ggtattacca gtggagcgcc
480
ctgctgcggg ccttgctcgc attcgaggcg tataccgaac tgtaccceaa cgcg
535

```

<210> 2376

<211> 178

<212> PRT

<213> Homo sapiens

<400> 2376

```

Xaa Ala Met Ser Leu Leu Ser Ser Gly Thr Leu Asp Ser Tyr Leu Glu
1      5      10      15
Arg His Lys Gln Leu Asp Ala Met Arg Met Leu His Phe Phe Ala Leu
20     25     30
Asp Glu Glu Asn Pro Ala Ser Ile Tyr Asn Cys Leu Arg Ala Ala Arg
35     40     45
Gly Asn Ala His Ala Val Arg Gly Arg Ile Thr Ala Asp Met Trp Glu
50     55     60
Asn Leu Asn Ala Thr Trp Leu Glu Met Arg Ser Ile Ala Ala Gly Gly
65     70     75     80
Leu Ala Arg His Gly Ile Ser His Phe Cys Asp Trp Val Lys Gln Arg

```

	85		90		95
Ser His Leu Phe Arg Gly Ala Thr Ser Gly Thr Ile Met Arg Asn Asp					
	100		105		110
Ala Tyr Arg Phe Ile Arg Leu Gly Thr Phe Val Glu Arg Ala Asp Asn					
	115		120		125
Thr Leu Arg Leu Leu Asp Ala Arg Tyr Glu Met Phe Gly Glu Glu Ser					
	130		135		140
Glu Glu Val Ser Asp Leu Ser Ala Arg Gly Tyr Tyr Gln Trp Ser Ala					
	145		150		155
Leu Leu Arg Ala Leu Ser Ser Phe Glu Ala Tyr Thr Glu Leu Tyr Pro					
	165		170		175
Asn Ala					

<210> 2377

<211> 622

<212> DNA

<213> Homo sapiens

<400> 2377

acgcgtgaag ggttgaggct tcagaagtgg tagggaagaa cagaagctcc cttctgaggg
 60
 agcaccaccagg agatgaaagg aaccaatcct ggggtgctcct gcaccaggct tatcaacccc
 120
 tgacagacaa atgaaaaact tctgtgatgg tgggacatga aaaaatatatt cacccttctg
 180
 ataaaaatgga accagcagat agaagtagga atttttctgt taggtgaaat gtttttaaaa
 240
 atatgtatatac aggaaaaagc ataaaaacagt attgactggc aaacatagaa ctggaatgta
 300
 aatataatgt tctttgcctt gaatgattta agtggcatga taaaactcat gccacagact
 360
 gggtaagaca agaatcttaa tccactctaa aaagaagaaa agcatagtaa aattctcctt
 420
 agagttagaa ttattaatag ttctatctta ctattttaatt taatcatagt taatgatgag
 480
 aatttcttaa atttaaaact tctgatgatg ctaaatgtgc atttctcatg attccttaaa
 540
 acaatttttg taaattctat tcttaggacc ttctgctttc agaaaaatta atgtcttgta
 600
 ttcttcgtat tggaggagat ct
 622

<210> 2378

<211> 109

<212> PRT

<213> Homo sapiens

<400> 2378

Met Ser Phe Ile Met Pro Leu Lys Ser Phe Arg Ala Lys Asn Ile Ile					
	1		5		10
Phe Thr Phe Glu Phe Tyr Val Cys Gln Ser Ile Leu Phe Tyr Ala Phe					
	20		25		30
Ser Cys Ile His Ile Phe Lys Asn Ile Ser Pro Asn Arg Lys Ile Pro					

```

          35              40              45
Thr Ser Ile Cys Trp Phe His Phe Ile Arg Arg Val Lys Tyr Phe Phe
  50              55              60
Met Ser His His His Arg Ser Phe Pro Phe Val Cys Gln Gly Leu Ile
  65              70              75
Ser Leu Val Gln Asp His Pro Gly Leu Val Pro Phe Ile Ser Trp Val
          85              90              95
Leu Pro Gln Lys Gly Ala Ser Val Leu Pro Tyr His Phe
          100              105

```

<210> 2379

<211> 342

<212> DNA

<213> Homo sapiens

<400> 2379

```

tcatgacctg gagacttcgg aaactcaaca agactgcagg gcacccaggg gcaccagccc
  60
cggtcaccgc agaggatcag tgcactttgc catctggcag atcaactcat ggcacaactg
  120
ggaaacataa cattcacgct tgtgaaccga gacgccatac cccagcgggtg ccgagagcaa
  180
cagtgctctgt caggtctggg cagatgaggg cctccaggac acgaggactc actcgtctac
  240
cctgccactc gggcagctgc tcgccactcc cctcctggag ggcaggacgg acaccacaca
  300
cacacacaag caggggaagct gtgcagcagt ggggagaaag ca
  342

```

<210> 2380

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2380

```

Met Thr Trp Arg Leu Arg Lys Leu Asn Lys Thr Ala Gly His Pro Gly
  1              5              10              15
Ala Pro Ala Pro Val Thr Ala Glu Asp Gln Cys Thr Leu Pro Ser Gly
          20              25              30
Arg Ser Thr His Gly Thr Thr Gly Lys His Asn Ile His Ala Cys Glu
          35              40              45
Pro Arg Arg His Thr Pro Ala Val Pro Arg Ala Thr Val Leu Cys Arg
          50              55              60
Ser Gly Gln Met Arg Ala Ser Arg Thr Arg Gly Leu Thr Arg Ser Pro
  65              70              75              80
Cys Pro Leu Gly Ser Cys Ser Pro Leu Pro Ser Trp Arg Ala Gly Arg
          85              90              95
Thr Pro His Thr His Thr Ser Arg Glu Ala Val Gln Gln Trp Gly Glu
          100              105              110
Ser

```

<210> 2381

<211> 434

<212> DNA

<213> Homo sapiens

<400> 2381

gtgcaccctg gccatatgga cgccagcgac gtcggcgctct tgcgtgacgt ggaaccgatc
 60
 ggcccaagta gagagatgga ttttgaatgg tgacgatgta cccgccgcag caagtggatg
 120
 ccgtcctctt tgacatggac ggaaccctgc tcaacacctt gccggcctgg tgcgtggcat
 180
 ctgagcatct gtggggcact tctctggctg acgctgacag cgccaagggt gacgggggca
 240
 ccgtcgacga cgctgttgag ctgtatctgc gagaccacc tcaggcagat cccagggcca
 300
 ccatacgagc tttcatggac atccttgacg ccaacctggc tggccacacc gagccgatgc
 360
 ccggagctga ccgctcgtg aagaggctgt caggtcatgt acccatcgct gtggtgtcga
 420
 attccccgac gcgt
 434

<210> 2382

<211> 116

<212> PRT

<213> Homo sapiens

<400> 2382

Met	Val	Thr	Met	Tyr	Pro	Pro	Gln	Gln	Val	Asp	Ala	Val	Leu	Phe	Asp
1				5					10					15	
Met	Asp	Gly	Thr	Leu	Leu	Asn	Thr	Leu	Pro	Ala	Trp	Cys	Val	Ala	Ser
			20					25					30		
Glu	His	Leu	Trp	Gly	Thr	Ser	Leu	Ala	Asp	Ala	Asp	Ser	Ala	Lys	Val
		35					40					45			
Asp	Gly	Gly	Thr	Val	Asp	Asp	Val	Val	Glu	Leu	Tyr	Leu	Arg	Asp	His
	50					55					60				
Pro	Gln	Ala	Asp	Pro	Gln	Ala	Thr	Ile	Glu	Arg	Phe	Met	Asp	Ile	Leu
65					70					75					80
Asp	Ala	Asn	Leu	Ala	Gly	His	Thr	Glu	Pro	Met	Pro	Gly	Ala	Asp	Arg
			85						90					95	
Leu	Val	Lys	Arg	Leu	Ser	Gly	His	Val	Pro	Ile	Ala	Val	Val	Ser	Asn
			100					105						110	
Ser	Pro	Thr	Arg												
			115												

<210> 2383

<211> 393

<212> DNA

<213> Homo sapiens

<400> 2383

acgcgtgcgt tcagatgagc gccggacgaa actcctcggc cgcttcggca ggcattggatt
 60
 catgtcggca cgggcctttg aacaggatcg ccgtcgcgtg gctatccgcc gcgggtgggg
 120

cagaaaaacgc ccactctccc ttccccaggc gccggccgctc gagtcgtcta cgcaacgcac
 180
 gtctacatag gtgacttttt cataccccca ctttcgtact cggatgggct cggcgtgctc
 240
 gatgtcggca cgaaaaatta aatgcactga atgcgggttg tcgcacagga tgcattctgt
 300
 ctttcttgat gccaccacc ttgttacata ttctgccatg caaaacacct tgtgattttt
 360
 ggccggagtgc aacatggtat gtgtatgcc ctg
 393

<210> 2384

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2384

Met	Leu	His	Ser	Ala	Lys	Asn	His	Lys	Val	Phe	Cys	Met	Ala	Glu	Tyr
1			5					10					15		
Val	Thr	Arg	Trp	Val	Ala	Ser	Arg	Lys	Thr	Arg	Cys	Ile	Leu	Cys	Asp
		20					25					30			
Asn	Pro	His	Ser	Val	His	Leu	Ile	Phe	Arg	Ala	Asp	Ile	Glu	His	Ala
		35				40					45				
Glu	Pro	Ile	Arg	Val	Arg	Lys	Trp	Gly	Tyr	Glu	Lys	Val	Thr	Tyr	Val
	50				55					60					
Asp	Val	Arg	Cys	Val	Asp	Asp	Ser	Thr	Ala	Gly	Ala	Trp	Gly	Arg	Glu
65				70				75						80	
Ser	Gly	Arg	Phe	Leu	Pro	His	Pro	Arg	Arg	Ile	Ala	Thr	Arg	Arg	Arg
		85						90					95		
Ser	Cys	Ser	Lys	Ala	Arg	Ala	Asp	Met	Asn	Pro	Cys	Leu	Pro	Lys	Arg
		100					105					110			
Pro	Arg	Ser	Phe	Val	Arg	Arg	Ser	Ser	Glu	Arg	Thr	Arg			
	115					120					125				

<210> 2385

<211> 347

<212> DNA

<213> Homo sapiens

<400> 2385

acgcgttccc aaagtaggat ggctgggata gagggaaagg acatctttca ggcttggtat
 60
 gcactgtgct gtggactctt gttgtggggt cctaggtctg cccagcattt tggggttcac
 120
 ccggtgacct totacgggtt tccatgcccc cagcaccacg tccatcatca tttctggggt
 180
 cccctcacct cagagagcct gcttcctatg actgcgtggg ccagctggag aaggacgacc
 240
 caagaccctt caagtctctg tgtcctgacc ccaagcatag gcctgagtgc tcctgggggc
 300
 caagggcctt tacgcactac tctctggggc ccaactgtctg cactctt
 347

<210> 2386

<211> 109
 <212> PRT
 <213> Homo sapiens

<400> 2386
 Met Ala Gly Ile Glu Gly Lys Asp Ile Phe Gln Ala Cys Tyr Ala Leu
 1 5 10 15
 Cys Cys Gly Leu Leu Trp Gly Pro Arg Ser Ala Gln His Phe Gly
 20 25 30
 Val His Pro Val Thr Leu Tyr Gly Phe Pro Cys Pro Gln His His Val
 35 40 45
 His His His Phe Trp Gly Pro Leu Thr Ser Glu Ser Leu Leu Pro Met
 50 55 60
 Thr Ala Trp Ala Ser Trp Arg Arg Thr Thr Gln Asp Pro Ser Ser Phe
 65 70 75 80
 Cys Val Leu Thr Pro Ser Ile Gly Leu Ser Ala Pro Gly Ala Gln Gly
 85 90 95
 Pro Leu Arg Thr Thr Leu Trp Gly Pro Leu Ser Ala Leu
 100 105

<210> 2387
 <211> 715
 <212> DNA
 <213> Homo sapiens

<400> 2387
 ncggcgcac ttcacctac ggaggggaga taatgagatc aattagaggc gccgtcacgc
 60
 cgccggagac agctgccgcc gcatagtaat caccgcggg ctgggtgcgc gggggctccc
 120
 cgctacctgc gcgcctgctg ctcccaccac gcggcaccga cccgggcgcg cccccggccc
 180
 ctgtccgcag cccacagcca caccgcgcac cctacacct cettgcgcct ctgctgggga
 240
 gctcaccccc tccactcgca cagtgcgctg cggcccgagg tgtgggaggt cccgggactt
 300
 ggggttgtgag tgccctgtgtg ggggtagggg cagggtgtccg cttgtgcgca tatgggcatg
 360
 agtgtacatg gcgtgtgcct ggagatgggc gaggtcaggc tggaaatgtgc cggcgtggca
 420
 cgtgtgtggg cccaaataga tgcgtgtgtg atcacatgtt gtgttcgtgt ttgcacctgc
 480
 tgtgcctgtg tgtccgtatt tgagtgtctt caggaatgtg ggtgggtgagt acccgatgtg
 540
 ggggtgcattc gcacttgtgc gtgtgtgtgt gtaggcgcgt gtgtgtgcgt gtgtgtgtta
 600
 ngggatacgt gtagatgtgc attagtgtga ctgtgtgtgc tcatgtgcct gtgcacgtgt
 660
 gtttgagggt tgtgtgcatg ggtagcgtct gtgagagcca tgtgtatatc tgcag
 715

<210> 2388
 <211> 58
 <212> PRT

<213> Homo sapiens

<400> 2388

```

Met Gly Met Ser Val His Gly Val Cys Leu Glu Met Gly Glu Cys Arg
 1             5             10             15
Leu Glu Cys Ala Gly Val Ala Arg Val Trp Ala Gln Ile Asp Ala Cys
          20             25             30
Val Ile Thr Cys Cys Val Arg Val Cys Thr Ser Cys Ala Cys Val Ser
          35             40             45
Val Phe Glu Cys Leu Gln Glu Cys Gly Trp
 50             55

```

<210> 2389

<211> 336

<212> DNA

<213> Homo sapiens

<400> 2389

```

ntcaccctgc cgccggaagg ttgctcgtac cgcctggcca tcgtcccat gaagaagtcg
60
tatccgggcc acgccaagcg cgtcatgttg ggtgtctggt cgtttttgcg acagttcatg
120
tataccaagt tcgttatcgt caccgacgac gatataacg cccgcgactg gaacgacgctg
180
atctggggcca tcaccacgcg catggacccc aagcgcgaca cgggtgatgat cgataaacg
240
ccgatcgact acctcgactt cgcctcgccg gtgtccggcc tgggttcgaa gatggggctc
300
gatccacgac acaaatggcc cggccacacc acccgn
336

```

<210> 2390

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2390

```

Xaa Thr Leu Pro Pro Glu Gly Cys Ser Tyr Arg Met Ala Ile Val Thr
 1             5             10             15
Met Lys Lys Ser Tyr Pro Gly His Ala Lys Arg Val Met Leu Gly Val
          20             25             30
Trp Ser Phe Leu Arg Gln Phe Met Tyr Thr Lys Phe Val Ile Val Thr
          35             40             45
Asp Asp Asp Ile Asn Ala Arg Asp Trp Asn Asp Val Ile Trp Ala Ile
          50             55             60
Thr Thr Arg Met Asp Pro Lys Arg Asp Thr Val Met Ile Asp Asn Thr
          65             70             75             80
Pro Ile Asp Tyr Leu Asp Phe Ala Ser Pro Val Ser Gly Leu Gly Ser
          85             90             95
Lys Met Gly Leu Asp Pro Thr His Lys Trp Pro Gly His Thr Thr Arg
          100             105             110

```

<210> 2391

<211> 388

<212> DNA

<213> Homo sapiens

<400> 2391

gtcgactaac ctgcgtacag cgcgccacct acgttttagtc gcgaagcgtg tcggctccat
 60
 gttcattccg gagctacacc atgaataaag tactacctga tccaccatc gatcccga
 120
 aagaccgcgt cgctttcaac cgcgccatcg accattacct gcttaccag ggcttccat
 180
 gcgtcaacga agacctgagt ttccaagacg ccctgctcta caccgccagc ctgctcgaca
 240
 gtgcctctgc caccggcgtg gattgcgggtg agctgctgca aagccctgaa cgggcggaaga
 300
 tcctggccgt gtggcatttg ctggaaattg caaaaaccac cgtagatcgc ttccccatcg
 360
 agtgcctgac cgcaccaaag ccctgcct
 388

<210> 2392

<211> 102

<212> PRT

<213> Homo sapiens

<400> 2392

Met	Asn	Lys	Val	Leu	Pro	Asp	Pro	Pro	Ile	Asp	Pro	Ala	Lys	Asp	Arg
1				5				10					15		
Val	Ala	Phe	Asn	Arg	Ala	Ile	Asp	His	Tyr	Leu	Pro	Thr	Gln	Gly	Phe
								25					30		
His	Cys	Val	Asn	Glu	Asp	Leu	Ser	Phe	Glu	Asp	Ala	Leu	Leu	Tyr	Thr
								40					45		
Ala	Ser	Leu	Leu	Asp	Ser	Ala	Ser	Ala	Thr	Ala	Leu	Asp	Cys	Gly	Glu
								55				60			
Leu	Leu	Gln	Ser	Pro	Glu	Arg	Ala	Lys	Ile	Leu	Ala	Val	Trp	His	Leu
65						70				75				80	
Leu	Glu	Ile	Ala	Lys	Thr	Thr	Val	Asp	Arg	Phe	Pro	Ile	Glu	Cys	Leu
						85				90				95	
Thr	Ala	Pro	Lys	Pro	Cys										
						100									

<210> 2393

<211> 411

<212> DNA

<213> Homo sapiens

<400> 2393

aaactgtcta ccgaggacca ggccgagcag gtagagattg tgaagcgcctc tgagtcggcg
 60
 atggtcaccg accccatcac tgcgcgcccg gatatgacca tcggggaagt agacgcgctg
 120
 tgcgcccgct tcgcgatctc cggcctgcgg gtggtagacg aggcgcggac cctgatgggg
 180
 atttgacca ccgcgatata gcgcttcgag cctgactttg accgcaaggt cagcgaggct
 240

atgacggcta tgccgcttgt tgttgccgcg gaggggtgat ctaagaagga agccctcgaa
 300
 ctgctctcgg ccaataaggt ggaaaagctg cccatcgctg atgctgataa taagctcacc
 360
 ggccttgatta ccgtcaagga ctttgtcaag accgagcagt accccaacgc g
 411

<210> 2394

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2394

Asn	Leu	Ser	Thr	Glu	Asp	Gln	Ala	Glu	Gln	Val	Glu	Ile	Val	Lys	Arg
1				5					10					15	
Ser	Glu	Ser	Gly	Met	Val	Thr	Asp	Pro	Ile	Thr	Ala	Arg	Pro	Asp	Met
			20					25					30		
Thr	Ile	Gly	Glu	Val	Asp	Ala	Leu	Cys	Ala	Arg	Phe	Arg	Ile	Ser	Gly
		35					40					45			
Leu	Pro	Val	Val	Asp	Glu	Asp	Gly	Thr	Leu	Met	Gly	Ile	Cys	Thr	Thr
	50					55					60				
Arg	Asp	Met	Arg	Phe	Glu	Pro	Asp	Phe	Asp	Arg	Lys	Val	Ser	Glu	Val
	65				70				75					80	
Met	Thr	Ala	Met	Pro	Leu	Val	Val	Ala	Arg	Glu	Gly	Val	Ser	Lys	Lys
			85						90					95	
Glu	Ala	Leu	Glu	Leu	Leu	Ser	Ala	Asn	Lys	Val	Glu	Lys	Leu	Pro	Ile
		100						105					110		
Val	Asp	Ala	Asp	Asn	Lys	Leu	Thr	Gly	Leu	Ile	Thr	Val	Lys	Asp	Phe
		115				120						125			
Val	Lys	Thr	Glu	Gln	Tyr	Pro	Asn	Ala							
	130					135									

<210> 2395

<211> 362

<212> DNA

<213> Homo sapiens

<400> 2395

aagcttttcag aggagtttgc taaagtgtta aggatttgca tattttcaac tttagtcata
 60
 tctaagtggcc ccaataaaac agcgcgccgc attggggggct ggcttttcac aacaactaac
 120
 ttagcaatat taatctgacc ttttcctggg gattgggcat ttagtaataa tgcggggcca
 180
 atatcatcat actttccaaa ttttttggat tttttagaca tcaactgaag ttgtgaccat
 240
 ttactgtctt tgtcttgatg gcaatctaaa caaacatctc ttgtattaag ttgttcactt
 300
 acccaaggat taggcactct aaaggcatga tcgctcgat catcgactcc catgtaacgc
 360
 gt
 362

<210> 2396

<211> 117

<212> PRT

<213> Homo sapiens

<400> 2396

```

Met Gly Val Asp Asp Arg Arg Asp His Ala Phe Arg Val Pro Asn Pro
 1             5             10             15
Trp Val Ser Glu Gln Leu Asn Thr Arg Asp Val Cys Leu Asp Cys His
             20             25             30
Gln Asp Lys Asp Ser Lys Trp Ser Gln Leu Gln Leu Met Ser Lys Lys
 35             40             45
Ser Lys Ile Phe Gly Lys Tyr Asp Asp Ile Gly Pro Ala Leu Leu Leu
 50             55             60
Asn Ala Gln Ser Pro Gly Lys Gly Gln Ile Asn Ile Ala Lys Leu Val
 65             70             75             80
Val Asp Glu Ser Gln Pro Pro Met Arg Arg Ala Val Leu Leu Gly His
             85             90             95
Leu Asp Met Thr Lys Val Glu Asn Met Gln Ile Leu Asn Thr Leu Ala
 100             105             110
Asn Ser Ser Glu Ser
 115

```

<210> 2397

<211> 449

<212> DNA

<213> Homo sapiens

<400> 2397

```

nacagcacac tccgcctect ccgacgatca tagctttcac gtcggacatg atcccccgcc
 60
tagtggtacta ctggtccttc tccgtccctc cctacgggga ccacacttcc tacaccatgg
 120
aagggtatcat caacaacact ctctccatct tcaaagtcgc agacttcaaa aacaaaagca
 180
agggaaaccc gtactctgac ctgggtaacc ataccacatg caggtatcgt gatttccgat
 240
acccacctgg acacccccag gagtataaac acaacatcta ctattggcat gtgattgcag
 300
ccaagctggc ttttatcatt gtcattggag acgtcatcta ctctgtgaaa tttttcattt
 360
catatgcaat tcccgatgta tcaaagcgca caaagagcaa gatccagaga gaaaaatacc
 420
taacccaaaa gcttcttcat gagaatcac
 449

```

<210> 2398

<211> 76

<212> PRT

<213> Homo sapiens

<400> 2398

```

Cys Thr Thr Gly Pro Ser Pro Ser Leu Pro Thr Gly Thr Thr Leu Pro
 1             5             10             15
Thr Pro Trp Lys Gly Thr Ser Thr Thr Leu Ser Pro Ser Ser Lys Ser

```

```

                20                25                30
Gln Thr Ser Lys Thr Lys Ala Arg Glu Thr Arg Thr Leu Thr Trp Val
      35                40                45
Thr Ile Pro His Ala Gly Ile Val Ile Ser Asp Thr His Leu Asp Thr
      50                55                60
Pro Arg Ser Ile Asn Thr Thr Ser Thr Ile Gly Met
      65                70                75

```

<210> 2399
 <211> 344
 <212> DNA
 <213> Homo sapiens

```

<400> 2399
acgcgtcatg cttcacgaaa cgggtcacgc gtttcattac caagcagctg gcaaacacaa
60
cttggtatttc gagcgggttg cgccagtcga gatcatggag ttctgtggcct actgcttgca
120
gtttctgacg atcgagcgcc tggccatgtc aggggaactt tcgggtaaaag aacaggaact
180
agtcaaaccc tttgtcggtc cggccaggct tggagggggt cgaaaacctt caacgccaca
240
aaacgggttcc agcactgggt ttataaacag cctaaaaatcc cgacaagtaa agaactcgat
300
accgtatggc ttgagatgcg acacacgctc ggggtggatt ggctc
344

```

<210> 2400
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 2400
Met Leu His Glu Thr Gly His Ala Leu His Tyr Gln Ala Ala Gly Lys
1      5      10      15
His Asn Leu Tyr Phe Glu Arg Val Ala Pro Val Glu Ile Met Glu Phe
20     25     30
Val Ala Tyr Cys Leu Gln Phe Leu Thr Ile Glu Arg Leu Ala Met Ser
35     40     45
Gly Glu Leu Ser Gly Lys Glu Gln Glu Leu Val Lys Pro Phe Ala Gly
50     55     60
Pro Ala Arg Leu Gly Gly Val Arg Lys Pro Thr Thr Pro Gln Asn Gly
65     70     75     80
Ser Ser Thr Gly Phe Ile Asn Ser Leu Lys Ser Arg Gln Val Lys Asn
85     90     95
Ser Ile Pro Tyr Gly Leu Arg Cys Asp Thr Arg Ser Gly Trp Ile Gly
100    105    110

```

<210> 2401
 <211> 479
 <212> DNA
 <213> Homo sapiens

<400> 2401

nntaccgagg taaaactcga tagcctcggt gtcaccgacc agatgcgctc tgggcgctgc
 60
 tggatgtttg ccgcgctcaa cgtattccgc caccgcgcgg ccaaggagct caacatcgat
 120
 gacttttagt tttcctttac ctacctcgag tacttcgaca aactagagcg cgccaacttc
 180
 gcgctcaacc aactgctgga tctcaccgaa gacggcaccg actgggatga ccgcgacgtg
 240
 gctacttccc tcgagctcac aggcgacgac ggcggctggt ggtcattttt caccaacctc
 300
 gtggacaagt acggcgagct cccggccgag gtcctgcctg aggtgcactc gtccggccac
 360
 accgaccaga tgaatcgaga tatcgccacc atcatccgcc gcgcgcgcga ccgtgcgggtg
 420
 gaagcgaggg gggatcgagg gggcatcgct aagcaagccc gccccgatat ccaacgcgt
 479

<210> 2402

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2402

Xaa	Thr	Glu	Val	Lys	Leu	Asp	Ser	Leu	Gly	Val	Thr	Asp	Gln	Met	Arg
1				5					10				15		
Ser	Gly	Arg	Cys	Trp	Met	Phe	Ala	Ala	Leu	Asn	Val	Phe	Arg	His	Arg
			20					25					30		
Ala	Ala	Lys	Glu	Leu	Asn	Ile	Asp	Asp	Phe	Glu	Phe	Ser	Phe	Thr	Tyr
		35					40					45			
Leu	Gln	Tyr	Phe	Asp	Lys	Leu	Glu	Arg	Ala	Asn	Phe	Ala	Leu	Asn	Gln
	50					55				60					
Leu	Leu	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Asp	Trp	Asp	Asp	Arg	Asp	Val
65				70					75				80		
Ala	Thr	Ser	Leu	Glu	Leu	Thr	Gly	Asp	Asp	Gly	Gly	Trp	Trp	Ser	Phe
			85				90						95		
Phe	Thr	Asn	Leu	Val	Asp	Lys	Tyr	Gly	Ala	Val	Pro	Ala	Glu	Val	Met
	115					120				125					
Ala	Thr	Ile	Ile	Arg	Arg	Ala	Ala	His	Arg	Ala	Val	Glu	Gly	Glu	Gly
	130				135					140					
Asp	Arg	Gly	Gly	Ile	Val	Lys	Gln	Ala	Arg	Pro	Asp	Ile	Gln	Arg	
145				150						155					

<210> 2403

<211> 387

<212> DNA

<213> Homo sapiens

<400> 2403

ntcgatgaag gcgataaccc gctggactcg tctgcggttc acccggaagc ctaccgctg
 60
 gtgcagcgta ttgccgccga gaccggccgt gatatccgtt cgctgatcgg tgacgccgcg
 120

ttctctaagc gcctggaccc gaagaagtac accgacgaaa ccttcgggtgt gccgaccatc
 180
 accgacatcc tgcaagagct ggaaaaacct ggccgcgacc cgcgccccga gttcaagacc
 240
 gccgagttcc aggacggtgt tgaagacctc aaggacctgc agccgggcat gatccctgaa
 300
 ggcggtgtca ccaacgtgac caactttggc gcctttgtgg atatcggcgt gcatcaggac
 360
 gggttggtgc acatctctgc actttcg
 387

<210> 2404
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 2404
 Xaa Met Asn Gly Asp Asn Pro Leu Asp Ser Ser Ala Val His Pro Glu
 1 5 10 15
 Ala Tyr Pro Leu Val Gln Arg Ile Ala Ala Glu Thr Gly Arg Asp Ile
 20 25 30
 Arg Ser Leu Ile Gly Asp Ala Ala Phe Leu Lys Arg Leu Asp Pro Lys
 35 40 45
 Lys Tyr Thr Asp Glu Thr Phe Gly Val Pro Thr Ile Thr Asp Ile Leu
 50 55 60
 Gln Glu Leu Glu Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr
 65 70 75 80
 Ala Glu Phe Gln Asp Gly Val Glu Asp Leu Lys Asp Leu Gln Pro Gly
 85 90 95
 Met Ile Leu Glu Gly Val Val Thr Asn Val Thr Asn Phe Gly Ala Phe
 100 105 110
 Val Asp Ile Gly Val His Gln Asp Gly Leu Val His Ile Ser Ala Leu
 115 120 125
 Ser

<210> 2405
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 2405
 ttgcaagtaa catcaaaagt catctacaga agcaaaagac aaaaaggccc ctccacctgc
 60
 aaattaaatg gaataatttg ctttatgaga agctcaccat tgggggtcatt cttatttttt
 120
 ctcaactcac atttcactac aaaccaagga aagctccctc atggaccgac atctggtgag
 180
 ccttcacttc tccccggca atgcctggcc acctgacacc tggcctccct cctctttcca
 240
 gcaatcctgg taccaacgaa tggctcacca ccacccaccc caatgcccg accgcagacc
 300
 tgcattcctc ccatctcaca gccccaaatc caaacgttta ttcattctac ctcccactct
 360

actcctcagc aatttcttcc accgtagact ctgggtaatt ggactgactg aagcccaggg
 420
 gtcagtttct gtcctaagag cgtccaggt ggctgcaccc tgtgcccaga gccaggcccc
 480
 ctgctatagg ctgctgcac tccccctgca ggtgctgggg acaccgcaac cctcctctg
 540
 gggacaccta ctgaccttg caggccctcg ggggtcactt ctcccaggaa gccgcctctg
 600
 ggtgaggtaa tatccctcta tcacagcatt ggccacacca cattgcaaac gctgctgggg
 660
 tccactgtct tcaccaatta caccatgagc tccacagact ccaggacctat ggcttctacc
 720
 tctcagttcc cagtgttagc tatggggccc agcacacagg gaacagcagt tcaattaccc
 780
 agttactga agggcagacc tgggatcata caggggagcaa ggaagcttga gcccttacc
 840
 gagaagggga agaacgcgt
 859

<210> 2406

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2406

Met Asp Arg His Leu Val Ser Leu His Leu Ser Pro Gly Asn Ala Trp
 1 5 10 15
 Pro Pro Asp Thr Trp Pro Pro Ser Ser Phe Gln Gln Ser Trp Tyr Gln
 20 25 30
 Arg Met Ala His His His Pro Pro Gln Cys Pro Asp Arg Arg Pro Ala
 35 40 45
 Phe Leu Pro Ser His Ser Pro Lys Ser Lys Pro Leu Phe Ile Leu Pro
 50 55 60
 Pro Ile Leu Leu Leu Thr Asn Phe Phe His Arg Arg Leu Trp Leu Ile
 65 70 75 80
 Gly Leu Thr Glu Ala Gln Gly Ser Val Ser Val Leu Arg Ala Leu Gln
 85 90 95
 Val Ala Ala Pro Cys Ala Gln Ser Gln Ala Pro Cys Tyr Arg Leu Ala
 100 105 110
 Ala Leu Pro Leu Gln Val Leu Gly Thr Pro Gln Pro Ser Ser Trp Gly
 115 120 125
 His Leu Leu Ala Phe Ala Gly Pro Arg Gly Ser Leu Leu Pro Gly Ser
 130 135 140
 Arg Leu Trp Val Arg
 145

<210> 2407

<211> 303

<212> DNA

<213> Homo sapiens

<400> 2407

nacgcgtggt ttatcttcag catggtgacg gcgattgggt tagccgttat ggctgcgggtc
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gtattcatcg agcaaggcca ggcacgtatc ccggtgcagt acgccaagcg gatggtgggg
 120
 cgccgaatgt ttggtggctc gacgacgtac attccgctca aggtaaacca atctggcgctt
 180
 atcccggtca tctttgcttc gtcgatccgt taccttcggg tgctctacgc aactttccgg
 240
 ccgcagacgt ccgcggcaaa gtggatcggt cactacttca cgcgcggtga ccatccggtg
 300
 tac
 303

<210> 2408

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2408

Xaa Ala Trp Phe Ile Phe Ser Met Val Ile Ala Ile Gly Leu Ala Val
 1 5 10 15
 Met Ala Ala Val Val Phe Ile Glu Gln Gly Gln Arg Arg Ile Pro Val
 20 25 30
 Gln Tyr Ala Lys Arg Met Val Gly Arg Arg Met Phe Gly Gly Ser Thr
 35 40 45
 Thr Tyr Ile Pro Leu Lys Val Asn Gln Ser Gly Val Ile Pro Val Ile
 50 55 60
 Phe Ala Ser Ser Ile Leu Tyr Leu Pro Val Leu Tyr Ala Thr Phe Arg
 65 70 75 80
 Pro Gln Thr Ser Ala Ala Lys Trp Ile Gly His Tyr Phe Thr Arg Gly
 85 90 95
 Asp His Pro Val Tyr
 100

<210> 2409

<211> 322

<212> DNA

<213> Homo sapiens

<400> 2409

ccatggtttc aagcccccat tgtgtcagcc cagagagcaa ctggagaccc tctgacacca
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 120
 cttccggcca aatgacctc cctaggctac caagacctg gcctaagggg agccgaggtc
 180
 tcggcccgac tgcagacgcc cgcaccctga ctccagatgc ctccagggca tccagtgagg
 240
 ccctgagggg cctgctgtgg etttgttctt gttggetggg ctgggggtct gacctggtga
 300
 gggacatgag tgtcagtgtg gg
 322

<210> 2410

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2410

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Met Val Ser Ser Pro His Cys Val Ser Pro Glu Ser Asn Trp Arg Pro
 1           5           10           15
Ser Asp Thr Thr Ser Arg Pro Asn Arg Arg Gly Ser Arg Asn Ser Asp
           20           25           30
Cys Gly Asn Cys Leu Gln Phe Ser Ser Gly Gln Met Thr Leu Pro Arg
           35           40           45
Leu Pro Arg Pro Trp Pro Lys Gly Ser Arg Gly Leu Gly Pro Thr Ala
           50           55           60
Asp Ala Arg Thr Leu Thr Pro Asp Ala Ser Glu Ala Ser Arg Trp Ala
           65           70           75           80
Leu Arg Gly Leu Leu Trp Leu Cys Ser Cys Trp Leu Gly Trp Gly Ser
           85           90           95
Asp Leu Val Arg Asp Met Ser Val Ser Val
           100           105

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<210> 2411

<211> 371

<212> DNA

<213> Homo sapiens

<400> 2411

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ccatgggctg ggtgctggag acacgagatc aggcaggccc tgccctggg gctcattcta
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gggtctcgcg cagacagggga gacagagggga gctgtgagag ccctgaggct gaggtagcttt
120
ctgggggaagc accatcccta gggacctcgc cgttcgggtca gtggccgctg ctgtcgggtg
180
gcagagcaga ggctggggcg agagtgggtca gcaggcctgc tggtaggcagc ttgtgcagga
240
agggaggatg gaggttggtc tgtggctggc aagaggggtgg catgcacgtc gctgaaaggc
300
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360
ggggggctgc g
371

```

<210> 2412

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2412

```

Met Gly Trp Val Leu Glu Thr Arg Asp Gln Ala Gly Pro Ala Pro Gly
 1           5           10           15
Ala His Ser Arg Val Cys Gly Arg Gln Gly Asp Arg Gly Ser Cys Glu
           20           25           30
Ser Pro Glu Ala Glu Trp Leu Ser Gly Glu Ala Pro Ser Leu Gly Thr
           35           40           45
Ser Ala Phe Gly Gln Trp Pro Leu Leu Ser Val Cys Arg Ala Glu Ala
           50           55           60
Gly Ala Arg Val Val Ser Arg Pro Ala Gly Gly Ser Leu Cys Arg Lys

```

65		70		75		80									
Gly	Gly	Trp	Arg	Leu	Ala	Cys	Gly	Trp	Gln	Glu	Gly	Gly	Met	His	Val
			85					90					95		
Ala	Glu	Arg	Gln	Ala	Trp	Ala	Arg	Gly	Leu	Gly	Val	Gly	Thr	Pro	Glu
			100					105					110		
Glu	Thr	Val	Gln	Cys	Gly	Val	Gly	Gly	Ala	Ala					
		115					120								

<210> 2413
 <211> 784
 <212> DNA
 <213> Homo sapiens

<400> 2413
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 120
 taggctcact gaggaattgg ggttcttctt gaagagcatg gagcccttgg aggacctcca
 180
 cagcaggcag agagacggca gcctcctggg atctgattgc ccagcccccac ttacacagggt
 240
 ggctgagggt agctcttccc atggagtgca tccttctctga tcagcctgag gagagcaggg
 300
 ccccaccatc ctgcacctgg tgcagaaaaa cctgtgaag ctgcactaca gaaagacacc
 360
 accaggtggc aggcctggag attgcatgga gggccgccc cccccaacca attctttgat
 420
 aatagcacag tggtgaagag agggggccat aaaagactga atcctgttgc atgccaggct
 480
 ggctctgccc aacatatatg agactgcaag ttctgcccatt gtgggctgtg tacccacaag
 540
 ccacaggctc ctctgaacct gtgaatcagg tcttggggagc tattcgagca ggctggattt
 600
 tctctctgac ctgcggggac ctgagagtaa gttacagact tcatgacctt tcaccccaaa
 660
 acacttgagt atgtatcacc taagaacaag ggcatttctc tgtagaacca caatgcaatt
 720
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 780
 gcgt
 784

<210> 2414
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 2414
Met Lys Ser Val Thr Tyr Ser Gln Val Pro Arg Gly Arg Gly Glu Asn
1 5 10 15
Pro Ala Cys Ser Asn Ser Ser Gln Asp Leu Ile His Arg Phe Arg Gly
20 25 30
Thr Cys Gly Leu Trp Val His Ser Pro Gln Trp Gln Asn Leu Gln Ser

35	40	45
His Ile Cys Trp Ala Glu Pro Ala Trp His Glu Gln Gly Phe Ser Leu		
50	55	60
Leu Trp Pro Pro Leu Phe Asn Thr Val Leu Leu Ser Lys Asn Trp Leu		
65	70	75
Gly Gly Ala Gly Pro Pro Cys Asn Leu Gln Ala Cys His Leu Val Val		
85	90	95
Ser Phe Cys Ser Ala Ala Ser Gln Gly Phe Ser Ala Pro Gly Ala Gly		
100	105	110
Trp Trp Gly Pro Ala Leu Leu Arg Leu Ile Arg Lys Asp Ala Leu His		
115	120	125
Gly Lys Ser Ser Pro Gln Pro Pro Val		
130	135	

<210> 2415

<211> 2164

<212> DNA

<213> Homo sapiens

<400> 2415

ctcgtgccag cgctcctcgcg ggtctgaatg gaaggggtcga ggtcgtcgtc ggcggcgagc
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120
ccccccacc cgcgcgcgcg catggaggtg ctgcggcgct ctctcggtctt cgctgcggag
180
atcatggacg cctttgatcg ctggcccaca gacaaggagc tgggtggccca ggctaaagca
240
ctaggccggg agtaactgca cgcgcggcct ttgcgcgcgc gcctctcctg gagcgtccca
300
gagcgtgcct cgcctgcccc tggaggacgc ctggctgagg tgtgcgcggt gctgctgcgc
360
ctggggcgat agctggagat gatccggccc agcgtctacc gcaacgtggc cgtcagctg
420
cacatctccc tgcagtctga gcctgtgggt accgatgcgt tcttggcggt ggctggccac
480
atcttctctg caggcatcac gtggggcaag gtggtgtccc tgtatgcggt ggccgcgggg
540
ctggccgtgg actgtgtgag gcaggccca cctgccatgg tccacgcctt cgtggactgc
600
ctgggggagt tegtgcgcaa gacctggca acctggctgc ggagacgcgg cggatggact
660
gatgtctca agtgtgtggt cagcacagac cctggcctcc gctccactg cctggtggct
720
gcaactgca gcttcggccg ctctctgaag gctgccttct tctgtgtgct gccagagaga
780
tgagctgccc acctggcagt ggccgcagcc tggccctctg ggcccaacgc aggaggccct
840
cagcaccga acacatcttc ctctccccc cccgagcctg gagcactcta acctcggaga
900
ccccetaag cccgttcttc cgcagaccca ggccctccgg aagggtgagt ggggaggggc
960
tttctgagc ctggagctgg gctttggggc agcctgcgac cctccccgct tgtgtccctt
1020

ctctctgtgat ctctgtgttt tcccttttct ttctggggcc aggaagtcag ggtcaactcc
 1080
 caggcctcag gtgaaggggc ccagaacacc tgctctcacc tgagccccag gtgaaggggc
 1140
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 1200
 cctgagcccc tggtaagagg gcccggaaca cctgctctca cctgagcccc aggtgaaggg
 1260
 gcccggaaca cctgctctca cctgagcccc aggtgaaggg gcccggaaca cttgctctca
 1320
 cctgagcccc aggtgaaggg gcccggaac acctctcacc tgaacccggg ggtcccatcc
 1380
 caggaagaag ggccatctca ggacatgagt cctcaggggc cctgcacatt caatctgaag
 1440
 gtgaccctgg cctggctgaa gctggaagag ctgtggggac tcagccctga aacagagcgt
 1500
 aagggtcaca tgctggttgc ttaatccgtt tctggaggaa gagtatgaca ccacttgtg
 1560
 atgggggtcct tgtgcgttgg ggaccggggc cggggggctc caggccagca cacctaacc
 1620
 atggatgtgg aacctacggc cgagaaggaa tggtgcatga gtcggatccc agtccattgt
 1680
 cagtggaggg tgagggtgac cccatctgct atttttgtgc tcactcctcat acaaccattt
 1740
 ggggatgtgc ctattagggc tccgtaagaa ctcagatgcc tgggaagccc agccccctag
 1800
 gtgccccacc acacagcctt cccttgacgc ctacatttct aggcacatgt gaggcattt
 1860
 tcctggagcc ccgagccagc cctgtccctc cccagtgcag catggcactc aggagataca
 1920
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 1980
 tcccgccagc gcttcgtgct ggggtggggc atgtgccagg acaggagggg cccggcgga
 2040
 agccagcccc ggactcatcg tgacattgag atccactgg agggtagggg tggtataataa
 2100
 cttctccaaa cgataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 2160
 aaaa
 2164

<210> 2416

<211> 213

<212> PRT

<213> Homo sapiens

<400> 2416

Met	Glu	Val	Leu	Arg	Arg	Ser	Ser	Val	Phe	Ala	Ala	Glu	Ile	Met	Asp
1				5					10					15	
Ala	Phe	Asp	Arg	Trp	Pro	Thr	Asp	Lys	Glu	Leu	Val	Ala	Gln	Ala	Lys
			20					25					30		
Ala	Leu	Gly	Arg	Glu	Tyr	Val	His	Ala	Arg	Leu	Leu	Arg	Ala	Gly	Leu
		35					40					45			
Ser	Trp	Ser	Ala	Pro	Glu	Arg	Ala	Ser	Pro	Ala	Pro	Gly	Gly	Arg	Leu

50	55	60
Ala Glu Val Cys Ala Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Met		
65	70	75
Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Ser		80
	85	90
Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly		95
	100	105
His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr		110
	115	120
Ala Val Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro		125
	130	135
Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys		140
	145	150
Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu		155
	160	165
Lys Cys Val Val Ser Thr Asp Pro Gly Leu Arg Ser His Trp Leu Val		170
	175	180
Ala Ala Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Val		185
	190	195
Leu Leu Pro Glu Arg	200	205
210		

<210> 2417

<211> 615

<212> DNA

<213> Homo sapiens

<400> 2417

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nnagatctttt ggaatgggca gaactactaa atacagttaa tgcaccaaca agggtaagta
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120
cagttgttagt ttttcacact ttaaaaaagg ctttcaatta taaaatcttt ctccattatt
180
acgttttttc acaactgtga tccacgccac agttgcaaat aatcaacata gaaaaattaa
240
ataacataat tgatgaaaag ttagtttttc acaaaaatac gaaaaatttc atcacctaga
300
gaggaaaatg ttatgacaac ctatttcgat aaaattgaaa aaatctcctt tgaggggagaa
360
aaatccacaa atccttttgc ttccaacat tatgatgcta atcaagtaat tttaggtaaa
420
actatggctg aacatttaacg cttaacgggtg tgttattggc ataccttttg ctggaatggg
480
aatgatatgt ttgggctagg ttctttggaa cgaagtggc agaaaaattc aaatttgctt
540
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600
tattattggt ttcat
615

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<210> 2418

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2418

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Met Thr Thr Tyr Phe Asp Lys Ile Glu Lys Ile Ser Phe Glu Gly Glu
 1              5              10              15
Lys Ser Thr Asn Pro Phe Ala Phe Lys His Tyr Asp Ala Asn Gln Val
              20              25              30
Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Thr Val Cys Tyr
              35              40              45
Trp His Thr Phe Cys Trp Asn Gly Asn Asp Met Phe Gly Leu Gly Ser
              50              55              60
Leu Glu Arg Ser Trp Gln Lys Asn Ser Asn Leu Leu Ala Gly Ala Glu
65              70              75              80
Gln Lys Ala Asp Ile Ala Phe Glu Phe Leu Asn Lys Leu Gly Val Pro
              85              90              95
Tyr Tyr Cys Phe His
              100

```

<210> 2419

<211> 318

<212> DNA

<213> Homo sapiens

<400> 2419

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aaattttcag aagtcctggt gttgcgcggt caaacagggg cgcaggaggg acgaccgcct
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ccccgtgacg ctgcttcttc ttctgcctg cagctgaggg gtctgttttg tgctgcttcc
120
gctccttctc cacgtacaca gggggcagct tagcctctgg gatgggagtg gcttcataca
180
tgagacacat gcccgagtcg aggtagatgt cgctgtcgtc ctgcggcgagg gtgggtggggg
240
tccagaacgg catgacttct gtctgcccac cgacatcttc gtagacatac tccatgttgt
300
aggcatcccc tcacgcgt
318

```

<210> 2420

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2420

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Met Glu Tyr Val Tyr Glu Asp Val Asp Gly Gln Thr Glu Val Met Pro
 1              5              10              15
Phe Trp Thr Pro Pro Thr Pro Pro Gln Asp Asp Ser Asp Ile Tyr Leu
              20              25              30
Asp Ser Gly Met Cys Leu Met Tyr Glu Ala Thr Pro Ile Pro Glu Ala
              35              40              45
Lys Leu Pro Pro Val Tyr Val Arg Lys Glu Arg Lys Arg His Lys Thr
              50              55              60
Asp Pro Ser Ala Ala Gly Arg Lys Lys Lys Gln Arg His Gly Glu Ala
65              70              75              80
Val Val Pro Pro Arg Ser Leu Phe Asp Arg Ala Thr Pro Gly Leu Leu

```

85 90 95

Lys Ile

<210> 2421
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 2421
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 tactggttgt ttgacagtgc agggccttggt cacagacgtg agccacaggg cagcacaacg
 120
 ctgtcgcaag tctgagtagg gattatcatg acggatacaa cttcagcccc gcgttacgcg
 180
 ctgcgtgggc tacagcttat tggctggcgt gacatgcaac acgcgctgga tttcctgttc
 240
 gcggacgggc agatgaaatc gggcacgctg gtggccatca acgcagaaaa gatgctggcg
 300
 gttgaagata atgcggaagt gaaaagcctg attgaagccg cggagtgttaa ataccgggcc
 360
 ggtattagcg tagtgcgcttc aattcgtaaa aagttccccc acgtggagtg gtgctcgcaa
 420

<210> 2422
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 2422
 Met Thr Asp Thr Thr Ser Ala Pro Arg Tyr Ala Leu Arg Gly Leu Gln
 1 5 10 15
 Leu Ile Gly Trp Arg Asp Met Gln His Ala Leu Asp Phe Leu Phe Ala
 20 25 30
 Asp Gly Gln Met Lys Ser Gly Thr Leu Val Ala Ile Asn Ala Glu Lys
 35 40 45
 Met Leu Ala Val Glu Asp Asn Ala Glu Val Lys Ser Leu Ile Glu Ala
 50 55 60
 Ala Glu Phe Lys Tyr Pro Ala Gly Ile Ser Val Val Arg Ser Ile Arg
 65 70 75 80
 Lys Lys Phe Pro His Ala Gly Val Cys Ser Arg
 85 90

<210> 2423
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 2423
 tgatcaagtc ggaggattcg gcaggggcgca gccatgaacg agaaggcgtc cgtctccaag
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 gagctcaacg ccaagcacia gaagatattg gaaggtcttc tacggcatcc tgagaataga
 120

gaatgcgcag actgcaagtc aaagggctct cgaaggggcaa gtgtgaatct aggtatcttt
 180
 atatgcata catgttctgg cattcataga agcctggggg tgcacatatc taaggtaaga
 240
 tctgccacc tggatacatg gctgccagag caagttgcat ttattcaatc aatgggaaac
 300
 gaaaaagcaa atagctattg ggaagcagag ctgcctccta actacgatag ggttgaata
 360
 gagaatttga t
 371

<210> 2424
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 2424
 Met Asn Glu Lys Ala Ser Val Ser Lys Glu Leu Asn Ala Lys His Lys
 1 5 10 15
 Lys Ile Leu Glu Gly Leu Leu Arg His Pro Glu Asn Arg Glu Cys Ala
 20 25 30
 Asp Cys Lys Ser Lys Gly Pro Arg Trp Ala Ser Val Asn Leu Gly Ile
 35 40 45
 Phe Ile Cys Met Thr Cys Ser Gly Ile His Arg Ser Leu Gly Val His
 50 55 60
 Ile Ser Lys Val Arg Ser Ala Thr Leu Asp Thr Trp Leu Pro Glu Gln
 65 70 75 80
 Val Ala Phe Ile Gln Ser Met Gly Asn Glu Lys Ala Asn Ser Tyr Trp
 85 90 95
 Glu Ala Glu Leu Pro Pro Asn Tyr Asp Arg Val Gly Ile Glu Asn Leu
 100 105 110

<210> 2425
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 2425
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 60
 ccgctcctga acggctacga gatgacctgc cgctgcgcg aacatgaagc cncgcccatt
 120
 acctcccgcc ctgcacgggg gttcggtttc accgcccacg cccagcccga ggaacgcccc
 180
 cgctgcaagg aagccggcat gaacgactgc ctgttcaagc ccatcagcct gaccaccctc
 240
 aaccagaaac tcgccgacgt cagcgcgcgc ccgctgccga gccaggccgc cttcagcctc
 300
 gacggcctgc acgcctgac cgggggcgag ccgctgctga tgcgtgcctt gatcgacgag
 360
 ctgctgagca gttgccaggc ggcccgcgag gcaactgctc gactgcccac c
 411

<210> 2426

<211> 137
 <212> PRT
 <213> Homo sapiens

<400> 2426
 Thr Gly Leu Gln Ala Trp Lys Asp Gly His Phe Asp Leu Val Ile Val
 1 5 10 15
 Asp Cys Asn Met Pro Val Leu Asn Gly Tyr Glu Met Thr Arg Arg Leu
 20 25 30
 Arg Glu His Glu Ala Xaa Ala Met Thr Ser Arg Pro Ala Arg Gly Phe
 35 40 45
 Gly Phe Thr Ala His Ala Gln Pro Glu Glu Arg Pro Arg Cys Lys Glu
 50 55 60
 Ala Gly Met Asn Asp Cys Leu Phe Lys Pro Ile Ser Leu Thr Thr Leu
 65 70 75 80
 Asn Gln Lys Leu Ala Asp Val Thr Pro Arg Pro Arg Pro Ser Gln Ala
 85 90 95
 Ala Phe Ser Leu Asp Gly Leu His Ala Leu Thr Gly Gly Glu Pro Leu
 100 105 110
 Leu Met Arg Arg Leu Ile Asp Glu Leu Leu Ser Ser Cys Gln Ala Ala
 115 120 125
 Arg Glu Ala Leu Leu Gly Leu Pro Ile
 130 135

<210> 2427
 <211> 293
 <212> DNA
 <213> Homo sapiens

<400> 2427
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 tggagcgtaa aatgttgcag agcccagcta gaagccagga ggagcagaca ccctgctgat
 120
 ggagcccaac aagaaagatg ttgtgtccct cctggtgagc gctgtccccg tgcacccgat
 180
 aatggcgaag aaaatgtgcc tctttcagga aaagtatagg aaatgagaga agactgtgac
 240
 aactcatgac ctgcatcctt aatatccagt gacttcatct ccccttcacg cgt
 293

<210> 2428
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 2428
 His Asn Lys Gly Leu Gly Ile Leu Val Pro Cys Ala Ile Xaa Ala Ala
 1 5 10 15
 Phe Leu Leu Ile Trp Ser Val Lys Cys Cys Arg Ala Gln Leu Glu Ala
 20 25 30
 Arg Arg Ser Arg His Pro Ala Asp Gly Ala Gln Gln Glu Arg Cys Cys
 35 40 45
 Val Pro Pro Gly Glu Arg Cys Pro Ser Ala Pro Asp Asn Gly Glu Glu

50 55
 Asn Val Pro Leu Ser Gly Lys Val
 65 70

60

<210> 2429
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 2429
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 atcgccgaga tggcggggct acaggctgct cagtcgatcc gggaatcctt gaacaaggct
 120
 gatgtcctgc tcaatgggggt agagacgtcg accgggtccgc agccgggtgc gcttgctttg
 180
 ctggaacagg ccgtacatga gctggatggc actggggatg ctgatcctcg cgccgctgag
 240
 ttggctgagc gcgcccgcga gatgtcgtat gacctcactg acctcgctgc ttcggctcgt
 300
 ggccatgcgg ctcgggctga agctgatccg caacggcttg aggaattggg gggctcgttg
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 gcggctattc agcggctggt gagggcgcg accaccacc tcgacgatct cctcgactcc
 420
 actgcggc
 428

<210> 2430
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 2430
 Ser Arg Arg Val Gly Glu Val Asp Ala Val Asp Pro Lys Pro His Glu
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 Asp Asp Asp Leu Ile Ala Glu Met Ala Gly Leu Gln Ala Ala Gln Ser
 20 25 30
 Ile Arg Glu Ser Leu Asn Lys Ala Asp Val Leu Leu Asn Gly Val Glu
 35 40 45
 Thr Ser Thr Gly Pro Gln Pro Gly Ala Leu Ala Leu Leu Glu Gln Ala
 50 55 60
 Val His Glu Leu Asp Gly Thr Gly Asp Ala Asp Pro Arg Ala Ala Glu
 65 70 75 80
 Leu Ala Glu Arg Ala Arg Gln Met Ser Tyr Asp Leu Thr Asp Leu Ala
 85 90 95
 Ala Ser Val Ala Gly His Ala Ala Arg Ala Glu Ala Asp Pro Gln Arg
 100 105 110
 Leu Glu Glu Leu Gly Gly Arg Leu Ala Ala Ile Gln Arg Leu Leu Arg
 115 120 125
 Ala Arg Thr Thr Thr Leu Asp Asp Leu Leu Asp Ser Thr Ala
 130 135 140

<210> 2431
 <211> 409

<212> DNA

<213> Homo sapiens

<400> 2431

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 120
 aatggcgagg taacaatttc tggggcaaaa aatgccgcat taccaatcct atttgctact
 180
 ttattatctg aggggtgatat caatttaagc aatgtaccgc ttttaaaga tattgccacc
 240
 actatcgagt tgtaaaaga gctgggtgct actgtactc agactcaaca ctgctgcat
 300
 attaatgcga aagaagttaa gaactatact gcttcttatg aattagttag aagtatgcgt
 360
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 409

<210> 2432

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2432

Met	Gly	Gln	Phe	Ile	Ile	Gln	Gly	Gly	Cys	Gln	Leu	Asn	Gly	Glu	Val
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Thr	Ile	Ser	Gly	Ala	Lys	Asn	Ala	Ala	Leu	Pro	Ile	Leu	Phe	Ala	Thr
			20					25					30		
Leu	Leu	Ser	Glu	Gly	Asp	Ile	Asn	Leu	Ser	Asn	Val	Pro	Leu	Leu	Lys
			35					40				45			
Asp	Ile	Ala	Thr	Thr	Ile	Glu	Leu	Leu	Lys	Glu	Leu	Gly	Ala	Thr	Ala
			50				55				60				
Thr	Gln	Thr	Gln	His	Cys	Val	His	Ile	Asn	Ala	Lys	Glu	Val	Lys	Asn
65					70					75				80	
Tyr	Thr	Ala	Ser	Tyr	Glu	Leu	Val	Arg	Ser	Met	Arg	Ala	Ser	Ile	Leu
			85						90				95		
Ala	Leu	Gly	Pro	Leu	Val	Ala	Arg	Phe	Gly	Glu	Ala				
			100					105							

<210> 2433

<211> 655

<212> DNA

<213> Homo sapiens

<400> 2433

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 120
 gctctatgat gctcacgtaa caatgaaatc acggaatctc tctctcagaa catttccccg
 180
 ttgtgaagca gcacgtgact ataattcttt cccaggttta cccctgaagt tcaagtgcga
 240

tgccccgtgca cagcacagag caggggacga taggaggcgt gccttctcca gctgaaccac
 300
 cgggccagcc gggcgggcag tgggggttgg ggggagggtt gacccattgg tgetgccacg
 360
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 420
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 480
 tgtgactgccc gtgttccaaa cacacccttt gcttttataa aaacccaac tgggagggtt
 540
 agcaaaaggc acagtttcag agcataataa agacagagca gaatgggaga ggaggttaat
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 655

<210> 2434

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2434

Met	Ala	His	Leu	Ile	Asn	Leu	Leu	Ser	His	Ser	Ala	Leu	Ser	Leu	Leu
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Cys	Ser	Glu	Thr	Val	Pro	Phe	Ala	Lys	Pro	Pro	Ser	Leu	Gly	Phe	Cys
				20				25					30		
Lys	Ser	Lys	Gly	Cys	Val	Trp	Asn	Thr	Ala	Val	Thr	Glu	Lys	Val	Leu
			35				40					45			
Phe	Ala	Gln	Ser	Ala	Arg	Pro	Leu	Leu	Leu	Ser	Leu	Met	Ser	Pro	Asp
			50			55					60				
Trp	Ala	Phe	Ile	Val	Pro	Cys	Thr	Glu	Ala	Ser	Leu	Ser	Pro	Arg	Ser
				70					75					80	
Cys	Leu	Phe	Gly	Arg	Gly	Ser	Thr	Asn	Gly	Ser	Thr	Leu	Pro	Pro	Thr
				85					90					95	
Pro	Thr	Ala	Arg	Pro	Ala	Gly	Pro	Val	Val	Gln	Leu	Glu	Lys	Ala	Arg
				100				105					110		
Leu	Leu	Ser	Ser	Pro	Ala	Leu	Cys	Cys	Ala	Gly	Ala	Leu	His	Leu	Asn
				115			120						125		
Phe	Arg	Gly	Lys	Pro	Gly	Lys	Arg	Leu							
			130				135								

<210> 2435

<211> 401

<212> DNA

<213> Homo sapiens

<400> 2435

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 120
 gcagatatgg accaagcggg ccagggtgag atgggcgcga agatgcgcga tatcggcgag
 180
 gctgcaccg cagctaaccg cttcttggtc cagcagctctg ttgctgagga gttctctgag
 240

aaactcgttg cggagtttga gaagctcaat ctgggcaatg gtagggacga aggtattacc
 300
 tgccgacctc tcgtcgagtc caaggctttg gagagcattg cggcattggg ggacgatgct
 360
 gcagaaaaagg gcgctacccat ctccaccggc ggtaagcgcg c
 401

<210> 2436

<211> 133

<212> PRT

<213> Homo sapiens

<400> 2436

Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Pro	Val	Gly	Arg	Thr	Leu	Leu	Lys
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Xaa	Ala	Ala	Asp	Asn	Val	Leu	Arg	Thr	Ser	Met	Glu	Leu	Gly	Xaa	Asn
			20					25					30		
Ala	Pro	Phe	Ile	Val	Phe	Glu	Asp	Ala	Asp	Ile	Asp	Gln	Ala	Val	Gln
		35					40					45			
Gly	Ala	Met	Gly	Ala	Lys	Met	Arg	Asn	Ile	Gly	Glu	Ala	Cys	Thr	Ala
	50					55					60				
Ala	Asn	Arg	Phe	Leu	Val	His	Glu	Ser	Val	Ala	Glu	Glu	Phe	Ser	Glu
	65				70					75				80	
Lys	Leu	Val	Ala	Glu	Phe	Glu	Lys	Leu	Asn	Leu	Gly	Asn	Gly	Met	Asp
			85					90						95	
Glu	Gly	Ile	Thr	Cys	Gly	Pro	Leu	Val	Glu	Ser	Lys	Ala	Leu	Glu	Ser
			100					105					110		
Ile	Ala	Ala	Leu	Val	Asp	Asp	Ala	Ala	Glu	Lys	Gly	Ala	Thr	Ile	Ser
			115				120						125		
Thr	Gly	Gly	Lys	Arg											
			130												

<210> 2437

<211> 449

<212> DNA

<213> Homo sapiens

<400> 2437

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 120
 atgggtatgta tttttcaagc tagacgttca taatggtaga acatgaggag gaaaactgcc
 180
 tcttaaatcc caccacttac tgtgacacag tgaccggtcc ctgcagcgga ctggatagtt
 240
 gtagcataggt cctggacgga aacagatggc actcaaaaagg tggcgcgag ttcagagaaa
 300
 tgccctatgta cggatttggg ccaatgcctc agcctgacct caggggacct cgggggtctg
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 420
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<210> 2438
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 2438
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 Cys Asp Thr Val Thr Gly Pro Cys Ser Gly Leu Asp Ser Cys Ile Arg
 20 25 30
 Val Leu Asp Gly Asn Arg Trp His Ser Lys Gly Gly Ala Gln Phe Arg
 35 40 45
 Glu Met Pro Met Tyr Gly Phe Gly Pro Met Pro Gln Pro Asp Leu Arg
 50 55 60
 Asp Leu Arg Gly Ser Ala Pro Arg Pro Pro Leu His Ile Cys Asp Pro
 65 70 75 80
 Thr His Phe His Pro Ser Ala Thr Phe Lys Phe Gln Ser Phe His Phe
 85 90 95
 Ile Ala Val

<210> 2439
 <211> 4425
 <212> DNA
 <213> Homo sapiens

<400> 2439
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 120
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 180
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 240
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 480
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<210> 2440

<211> 1306

<212> PRT

<213> Homo sapiens

<400> 2440

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Thr	Asp	Asn	Ile	Lys	Lys	Thr	Leu	His	Lys	Phe	Cys	Gly	Pro	Ser	Pro
		20					25						30		
Val	Val	Phe	Ser	Asp	Val	Asn	Ser	Met	Tyr	Leu	Ser	Ser	Thr	Glu	Pro
		35					40					45			
Pro	Ala	Ala	Ala	Glu	Trp	Ala	Cys	Leu	Leu	Arg	Pro	Leu	Arg	Gly	Arg
	50					55					60				
Glu	Pro	Glu	Gly	Val	Trp	Asn	Leu	Leu	Ser	Ile	Val	Arg	Glu	Met	Phe
65				70					75					80	
Lys	Arg	Arg	Asp	Ser	Asn	Ala	Ala	Pro	Leu	Leu	Glu	Ile	Leu	Thr	Asp
			85						90					95	
Gln	Cys	Leu	Thr	Tyr	Glu	Gln	Ile	Thr	Gly	Trp	Trp	Tyr	Ser	Val	Arg
		100						105					110		
Thr	Ser	Ala	Ser	His	Ser	Ser	Ala	Ser	Gly	His	Thr	Gly	Arg	Ser	Asn
		115				120						125			
Gly	Gln	Ser	Glu	Val	Ala	Ala	His	Ala	Cys	Ala	Ser	Met	Cys	Asp	Glu
	130				135						140				
Met	Val	Thr	Leu	Trp	Arg	Leu	Ala	Val	Leu	Asp	Pro	Ala	Leu	Ser	Pro
145					150					155				160	
Gln	Arg	Arg	Arg	Glu	Leu	Cys	Thr	Gln	Leu	Arg	Gln	Trp	Gln	Leu	Lys
			165						170					175	
Val	Ile	Glu	Asn	Val	Lys	Arg	Gly	Gln	His	Lys	Lys	Thr	Leu	Glu	Arg
		180					185						190		
Leu	Phe	Pro	Gly	Phe	Arg	Pro	Ala	Val	Glu	Ala	Cys	Tyr	Phe	Asn	Trp
		195					200					205			
Glu	Glu	Ala	Tyr	Pro	Leu	Pro	Gly	Val	Thr	Tyr	Ser	Gly	Thr	Asp	Arg
		210				215					220				
Lys	Leu	Ala	Leu	Cys	Trp	Ala	Arg	Ala	Leu	Pro	Ser	Arg	Pro	Gly	Ala
225					230					235				240	
Ser	Arg	Ser	Gly	Gly	Leu	Glu	Glu	Ser	Arg	Asp	Arg	Pro	Arg	Pro	Leu
			245						250					255	
Pro	Thr	Glu	Pro	Ala	Val	Arg	Pro	Lys	Glu	Pro	Gly	Thr	Lys	Arg	Lys

[illegible]

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Gln Ala Lys Leu Lys Lys Ile Leu Asp Lys Leu Leu Asp Arg Glu Ser					
	725		730		735
Gln Thr His Lys Pro Gln Thr Leu Ser Ser Phe Tyr Ser Ser Ser Arg					
	740		745		750
Pro Thr Thr Ala Ser Gln Arg Ser Pro Ser Lys His Gly Gly Pro Ser					
	755		760		765
Ala Pro Gly Ala Leu Gln Pro Leu Thr Ser Gly Ser Ala Gly Pro Ala					
	770		775		780
Gln Pro Gly Ser Val Ala Gly Ala Gly Pro Gly Pro Thr Glu Gly Phe					
785		790		795	800
Thr Glu Lys Asn Val Pro Glu Ser Ser Pro His Ser Pro Cys Glu Gly					
	805		810		815
Leu Pro Ser Glu Ala Ala Leu Thr Pro Arg Pro Glu Gly Lys Val Pro					
	820		825		830
Ser Arg Leu Ala Leu Gly Ser Arg Gly Gly Tyr Asn Gly Arg Gly Trp					
	835		840		845
Gly Ser Ser Gly Arg Pro Lys Lys Lys His Thr Gly Met Ala Ser Ile					
	850		855		860
Asp Ser Ser Ala Pro Glu Thr Thr Ser Asp Ser Ser Pro Thr Leu Ser					
	865		870		875
Arg Arg Pro Leu Arg Gly Gly Trp Ala Pro Thr Ser Trp Gly Arg Gly					
	885		890		895
Gln Asp Ser Asp Ser Ile Ser Ser Ser Ser Asp Ser Leu Gly Ser					
	900		905		910
Ser Ser Ser Ser Gly Ser Arg Ala Ala Ser Ala Ser Gly Gly Ala Arg					
	915		920		925
Ala Lys Thr Val Glu Val Gly Arg Tyr Lys Gly Arg Arg Pro Glu Ser					
	930		935		940
His Ala Pro His Val Pro Asn Gln Pro Ser Glu Ala Ala Ala His Phe					
	945		950		955
Tyr Phe Glu Leu Ala Lys Thr Val Leu Ile Lys Ala Gly Gly Asn Ser					
	965		970		975
Ser Thr Ser Ile Phe Thr His Pro Ser Ser Ser Gly Gly His Gln Gly					
	980		985		990
Pro His Arg Asn Leu His Leu Cys Ala Phe Glu Ile Gly Leu Tyr Ala					
	995		1000		1005
Leu Gly Leu His Asn Phe Val Ser Pro Asn Trp Leu Ser Arg Thr Tyr					
	1010		1015		1020
Ser Ser His Val Ser Trp Ile Thr Gly Gln Ala Met Glu Ile Gly Ser					
	1025		1030		1035
Ala Ala Leu Thr Ile Leu Val Glu Cys Trp Asp Gly His Leu Thr Pro					
	1045		1050		1055
Pro Glu Val Ala Ser Leu Ala Asp Arg Ala Ser Arg Ala Arg Asp Ser					
	1060		1065		1070
Asn Met Val Arg Ala Ala Ala Glu Leu Ala Leu Ser Cys Leu Pro His					
	1075		1080		1085
Ala His Ala Leu Asn Pro Asn Glu Ile Gln Arg Ala Leu Val Gln Cys					
	1090		1095		1100
Lys Glu Gln Asp Asn Leu Met Leu Glu Lys Ala Cys Met Ala Val Glu					
	1105		1110		1115
Glu Ala Ala Lys Gly Gly Gly Val Tyr Pro Glu Val Leu Phe Glu Val					1120

1125 1130 1135
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 1140 1145 1150
 Thr Ala Arg Glu Gly Ala Thr Ser Cys Ser Ala Ser Gly Ile Arg Ala
 1155 1160 1165
 Gly Gly Glu Ala Gly Arg Gly Met Pro Glu Gly Arg Gly Gly Pro Gly
 1170 1175 1180
 Thr Glu Pro Val Thr Val Ala Ala Ala Val Thr Ala Ala Thr
 1185 1190 1195 1200
 Val Val Pro Val Ile Ser Val Gly Ser Ser Leu Tyr Pro Gly Pro Gly
 1205 1210 1215
 Leu Gly His Gly His Ser Pro Gly Leu His Pro Tyr Thr Ala Leu Gln
 1220 1225 1230
 Pro His Leu Pro Cys Ser Pro Gln Tyr Leu Thr His Pro Ala His Pro
 1235 1240 1245
 Ala His Pro Met Pro His Met Pro Arg Pro Ala Val Phe Pro Val Pro
 1250 1255 1260
 Ser Ser Ala Tyr Pro Gln Val Arg Pro Val Phe Cys Trp Gly Val Arg
 1265 1270 1275 1280
 His Gly Lys Ile Leu Gly Ile His Arg Gly Leu Glu Trp Val Leu Trp
 1285 1290 1295
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<210> 2441

<211> 2244

<212> DNA

<213> Homo sapiens

<400> 2441

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 120
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 gcctcggggc ggaagggtac aaagcccccgc cgtgtgttct gccacagagt ctcttgaaa
 360
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 420
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 480
 gatgcctccg accttttgga tctcttttct gcacctctca ggggacaggt ccgctctgta
 540
 cggcgctgcc tacgagaaac ccaagttcat tactgcagcc aaaggaaaag tgcaggcggt
 600
 gggaggctcc tgcaagggtga tgcgtctggc cataagtccc actgccttct cccacctgct
 660
 ggctgtgcc cagcagttcc ggaagcagac ccaggcccag gtgtacagtg aggacatggc
 720

cctgaacata ggctcggaaac cagaaggcct gcaggtggaa gagaaggagc gccctgtgca
780
gaggctcagt agcgtcctgg ggccctcgga ggagcttctg cagccgctat tccccctgct
840
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900
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960
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1020
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1080
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1140
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1200
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1260
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1320
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1380
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1440
gagcttctctg tcccatatat tagtggagag attggtcgcc atgaacttgc aagagtgcga
1500
ggtggcagtc ctgctggacc tggcacggtc ctaccagagc ttgaagaggc acatggagag
1560
cgtggagcac aggagatctg ttggccgttg ggaagccaat tggagaaaac gtgcgtctcc
1620
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1800
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1920
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1980
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2040
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2100
ccagaagact attcagaccg tgagcctgtt ttgtatttga gtgttccact aaacaaacaa
2160
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2220
aaaaaaaaa aaaaaaaaaa aaaa
2244

<210> 2442

<211> 168

<212> PRT

<213> Homo sapiens

<400> 2442

```

Met Gly Cys Arg Thr Lys Pro Ser Gly Ser Ala Gly Leu Asp Leu Pro
 1           5           10           15
Pro Ile Ser Cys Trp Gly Pro Ser Thr Cys Leu Cys Pro Trp Leu Cys
           20           25           30
Pro Ser Ala Asn Pro Ser Pro Pro Gly Ser His Pro Gln Leu Pro
 35           40           45
Ala Arg Ser Pro Leu Pro Gly Pro Leu Pro Ser Pro Trp Cys Ser Leu
 50           55           60
Ser Gln Gly Pro Ser Pro Ser Asp Phe Pro Gln Gly Ser Arg Leu Asp
 65           70           75           80
Leu Glu Leu Cys Leu Pro Val Cys Ala Met Gly Ser Ala Ser Gly Leu
           85           90           95
Glu Leu Arg Leu Phe Pro Gly Pro Gly Gln Gly Arg Pro Pro Leu Gly
          100          105          110
Gly Ala Gly Ala Glu Leu Leu Arg Pro Glu Asp Tyr Ser Asp Arg Glu
          115          120          125
Pro Val Phe Asp Leu Ser Val Pro Leu Asn Lys Gln Gln Lys Pro Lys
          130          135          140
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
          145          150          155          160
Lys Lys Lys Lys Lys Lys Lys Lys
          165

```

<210> 2443

<211> 361

<212> DNA

<213> Homo sapiens

<400> 2443

```

nccgtgcgcg ctattcttgcg tcgtacgccc tccaggggaag atgaaaaaat gctacaaaacg
 60
gccgatggac gattgcgcat tgatatcgaa tccatgcgca cttttgtaga gggcaaaagaa
 120
gtccatttga cgaaaaacga atttttaatt gtgcagactt tgtttacgca ccccaataag
 180
atctatacgc gcgatgaaat tatcgaaatc accttcggaa tggattatga ggcctttgac
 240
cgtgccattg atacctatat caaaaacatt cgccagaaga ttgaagcgga tccgaaaaac
 300
cccgctctata tccgcacggt ttatgggtgtc gggtatctgc ccggaggcct tgatgaagct
 360
t
 361

```

<210> 2444

<211> 120

<212> PRT

<213> Homo sapiens

<400> 2444

```

Xaa Val Arg Ala Ile Leu Arg Arg Thr Pro Ser Arg Glu Asp Glu Lys
 1           5           10           15
Met Leu Gln Thr Ala Asp Gly Arg Leu Arg Ile Asp Ile Glu Ser Met
          20           25           30
Arg Thr Phe Val Glu Gly Lys Glu Val His Leu Thr Lys Asn Glu Phe
          35           40           45
Leu Ile Val Gln Thr Leu Phe Thr His Pro Asn Lys Ile Tyr Thr Arg
          50           55           60
Asp Glu Ile Ile Glu Val Thr Phe Gly Met Asp Tyr Glu Ala Phe Asp
65           70           75           80
Arg Ala Ile Asp Thr His Ile Lys Asn Ile Arg Gln Lys Ile Glu Ala
          85           90           95
Asp Pro Lys Asn Pro Val Tyr Ile Arg Thr Val Tyr Gly Val Gly Tyr
          100          105          110
Leu Pro Gly Gly Phe Asp Glu Ala
          115          120

```

<210> 2445

<211> 403

<212> DNA

<213> Homo sapiens

<400> 2445

```

agatctgttg aatgaagcag gtgccactta gacattcact tcaactgactc caaccacaac
60
ctcccccttca ttgatatacc tgctcttggc agaaggatgg agaaagagca tcgcacaaag
120
aggaagcattg tttatcctgt tcagattact gcttctgccca ggctgctgct gctgttgggt
180
cttgccacatt tgctctttat taagcaaatg tcagagctgg gtgctggcaa gggaatcccc
240
tgtatttaca caggtaaacc tgagagccag agggcccccac accatctctgg ctgcgaggga
300
caagctatta gagttaataa cagtgcactg gcattccttc aaaatcctaa tgggaagcata
360
aataaaaaa ggaagtccc ctttaccacaa gaacctgaaa aan
403

```

<210> 2446

<211> 102

<212> PRT

<213> Homo sapiens

<400> 2446

```

Met Glu Lys Glu His Arg Thr Lys Arg Lys His Val Tyr Pro Val Gln
 1           5           10           15
Ile Thr Ala Ser Ala Arg Leu Leu Leu Leu Gly Ser Ala His Leu
          20           25           30
Leu Phe Ile Lys Gln Met Ser Glu Leu Gly Ala Gly Lys Gly Ile Pro
          35           40           45
Cys Ile Tyr Thr Gly Lys Pro Glu Ser Gln Arg Ala Pro Asn His Pro
          50           55           60
Gly Cys Glu Gly Gln Ala Ile Arg Val Asn Asn Ser Ala Leu Ala Phe

```

```

65              70              75              80
Leu Gln Asn Pro Asn Gly Ser Ile Asn Lys Lys Arg Lys Val Pro Phe
      85              90              95
Thr Gln Glu Pro Glu Lys
      100

```

```

<210> 2447
<211> 744
<212> DNA
<213> Homo sapiens

```

```

<400> 2447
naccgcgtcga ggtttgccag tcacgggttg cgggtggggc aggtactact caccgtcaat
60
gacctgggtgc ggccacttc gtaccgcaat gcctgggtcaa cctcgacac tttgctgggg
120
ttgggcgtgc tgccgatcgt caacgagaac gacacggctgc ccaccggaga aattcggttt
180
ggcgataaatg atcggtctgc tgccctggta gccgagctgg tgcgcgtca agccctcat
240
ctgctctctg acgttgacgc cttgtacacc gcccatccgg attcaccgga tgctcgctgc
300
gtggagggttg tggaggacat cgatgcattg gatgtcgata cccataaagc tggttcgggg
360
gtgggaacgc gcggcatgac cagcaaaact gaagccgccc gaatggccac ctgtgccggg
420
gtaccgggtg tactcgacgc ggcgtgtgat gcccggacg tctctggctg tgccccgtg
480
ggtacctact tccgcccgtc ggcgacgcga cggccccgac ggttgctgtg gttggccgac
540
gctgccaccc cgcagggaca gatcgtcatc gacgacggag ctgtcgaaagc tttgacacag
600
cgtcattcct cgttggtggc ggtgggtgtg actcgggtac acggggattt ccaagcaggc
660
gaccagtgta cgatcctggc ctccgacggt cgagttgttg gtcgcggtat cgcccagttc
720
tcccatgatg aggtgcgcgt catg
744

```

```

<210> 2448
<211> 248
<212> PRT
<213> Homo sapiens

```

```

<400> 2448
Xaa Ala Ser Arg Phe Ala Ser His Gly Leu Arg Val Gly Gln Val Leu
1      5      10      15
Leu Thr Val Asn Asp Leu Val Arg Pro Thr Ser Tyr Arg Asn Ala Trp
      20      25      30
Ser Thr Leu Asp Thr Leu Leu Gly Leu Gly Val Val Pro Ile Val Asn
      35      40      45
Glu Asn Asp Thr Val Ala Thr Gly Glu Ile Arg Phe Gly Asp Asn Asp
      50      55      60
Arg Leu Ala Ala Leu Val Ala Glu Leu Val Arg Ala Gln Ala Leu Ile

```



```

65              70              75              80
Leu Leu Ser Asp Val Asp Ala Leu Tyr Thr Ala His Pro Asp Ser Pro
      85              90              95
Asp Ala Arg Arg Val Glu Val Val Glu Asp Ile Asp Ala Leu Asp Val
      100              105              110
Asp Thr His Lys Ala Gly Ser Gly Val Gly Thr Gly Gly Met Thr Thr
      115              120              125
Lys Leu Glu Ala Ala Arg Met Ala Thr Cys Ala Gly Val Pro Val Val
      130              135              140
Leu Ala Ala Ala Val Asp Ala Pro Asp Val Leu Ala Gly Ala Pro Val
145              150              155              160
Gly Thr Tyr Phe Arg Pro Leu Ala Thr Arg Arg Pro Arg Arg Leu Leu
      165              170              175
Trp Leu Ala Asp Ala Ala Thr Pro Gln Gly Gln Ile Val Ile Asp Asp
      180              185              190
Gly Ala Val Glu Ala Leu Thr Gln Arg His Ser Ser Leu Leu Ala Val
      195              200              205
Gly Val Thr Arg Val His Gly Asp Phe Gln Ala Gly Asp Pro Val Thr
      210              215              220
Ile Leu Ala Ser Asp Gly Arg Val Val Gly Arg Gly Ile Ala Gln Phe
225              230              235              240
Ser His Asp Glu Val Arg Val Met
      245

```

<210> 2449

<211> 296

<212> DNA

<213> Homo sapiens

<400> 2449

```

gtgcactttg ttacagccct ggaacatgaa cacatgccgt catcaactcc caaaaatctc
60
ctactgctct cccctectcc ctgggcccctg tcctatcccc agaggccaga caggccttcc
120
tcgcatgcaa gagtctccct cgccctgcgc gacagtggcc tccatctacc tgccctgtctt
180
gctggactcc agaactcc agtcctttcc cccttggggg ttgggggggg cccccctttt
240
tttcccccc ctttccctct tcattccaca ggaggccagc ctcaacatcc cncccc
296

```

<210> 2450

<211> 90

<212> PRT

<213> Homo sapiens

<400> 2450

```

Met Asn Thr Cys Arg His Gln Leu Pro Lys Ile Ser Tyr Cys Ser Pro
1              5              10              15
Leu Leu Pro Gly Pro Cys Pro Ile Pro Arg Gly Gln Thr Gly Leu Pro
      20              25              30
Arg Met Gln Glu Ser Pro Ser Pro Cys Arg Thr Val Ala Ser Ile Tyr
      35              40              45
Leu Pro Val Leu Leu Asp Ser Arg Thr Leu Gln Ser Phe Pro Pro Trp

```

```

      50              55              60
Gly Leu Gly Gly Ala Pro Pro Phe Phe Pro Pro Leu Ser Leu Phe Ile
65              70              75              80
Pro Gln Glu Ala Ser Leu Asn Ile Pro Xaa
      85              90

```

<210> 2451

<211> 589

<212> DNA

<213> Homo sapiens

<400> 2451

```

nacgcgtgac tggattgtct aacgggtgag gaatcgagcg gttacgatgt cgggccgcatc
60
tgcaacgatg atcttgtgag cgaatgtattg accggtgtgt gggccgatct tgtgggccag
120
gagaaggctg tcggggtcct gcgtcgtgcc gccgaatcgc agccggggcg ctcgtcccat
180acgcatggct cattacgggt ccgcctggat caggtcggtc gaatgctcgc      240
aaggcctttg cagcggcgct acagtgcgtc gaccatggat gcgggcagtg caatgcctgt
300
cgaaccngcc tgtcaggcgc ccatacctgac gtcaccctcg tgcgtactga ggcgctgtct
360
attggcgctg attgaggtcg tgaatatgggt ttgttcgagc gggcgatgaa ttccgggtccc
420
cgggggcgctc ccagggttgt cgtcgtcgaa gatgccgacc gcatcactga acgcgagagt
480
gacgcctttg ttaaagctat cgaggagcct gcgccgaaaa ccgtctgtgt gctgtgtgccc
540
cctactccag aggacgtcat cgtcacgatac aggtcgagat gtcggcgccc
589

```

<210> 2452

<211> 121

<212> PRT

<213> Homo sapiens

<400> 2452

```

Leu Asp Cys Ser Thr Gly Glu Glu Ser Ser Gly Tyr Asp Val Gly Pro
1              5              10              15
Ile Cys Asn Asp Asp Leu Val Ser Asp Val Leu Thr Gly Val Trp Ala
20              25              30
Asp Leu Val Gly Gln Glu Lys Ala Val Gly Val Leu Arg Arg Ala Ala
35              40              45
Glu Ser Gln Pro Gly Arg Ser Ser His Ala Met Ser His Ala Trp Leu
50              55              60
Ile Thr Gly Pro Pro Gly Ser Gly Arg Ser Asn Ala Ala Lys Ala Phe
65              70              75              80
Ala Ala Ala Leu Gln Cys Val Asp His Gly Cys Gly Gln Cys Asn Ala
85              90              95
Cys Arg Thr Xaa Leu Ser Gly Ala His Pro Asp Val Thr Leu Val Arg
100              105              110
Thr Glu Ala Leu Ser Ile Gly Val Asp
115              120

```

<210> 2453
 <211> 695
 <212> DNA
 <213> Homo sapiens

<400> 2453
 nnacgcgtca gccatctgtg agtgctcaca ctatacacac atccccgggc acactcaggg
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 agattcacac attcctacga gcacacatgt gcctgcattga gttattcccc atgtgaacac
 120
 acagggttggc acacgcacat gcccctgggt atgctcatgt ccattcatcc atcccagcct
 180
 gtgcacgtcc tctcactcct gtgttcacac ctatgcccaa atgaaccaag ggacacacat
 240
 gcacaccctt atgtggtgca cacacactcg tgcacacgga gccacaccag cacatgctca
 300
 gaggcatttg tgtgcgtggg catttgacgc atgactcaga acggagtatg ggggtggcgcg
 360
 gcgtggctgg ggaggtccca tcagcccgcc tctgaaaccc tcccaacctg cccatcctgg
 420
 ccaggcact gtgtctccgg cttgggcttc agcccggac cccaggacac cccggacaaa
 480
 gaggagctgc tctcgtctga agcctgctac gaatgcagga tcaatggcct ctcccctgg
 540
 gaccggccac gacgcagtgc ccacaggag caccaggatga catgggtgct gcaataggca
 600
 ggggtggcca gggaatgggt gagggtggga aagaggctgt ggacccgact tagtcatgtc
 660
 agcccccca agaaggagca ccaggctcca gatct
 695

<210> 2454
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 2454
 Met Ser Tyr Ser Pro Cys Glu His Thr Gly Trp His Thr His Met Pro
 1 5 10 15
 Leu Gly Met Leu Met Ser Ile His Pro Ser Gln Pro Val His Val Leu
 20 25 30
 Ser Leu Leu Cys Ser His Leu Cys Pro Asn Glu Pro Arg Asp Thr His
 35 40 45
 Ala His Pro Tyr Val Val His Thr His Ser Cys Thr Arg Ser His Thr
 50 55 60
 Ser Thr Cys Ser Glu Ala Phe Val Cys Val Gly Ile Cys Ser Met Thr
 65 70 75 80
 Gln Asn Gly Val Trp Gly Gly Ala Ala Trp Leu Gly Arg Ser His Gln
 85 90 95
 Pro Ala Ser Glu Thr Leu Pro Thr Cys Pro Ser Trp Pro Arg His Cys
 100 105 110
 Val Ser Gly Leu Gly Phe Ser Pro Gly Pro Gln Asp Thr Pro Asp Lys
 115 120 125
 Glu Glu Leu Leu Ser Ser Glu Ala Cys Tyr Glu Cys Arg Ile Asn Gly

```

      130                      135                      140
Leu Ser Pro Arg Asp Arg Pro Arg Arg Ser Ala His Arg Asp His Gln
145                      150                      155                      160
Val Thr Trp Val Leu His
      165

```

<210> 2455
 <211> 378
 <212> DNA
 <213> Homo sapiens

```

<400> 2455
acgcgtcggc agaagcgta gctgaccgtc ggagccgac tgccccagg cgtcgtcagc
60
ggaaccgcgc agaaggaat ccacgcgctg ccgatcatga aggcgctccc catgggcgtc
120
aaagaactgc ttctgggcga atcgaagtgg caggacgagt tgatcaacaa cttcatcgtc
180
gcgctgtttg caggcggtgt gttgctgttc gcggtgctgg tgctgctgta ccggcgcttg
240
ctgcgcgcgt tcatcaacgt gatgtcgtg gcggtggcac cgctgggcgg gttgatcggc
300
ctgtggcgta ccaacacgcc gatctcgatg ccggtctata tcggcttgat catgctgctc
360
ggcatcgtcg ccaagaat
378

```

<210> 2456
 <211> 126
 <212> PRT
 <213> Homo sapiens

```

<400> 2456
Thr Arg Arg Gln Lys Arg Gln Leu Thr Val Gly Ala Asp Leu Ser Pro
1      5      10      15
Gly Val Val Ser Gly Thr Ala Gln Lys Glu Ile His Ala Leu Pro Ile
20     25     30
Met Lys Ala Leu Pro Met Gly Val Lys Glu Leu Val Leu Gly Glu Ser
35     40     45
Lys Trp Gln Asp Glu Leu Ile Asn Phe Ile Val Ala Leu Phe Ala
50     55     60
Gly Val Val Leu Leu Phe Ala Val Leu Val Leu Tyr Arg Arg Leu
65     70     75     80
Leu Pro Pro Phe Ile Asn Val Met Ser Leu Ala Val Ala Pro Leu Gly
85     90     95
Gly Leu Ile Gly Leu Trp Leu Thr Asn Thr Pro Ile Ser Met Pro Val
100    105    110
Tyr Ile Gly Leu Ile Met Leu Leu Gly Ile Val Ala Lys Asn
115    120    125

```

<210> 2457
 <211> 754
 <212> DNA
 <213> Homo sapiens

<400> 2457
 cctaggaatt taccaccatc aaagacttac attaaccagc tatccatgaa ctcacctgag
 60
 atgagcgaat gtgacatctt gcacactctg cgtgggtctt ctgggctccg gatcagctcc
 120
 tatgtcaact ggataaagga tcaccttattc aaacagggaa tgaaggctga gcattgctagc
 180
 tcgcttctag aactggcacc caccactaag tgtagctcag tgaatatga tgttgaataa
 240
 gtagaggaat acttcgctcg acagatctca tccttctgta gtatcgactg tgccaccatc
 300
 ttgcagctgc atgaaattcc cagtctgcag tccatctaca ccttgatgc cgcgattcta
 360
 aaaggcccg gtcttttttg gatgagcatt tttctaagat ggctgctgag actgatcctc
 420
 ataagtctgc tgagattacc aagaacctac ttccagccac gctgcaactc attgacacct
 480
 atgcctcgtt caccagagcc tatttgctgc aaaactttaa tgaagaggga acaactgaga
 540
 aaccttccaa ggagaaactg caaggctttg ctgctgtttt ggctattggc tctagcaggt
 600
 gcaaggcaaa tactctgggt ccgacactgg ttcagaattt gccatcgta gtgcgactg
 660
 tgtgtgagtc ctggaacaac atcaatacca atgaatttcc caatattgga tcctggcgca
 720
 atgcctttgc caatgacacc atcccttcac gcgt
 754

<210> 2458
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 2458
 Met Asn Ser Pro Glu Met Ser Glu Cys Asp Ile Leu His Thr Leu Arg
 1 5 10 15
 Trp Ser Ser Arg Leu Arg Ile Ser Ser Tyr Val Asn Trp Ile Lys Asp
 20 25 30
 His Leu Ile Lys Gln Gly Met Lys Ala Glu His Ala Ser Ser Leu Leu
 35 40 45
 Glu Leu Ala Ser Thr Thr Lys Cys Ser Ser Val Lys Tyr Asp Val Glu
 50 55 60
 Ile Val Glu Glu Tyr Phe Ala Arg Gln Ile Ser Ser Phe Cys Ser Ile
 65 70 75 80
 Asp Cys Ala Thr Ile Leu Gln Leu His Glu Ile Pro Ser Leu Gln Ser
 85 90 95
 Ile Tyr Thr Leu Asp Ala Ala Ile Leu Lys Gly Pro Gly Leu Phe Gly
 100 105 110
 Met Ser Ile Phe Leu Arg Trp Leu Leu Arg Leu Ile Leu Ile Ser Arg
 115 120 125
 Leu Arg Leu Pro Arg Thr Tyr Phe Gln Pro Arg Cys Asn Ser Leu Thr
 130 135 140
 Pro Met His Arg Ser Pro Glu Pro Ile Cys Cys Lys Thr Leu Met Lys

```

145             150             155             160
Arg Glu Gln Leu Arg Asn Leu Pro Arg Arg Asn Cys Lys Ala Leu Leu
165             170             175
Leu Phe Trp Leu Leu Ala Leu Ala Gly Ala Arg Gln Ile Leu Trp Val
180             185             190
Arg His Trp Phe Arg Ile Cys His Arg Gln Cys Arg Leu Cys Val Ser
195             200             205
Pro Gly Thr Thr Ser Ile Pro Met Asn Phe Pro Ile Leu Asp Pro Gly
210             215             220
Ala Met Pro Leu Pro Met Thr Pro Ser Leu His Ala
225             230             235

```

<210> 2459

<211> 382

<212> DNA

<213> Homo sapiens

<400> 2459

```

accggtgcac agatcgttct gcccgctgc actgccccgc tcaagcaaat cgctatcaac
60
gctggtcttg agggcgccgt cgtggctgag aaggtcgtg gtctgccccg aggacaggcg
120
ctcaacgcgg ccaatgacga gtatgtcgac atggtagagg ccggcatcat tgacccggcc
180
aaggtgaccc gttcggctct gcagaacgcc gcgtccatcg cggccctgtt cctcaccact
240
gaagccgtca tcgctgacaa gcccgagcct gttaaggctc ccgtggcg cggtgatatg
300
gacggtatgg gtggcatggg cggcgatgat tgatcgtgta ttgccttcgc tgatttgagt
360
gggatgccac ttgccccag gc
382

```

<210> 2460

<211> 110

<212> PRT

<213> Homo sapiens

<400> 2460

```

Thr Gly Ala Gln Ile Val Leu Ala Ala Cys Thr Ala Pro Leu Lys Gln
1             5             10             15
Ile Ala Ile Asn Ala Gly Leu Glu Gly Gly Val Val Ala Glu Lys Val
20             25             30
Ala Gly Leu Pro Ala Gly Gln Gly Leu Asn Ala Ala Asn Asp Glu Tyr
35             40             45
Val Asp Met Val Glu Ala Gly Ile Ile Asp Pro Ala Lys Val Thr Arg
50             55             60
Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Ala Leu Phe Leu Thr Thr
65             70             75             80
Glu Ala Val Ile Ala Asp Lys Pro Glu Pro Val Lys Ala Pro Ala Gly
85             90             95
Gly Gly Asp Met Asp Gly Met Gly Gly Met Gly Gly Met Met
100             105             110

```

<210> 2461
 <211> 558
 <212> DNA
 <213> Homo sapiens

<400> 2461
 tccggacaaa aggggttcaat cgaagtatgg ttagcctttt ccaagtcgcc aggacggacc
 60
 tgcaatgctg tttgtcgtca tgctcggggg caagcaccca cgggctaaaa tcgaaattca
 120
 cgatgtggta ttgcagtcg cggatagcgt gcaacacacc tacaccaat tgcgcgacgg
 180
 ctgggttcggc agccctaagg tgtgcatac gatgcgtgga tggcgcgcga tggcgcgcac
 240
 ggctggaaa tcgaactcag ccagatggcg ccgcctgccg acgcgcacga cctgtacttc
 300
 atcaacctcg gcggctacga ggccaacgct ttggcgagg cccatcatta cctgctgggtg
 360
 gtgcgccggg acaaacagga agccaagcgc aaggggcagc ggcaaatgtt gcaacactgg
 420
 tcccaggccc acaccgatgg cgtaatggat atcgacgact gcttgccgat tgatctgggtg
 480
 gacggtcgct atgttcacct ggtgcaagcg ccgcaccagc cgatcatcca gcacaacgac
 540
 tacatcatcc tgccgcga
 558

<210> 2462
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 2462
 Met Val Ser Leu Phe Gln Val Ala Arg Thr Asp Leu Gln Cys Cys Leu
 1 5 10 15
 Ser Ser Cys Ser Gly Ala Ser Thr His Gly Leu Lys Ser Lys Phe Thr
 20 25 30
 Met Trp Tyr Ser Gln Ser Arg Ile Arg Cys Asn Thr Pro Thr Pro Asn
 35 40 45
 Cys Ala Thr Ala Gly Ser Ala Ala Leu Arg Cys Ala Tyr Arg Cys Val
 50 55 60
 Asp Gly Arg Arg Trp Arg Arg Leu Glu Ser Arg Thr Gln Pro Asp
 65 70 75 80
 Gly Ala Ala Cys Arg Arg Ala Ser Pro Val Leu His Gln Pro Arg Arg
 85 90 95
 Leu Arg Gly Gln Arg Phe Trp Arg Gly Pro Ser Leu Pro Ala Gly Gly
 100 105 110
 Arg Pro Gly Gln Thr Gly Ser Gln Ala Gln Gly Ala Ala Ala Asn Val
 115 120 125
 Ala Thr Leu Val Pro Gly Pro His Arg Trp Arg Asn Gly Tyr Arg Arg
 130 135 140
 Leu Leu Ala Asp
 145

<210> 2463
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 2463
 cccagggggt aagccatgag cctgttgagc caagtggccc gggcgccgtt gagcgccaag
 60
 ttccgctctgc tgattattct gttatacgtc gcgctggcgc tgtgngcgcc gctgctggcg
 120
 ccctatggcg aaaccagggt ggtgggtgaa ggcttcgcgc cgtggagcgg ccagtttttg
 180
 ctgggcaccg ataacctggg gcgcgacatg ttcagccgcc tgatgtacgg cgcgcgcaat
 240
 accttgggca ttgccttctt gacgacgacg ctggcgcttc tgctcggtgg tttgagcggg
 300
 ttggtcgcgg cgatcaaggg cgggtgggtc gac
 333

<210> 2464
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 2464
 Met Ser Leu Leu Ser Gln Val Ala Arg Ala Pro Leu Ser Ala Lys Phe
 1 5 10 15
 Gly Leu Leu Ile Ile Leu Leu Tyr Val Ala Leu Ala Leu Xaa Ala Pro
 20 25 30
 Leu Leu Ala Pro Tyr Gly Glu Thr Gln Val Val Gly Glu Gly Phe Ala
 35 40 45
 Pro Trp Ser Gly Gln Phe Leu Leu Gly Thr Asp Asn Leu Gly Arg Asp
 50 55 60
 Met Phe Ser Arg Leu Met Tyr Gly Ala Arg Asn Thr Leu Gly Ile Ala
 65 70 75 80
 Phe Leu Thr Thr Thr Leu Ala Phe Leu Leu Gly Gly Leu Ser Gly Leu
 85 90 95
 Val Ala Ala Ile Lys Gly Gly Trp Val Asp
 100 105

<210> 2465
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 2465
 nntcatgagg acatttcctt catatttggt ggtggtaaata cctcctggg acacggggga
 60
 atgaccagag gctggcgccc cacctggcag gaacagatgc cagctctgct gcagccatcg
 120
 ccccttgagc ggggtggctct gtgcctcttt ctgcactgct ggtgggtggg gctgttggt
 180
 ggggtgatga taccggctgc cagagatggc tcagggtcca gctgctgggc tatctcaggc
 240

actggctgct gggctatctc ggggtgccgc tgctgggcta tctcaggcgc tggctgctgc
 300
 tgggtgtctc cgggtgctgg ctgttgggac gtctcctgtc ctggcactgg gctctcgggt
 360
 gctgggtgcc agctgtctgc taccttgac tgggctctgg gcactcactg cactcgggct
 420
 tttccatctc cgac
 434

<210> 2466
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 2466
 Trp Ile Pro Ala Ala Arg Asp Gly Ser Gly Ala Ser Cys Trp Ala Ile
 1 5 10 15
 Ser Gly Thr Gly Cys Trp Ala Ile Ser Gly Ala Gly Cys Trp Ala Ile
 20 25 30
 Ser Gly Ala Gly Cys Cys Trp Ala Val Ser Gly Ala Gly Cys Trp Asp
 35 40 45
 Val Ser Cys Pro Gly Thr Gly Leu Ser Gly Ala Gly Cys Gln Leu Leu
 50 55 60
 Pro Thr Leu His Trp Ala Leu Gly Thr His Cys Thr Arg Ala Phe Pro
 65 70 75 80
 Ser Pro

<210> 2467
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 2467
 atggactcca ccggcaccgg agcagggggg aaggggaaga agggagcggc cgggcgcaag
 60
 gtcggcgggc caaggaagaa gtcgggtgtc aggtccgtga aggcgggtct ccagttcccc
 120
 gtcggccgca tcgggcgcta cttgaagaag ggccgctacg cgcagcgtgt cggcaccggc
 180
 gccccgtct acctcgccgc tgctctcgaa tacctcgccg ctgaggttct ggagctcgcc
 240
 ggtaagtgtc ccagggaaca caagaagact cgcattattc cgcgccacgt gcttctggcg
 300
 atccgg
 306

<210> 2468
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 2468
 Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Lys Gly Ala

```

      1           5           10           15
Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser
      20           25           30
Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Leu
      35           40           45
Lys Lys Gly Arg Tyr Ala Gln Arg Val Gly Thr Gly Ala Pro Val Tyr
      50           55           60
Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val Leu Glu Leu Ala
      65           70           75           80
Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile Ile Pro Arg His
      85           90           95
Val Leu Leu Ala Ile Arg
      100

```

<210> 2469

<211> 489

<212> DNA

<213> Homo sapiens

<400> 2469

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gccggcggtgg cacatggcctt ccctgaagcc agcattgcc tggccaagga agctttgcag
60
aacagatgag atttcagctg ggacttgcag ccaagtggga tttggccttt tggggagaag
120
ggaaaggcca ttcaaaggcc agggacagag tatggtcaaa ggcattggaga tgaggaagag
180
gggaccagag cagaggggtca ggttggaagg cgagttgggg tcaatctgca aaggggctga
240
cgtgccaggt aaaaaacagg agcacagttt agttttgtcg gatcatttca ggtggaaggg
300
cagtggaagt gttggagaaa acactttttg gtgtcgttac attgaatctg ctcattcata
360
agaataaaac ttatttcat agagtatttg tatggctcaa aataggatat aagaattaag
420
aaaaagaatt ttagatttaa aatgaaaagg cacctacaaa agtagagtgg tagagttacc
480
aacgtggag
489

```

<210> 2470

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2470

```

Met Ala Ser Leu Lys Pro Ala Leu Pro Trp Pro Arg Lys Leu Cys Arg
1           5           10           15
Thr Asp Glu Ile Ser Ala Gly Thr Cys Ser Gln Val Gly Phe Gly Leu
      20           25           30
Leu Gly Arg Arg Glu Arg Ala Phe Lys Gly Gln Gly Gln Ser Met Val
      35           40           45
Lys Gly Met Glu Met Arg Lys Arg Gly Pro Glu Gln Arg Val Arg Leu
      50           55           60
Glu Ser Glu Leu Gly Ser Ile Cys Lys Gly Ala Asp Val Pro Gly Lys

```

```

65              70              75              80
Lys Gln Glu His Ser Leu Val Leu Ser Asp His Phe Arg Trp Lys Gly
              85              90              95
Ser Gly Asn Val Gly Glu Asn Thr Phe Trp Cys Arg Tyr Ile Glu Ser
              100              105              110
Ala His Leu
              115

```

```

<210> 2471
<211> 779
<212> DNA
<213> Homo sapiens

```

```

<400> 2471
tggccatcct ccgtgacatg tacacttcca atatgccggt gtttgagccg ttcatagatc
60
ctcacatggt ggccttgac ttctttcaca gtgaggacct ctgcttcatg aggcctataa
120
gaagaggagc taaggactat ttgtcatgg gggcgccaat ccactgcac ttctactata
180
attctctcat ttctgaggc aatatcagct ccaagatgtg tccaggagtt cttaggataa
240
gcactgtaaa gatgaacttt ccataaaacc ccaattgttc ctgggtcaat atgaattcca
300
ttcatacggt cacaaaagac tccctctgag gctctaagga gaatcagaag cttttgttcc
360
ttttctaagg gattttctaa agtaccaact ttcagctccc cgctgcaat gaccatgcat
420
gccacactca gaacattgct tctgtccaca gggaagtcta aggtcccat cacatacagc
480
cctttgaaga attggaaaat ctgtatccac aaggacagtt ctgttgggta aaatgagaac
540
gtcatcccca gggcctggaa tggatttgtt gtatcctccc cagccttctt caacaccttg
600
ccatgtttca gggaggggacc attttaaaagc tgattcaggg gcagaggtag aagctgaaat
660
agttgggggc ataccttctc tcaccggag aatgacttga acttggcctt cacctaaaac
720
cagataggtg agttgcctca gctggctatt gaagaaccag tcacagcctt ggttctggc
779

```

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<210> 2472
<211> 181
<212> PRT
<213> Homo sapiens

```

```

<400> 2472
Met Thr Phe Ser Phe Tyr Pro Thr Glu Leu Ser Leu Trp Ile Gln Ile
1              5              10              15
Phe Gln Phe Phe Lys Gly Leu Tyr Val Met Gly Thr Leu Asp Phe Pro
              20              25              30
Val Asp Arg Ser Asn Val Leu Ser Val Ala Cys Met Val Ile Ala Gly
              35              40              45
Gly Glu Leu Lys Val Gly Thr Leu Glu Asn Pro Leu Glu Lys Glu Gln

```

```

      50              55              60
Lys Leu Leu Ile Leu Leu Arg Ala Ser Glu Gly Val Phe Cys Asp Arg
65              70              75              80
Met Asn Gly Ile His Ile Asp Pro Gly Thr Ile Gly Val Tyr Gly Lys
      85              90              95
Val His Leu Tyr Ser Ala Tyr Pro Lys Asn Ser Trp Thr His Leu Gly
      100              105              110
Ala Asp Ile Ala Ser Gly Asn Glu Arg Ile Ile Val Glu Asp Ala Val
      115              120              125
Asp Trp Arg Pro His Asp Lys Ile Val Leu Ser Ser Ser Tyr Glu
      130              135              140
Pro His Glu Ala Glu Val Leu Thr Val Lys Glu Val Lys Gly His His
145              150              155              160
Val Arg Ile Tyr Glu Arg Leu Lys His Arg His Ile Gly Ser Val His
      165              170              175
Val Thr Glu Asp Gly
      180

```

<210> 2473

<211> 698

<212> DNA

<213> Homo sapiens

<400> 2473

```

nngtgcacca agaaatggca gcctgacaag ctggtggttg tatggactcg gcggaaccga
60
cgcatctgct ccaaggccca cagctggcag ccgngggcat ccagaaccca taccggggga
120
ccgtggtgtg gatggtacnc tgagaatgtg gacatctctg tgaccctcta cagggacccc
180
cacgtggacc agtatgaggc caaagagtgg acattttatta ttgaaaatga gtctaagggg
240
cagcggaagg tgctggccac ggccgaggtg gacctggccc gccatgccag ggcccggtgc
300
ntgtccaagt ccnactgag gctgcggctg aagccaaagt cagtgaagac ggtgcaggct
360
gagctgagcc tcaactcttc cgggggtgctg ctgcgggagg gccgtgccac ggacgatgac
420
atgcagagtc tcgcaagcct catgagtgtg aagcctagtg atgtggggcaa cttggatgac
480
tttgctgaga gtgatgaaga tgaggctcat ggcccaggag ccccggaggc ccgggctcga
540
gtcccccagc caggtgggct cacagcctgc tgtggatcga gactgccaa acctggggag
600
ggagggttac ccgggccacc agccacttgc tgtgccgcc ctgtgatggg aactcattac
660
tgcccaggga gtcccaacca acccagcagc ctcaattg
698

```

<210> 2474

<211> 232

<212> PRT

<213> Homo sapiens

<400> 2474

Xaa Cys Thr Lys Lys Trp Gln Pro Asp Lys Leu Val Val Val Trp Thr
 1 5 10 15
 Arg Arg Asn Arg Arg Ile Cys Ser Lys Ala His Ser Trp Gln Pro Xaa
 20 25 30
 Ala Ser Arg Thr His Thr Gly Ala Pro Trp Cys Gly Trp Tyr Xaa Glu
 35 40 45
 Asn Val Asp Ile Ser Val Thr Leu Tyr Arg Asp Pro His Val Asp Gln
 50 55 60
 Tyr Glu Ala Lys Glu Trp Thr Phe Ile Ile Glu Asn Glu Ser Lys Gly
 65 70 75 80
 Gln Arg Lys Val Leu Ala Thr Ala Glu Val Asp Leu Ala Arg His Ala
 85 90 95
 Arg Ala Arg Ala Xaa Ser Lys Ser Xaa Leu Arg Leu Lys Pro
 100 105 110
 Lys Ser Val Lys Thr Val Gln Ala Glu Leu Ser Leu Thr Leu Ser Gly
 115 120 125
 Val Leu Leu Arg Glu Gly Arg Ala Thr Asp Asp Met Gln Ser Leu
 130 135 140
 Ala Ser Leu Met Ser Val Lys Pro Ser Asp Val Gly Asn Leu Asp Asp
 145 150 155 160
 Phe Ala Glu Ser Asp Glu Asp Glu Ala His Gly Pro Gly Ala Pro Glu
 165 170 175
 Ala Arg Ala Arg Val Pro Gln Pro Gly Gly Leu Thr Ala Cys Cys Gly
 180 185 190
 Ser Arg Leu Pro Arg Pro Gly Glu Gly Gly Leu Pro Gly Pro Pro Ala
 195 200 205
 Thr Cys Cys Ala Arg Pro Val Met Gly Thr His Tyr Cys Pro Gly Ser
 210 215 220
 Pro Asn Gln Pro Ser Ser Leu Asn
 225 230

<210> 2475

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 2475

ngcgcgcccg agatgcaggt gagcaagagg atgctggcgg ggggcgtgag gagcatgccc
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 agccccctcc tggcctgctg gcagcccatc ctccctgttg tgctgggctc agtgcgtgca
 120
 ggctcggcca cgggtgccc gccccgtgc gagtgctccg cccaggaccg cgctgtgctg
 180
 tgccaccgca agcgccttctt ggagctcccc gagggcatcc ccaccgagac gcgcctgctg
 240
 gacctaggca agaaccgcat caaaacgctc aaccaggacg agttcgccag cttcccgcac
 300
 ctggaggagc tggagctcaa cgagaacatc gtgagcgccg tggagcccg cgccttcaac
 360
 aacctcttca acctccggac gctgggtctc cgcagcaacc gcctgaagct catcccgtca
 420
 ggcgtcttca ctggcctcag caacctgacc aagctggaca tcagcgagaa caagatcggt
 480

atcctactgg actacatggt tcaggacctg tacaacctca agtcactgga ggttggcgac
 540
 aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc tcaacagcct ggagcagctg
 600
 acgctggaga aatgcaacct gacctccatc cccaccgagg cgctgtccca cctgcacggc
 660
 ctcatcgctc tgaggctccg gcacctcaac atcaatgcc a tccgggacta ctccttcaag
 720
 aggcgtgacc gactcaaggt ctggagatc tccactggc cctacttgga caccatgaca
 780
 cccaactgcc tctacggcct caacctgacg tccctgtcca tcacacactg caatctgacc
 840
 gctgtgcctt acctggccgt ccgccaccta gtctatctcc gcttctctaa cctctctac
 900
 aacccccatca gcaccattga gggctccatg ttgcatgagc tgctccggct gcaggagatc
 960
 cagctggtgg gcgggcagct gcccggtgg agccctgctt tccggcgctt caactacctg
 1020
 cgctgtgctca atgtctctgg caaccagctg accacactgg aggaatcagt cttccactcg
 1080
 gtgggcaacc tggagacact catcctggac tccaaccgcg tggcctgcga ctgtcgctc
 1140
 ctgtgggtgt tccggcgccg tggcctacaa acttcaaccg gcagcagccc acgtgcgcca
 1200
 cgccccagtt tgtccagggg caaggagttc aaggacttcc ctgattgtct a
 1251

<210> 2476

<211> 417

<212> PRT

<213> Homo sapiens

<400> 2476

Xaa	Ala	Pro	Glu	Met	Gln	Val	Ser	Lys	Arg	Met	Leu	Ala	Gly	Gly	Val
1			5					10					15		
Arg	Ser	Met	Pro	Ser	Pro	Leu	Leu	Ala	Cys	Trp	Gln	Pro	Ile	Leu	Leu
		20						25				30			
Leu	Val	Leu	Gly	Ser	Val	Leu	Ser	Gly	Ser	Ala	Thr	Gly	Cys	Pro	Pro
		35					40					45			
Arg	Cys	Glu	Cys	Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys
	50					55				60					
Arg	Phe	Val	Ala	Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	Leu
	65				70				75					80	
Asp	Leu	Gly	Lys	Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	Phe	Ala
			85					90						95	
Ser	Phe	Pro	His	Leu	Glu	Glu	Leu	Glu	Leu	Asn	Glu	Asn	Ile	Val	Ser
		100						105					110		
Ala	Val	Glu	Pro	Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Thr	Leu
		115					120					125			
Gly	Leu	Arg	Ser	Asn	Arg	Leu	Lys	Leu	Ile	Pro	Leu	Gly	Val	Phe	Thr
	130					135					140				
Gly	Leu	Ser	Asn	Leu	Thr	Lys	Leu	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val
	145				150					155				160	
Ile	Leu	Leu	Asp	Tyr	Met	Phe	Gln	Asp	Leu	Tyr	Asn	Leu	Lys	Ser	Leu

65					170					175						
Glu	Val	Gly	Asp	Asn	Asp	Leu	Val	Tyr	Ile	Ser	His	Arg	Ala	Phe	Ser	
180					185					190						
Gly	Leu	Asn	Ser	Leu	Glu	Gln	Leu	Thr	Leu	Glu	Lys	Cys	Asn	Leu	Thr	
195					200					205						
Ser	Ile	Pro	Thr	Glu	Ala	Leu	Ser	His	Leu	His	Gly	Leu	Ile	Val	Leu	
210					215					220						
Arg	Leu	Arg	His	Leu	Asn	Ile	Asn	Ala	Ile	Arg	Asp	Tyr	Ser	Phe	Lys	
225					230					235					240	
Arg	Leu	Tyr	Arg	Leu	Lys	Val	Leu	Glu	Ile	Ser	His	Trp	Pro	Tyr	Leu	
245					250					255						
Asp	Thr	Met	Thr	Pro	Asn	Cys	Leu	Tyr	Gly	Leu	Asn	Leu	Thr	Ser	Leu	
260					265					270						
Ser	Ile	Thr	His	Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	
275					280					285						
His	Leu	Val	Tyr	Leu	Arg	Phe	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	
290					295					300						
Thr	Ile	Glu	Gly	Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	
305					310					315					320	
Gln	Leu	Val	Gly	Gly	Gln	Leu	Ala	Gly	Trp	Ser	Pro	Ala	Phe	Arg	Gly	
325					330					335						
Leu	Asn	Tyr	Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	
340					345					350						
Leu	Glu	Glu	Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	
355					360					365						
Leu	Asp	Ser	Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	
370					375					380						
Arg	Arg	Arg	Gly	Leu	Gln	Thr	Ser	Thr	Gly	Ser	Ser	Pro	Arg	Ala	Pro	
385					390					395					400	
Arg	Pro	Ser	Leu	Ser	Arg	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	
405					410					415						
Leu																

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<210> 2477
<211> 548
<212> DNA
<213> Homo sapiens
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400> 2477
nagactgcga tcagacgcgc gtgccagct gaaccagggt cgtgagaagg ctgccttcag
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gtggccgggg gtcctctcca gctgtctctg gacggaggga cgggaagtg ccagaagggg
120
aagtgtgagg agttccctgc cagcctgtca tcagtctccc cagggtcttg agcggcggcc
180
ctgctcctgt ccgtgaccat ggaccctctg gagaccctta tcaaggatgg catcctctac
240
cagcagcatg tcaagtttgg caagaagtg tggcggaagg tgtgggctct gctgtatgca
300
ggaggcccat caggcgtggc acggctggag aactgggagg tccgggatgg tggcctggga
360
gcagcgggtg acaggtcggc ggggcctggc cggcgagggg agcgacgggt catccgcctg
420

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gctgactgtg tgtccgtgct gccggctgac ggcgagagct gcccccgga caccggtgcc
 480
 ttctgtctca ccaccaccga gcgaagccat ctactggctg ctcagcaccg ccaggcctgg
 540
 atgggccc
 548

<210> 2478<211> 113

<212> PRT

<213> Homo sapiens

<400> 2478

Leu	Glu	Thr	Pro	Ile	Lys	Asp	Gly	Ile	Leu	Tyr	Gln	Gln	His	Val	Lys
1			5					10					15		
Phe	Gly	Lys	Lys	Cys	Trp	Arg	Lys	Val	Trp	Ala	Leu	Leu	Tyr	Ala	Gly
		20						25				30			
Gly	Pro	Ser	Gly	Val	Ala	Arg	Leu	Glu	Asn	Trp	Glu	Val	Arg	Asp	Gly
		35				40					45				
Gly	Leu	Gly	Ala	Ala	Gly	Asp	Arg	Ser	Ala	Gly	Pro	Gly	Arg	Arg	Gly
	50					55				60					
Glu	Arg	Arg	Val	Ile	Arg	Leu	Ala	Asp	Cys	Val	Ser	Val	Leu	Pro	Ala
65			70						75				80		
Asp	Gly	Glu	Ser	Cys	Pro	Arg	Asp	Thr	Gly	Ala	Phe	Leu	Leu	Thr	Thr
			85					90					95		
Thr	Glu	Arg	Ser	His	Leu	Leu	Ala	Ala	Gln	His	Arg	Gln	Ala	Trp	Met
			100					105					110		

Gly

<210> 2479

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2479

gaattcatgg aggtctatga ggaggatgaa gaatatgcgt atgaaaaata tgaaacccat
 60
 ttccgcacga gctggatgga ggagaccgca ggcaccttct cactgaactg gtatcgacgc
 120
 aggtactgga atgacaatga agcagcagaa aggcttgcgt tgatgtgggc taaaaccttc
 180
 aaatatgcgt cgataaacgt ctctggcag accgggatta gcaatagcga cgacgagggc
 240
 aatgaagatg aagacatggt ctacgccggt atctccattc cgctgggagg cggggcgatc
 300
 tctaactcct ggtatcgtga atat
 324

<210> 2480

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2480


```

Glu Phe Met Glu Val Tyr Glu Glu Asp Glu Glu Tyr Ala Tyr Glu Lys
 1             5             10             15
Tyr Glu Thr His Phe Gly Thr Ser Trp Met Glu Glu Thr Ala Gly Thr
      20             25             30
Phe Ser Leu Asn Trp Tyr Arg Ser Arg Tyr Trp Asn Asp Asn Glu Ala
      35             40             45
Ala Glu Arg Leu Ala Leu Met Trp Ala Lys Thr Phe Lys Tyr Ala Ser
      50             55             60
Ile Asn Val Ser Trp Gln Thr Gly Ile Ser Asn Ser Asp Asp Glu Gly
      65             70             75             80
Asn Glu Asp Glu Asp Met Phe Tyr Ala Gly Ile Ser Ile Pro Leu Gly
      85             90             95
Gly Gly Ala Tyr Ser Asn Ser Trp Tyr Arg Glu Tyr
      100             105

```

<210> 2481

<211> 484

<212> DNA

<213> Homo sapiens

<400> 2481

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gcgttcacta acgcttcaac aaactcttac aagcgtcttg ttccctgggtt cgaagcacct
60
ggtatgttgg cttactcagc tcgtaaccgt tctgcttcta tccgatatcc atacgttgca
120
agccctaaag gcaagcgtat tgaagctcgt ttccctgatc caaccgctaa cccataccta
180
gcatttttcag ctatgttgat ggctgggtatc gatggtatca aaaacaagat tcaccctggc
240
gatgcagcag acaaagattt gtacgacctt ccagctgaag aagcagccgc tatccctcaa
300
gttgcttagca gcttagaaga agcgcttaag tgcctagatc aagaccgtga gttcttgact
360
caagggtggcg ttttctctga cgacatgatc gatgcttaca tcgctcttaa agcagaagaa
420
gcacagcgtg ttgcaatgac aacaacacca cttgagttcg aactttacta cagcctataa
480
gctt
484

```

<210> 2482

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2482

```

Ala Phe Thr Asn Ala Ser Thr Asn Ser Tyr Lys Arg Leu Val Pro Gly
 1             5             10             15
Phe Glu Ala Pro Val Met Leu Ala Tyr Ser Ala Arg Asn Arg Ser Ala
      20             25             30
Ser Ile Arg Ile Pro Tyr Val Ala Ser Pro Lys Gly Lys Arg Ile Glu
      35             40             45
Ala Arg Phe Pro Asp Pro Thr Ala Asn Pro Tyr Leu Ala Phe Ser Ala
      50             55             60

```

```

Met Leu Met Ala Gly Ile Asp Gly Ile Lys Asn Lys Ile His Pro Gly
65              70              75              80
Asp Ala Ala Asp Lys Asp Leu Tyr Asp Leu Pro Ala Glu Glu Ala Ala
85              90              95
Ala Ile Pro Gln Val Ala Ser Ser Leu Glu Glu Ala Leu Lys Cys Leu
100             105             110
Asp Gln Asp Arg Glu Phe Leu Thr Gln Gly Gly Val Phe Ser Asp Asp
115             120             125
Met Ile Asp Ala Tyr Ile Ala Leu Lys Ala Glu Glu Ala Gln Arg Val
130             135             140
Ala Met Thr Thr Thr Pro Leu Glu Phe Glu Leu Tyr Ser Leu
145             150             155

```

<210> 2483

<211> 477

<212> DNA

<213> Homo sapiens

<400> 2483

```

acgcgtgttta gccaaatctt ggttctctccc gttctctcct taccgcagcc tgaggccctt
60
ctggagaaca ggcagcctct gaggaaacct ctgatccccc atcagccacc ccctgccttg
120
cgtccccagc cgcttctctc tggccttggt cccctctccc tgtgaaggag agaacagttt
180
cggtgtgccc tgagatgctg gcagcctcgc agtcagggca gtgggcgcct cccaccttga
240
aatgggtcctt cgtggtgcag ttctgcttac ggggtagact ttgttgccct ccacagagga
300
cagtttagggt gggcaggaag gaagtctctg ccacaagtct gcattccagg ctgtttccag
360
aagtgggaat tctctcgtgc cctggagtct gggaatgcat ttttagtttc ccagcttcag
420
gtagaattga aattgagtga gccaacccac cacatccatc tggagccagg aactagt
477

```

<210> 2484

<211> 130

<212> PRT

<213> Homo sapiens

<400> 2484

```

Met His Ser Gln Thr Pro Gly His Glu Arg Ile Pro Thr Ser Gly Asn
1              5              10              15
Ser Leu Glu Cys Arg Leu Val Ala Glu Thr Ser Phe Leu Pro Thr Leu
20             25             30
Thr Val Leu Cys Gly Arg Gln Gln Ser Leu Pro Arg Lys Gln Asn Cys
35             40             45
Thr Thr Lys Asp His Phe Lys Val Gly Gly Ala His Cys Pro Asp Cys
50             55             60
Arg Pro Ala Ser Ile Ser Gly Pro Ala Glu Thr Val Leu Ser Phe Thr
65             70             75             80
Gly Lys Gly Glu Gln Gly Gln Glu Glu Ala Ala His Asp Ala Gly Asp
85             90             95

```

Gly Val Ala Asp Arg Gly Ser Glu Val Ser Ser Glu Ala Ala Cys Ser
 100 105 110
 Pro Glu Gly Pro Gln Ala Arg Val Arg Arg Glu Arg Glu Glu Pro Arg
 115 120 125
 Phe Gly
 130

<210> 2485
 <211> 608
 <212> DNA
 <213> Homo sapiens

<400> 2485
 accggtgagg cgaagtgcgg tggcaattac gcagcttcgc tgcgttccca gatcgatgcc
 60
 aagacccgcg actgcaacga ggtgctcttt gtcgatgcag ttgaacatcg ctggatcgag
 120
 gagctggggt gtatgaactt catggccatc agcaaagacg gtcagctcgt caccctcgag
 180
 ctagtctgga ccatcctcgc tggcgtgacc cgcaagtcca ttctggaagt tgccccgcac
 240
 ctcggtcttt aaccagtgga gcgcaagatc gatgttgacg agctccttga tggcgcttcg
 300
 tctggcgagt tcccgggaagt ctctgcctgt ggtaccgcg cggttgctac accgatcggc
 360
 tctttcctag atggagatag cgacgtgaag gtctctgagc ccaccggaaa gaccacgatg
 420
 gagatccgct gcgctctgct ggatatccag ttcggacgcg ctgaggacac ccatggctgg
 480
 ttgaagcgag tctgctgacg gcgtcgacga ccattggggc cgcccccaat gatgtgttca
 540
 cgatcgggct acgacggtgt cgatgacaat gtcttgcggc tggaaagggtt gcccgacggt
 600
 gaacgcgt
 608

<210> 2486
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 2486
 Thr Gly Glu Ala Lys Cys Gly Gly Asn Tyr Ala Ala Ser Leu Arg Ser
 1 5 10 15
 Gln Ile Asp Ala Lys Thr Arg Asp Cys Asn Glu Val Leu Phe Val Asp
 20 25 30
 Ala Val Glu His Arg Trp Ile Glu Glu Leu Gly Gly Met Asn Phe Met
 35 40 45
 Ala Ile Ser Lys Asp Gly Gln Leu Val Thr Pro Glu Leu Ala Gly Thr
 50 55 60
 Ile Leu Arg Gly Val Thr Arg Lys Ser Ile Leu Glu Val Ala Pro Asp
 65 70 75 80
 Leu Gly Leu Glu Pro Val Glu Arg Lys Ile Asp Val Asp Glu Leu Leu
 85 90 95

```

Asp Gly Val Arg Ser Gly Glu Phe Pro Glu Val Phe Ala Cys Gly Thr
      100      105      110
Ala Ala Val Val Thr Pro Ile Gly Ser Phe Leu Asp Gly Asp Thr Asp
      115      120      125
Val Lys Val Ser Glu Pro Thr Gly Lys Thr Thr Met Glu Ile Arg Arg
      130      135      140
Arg Leu Leu Asp Ile Gln Phe Gly Arg Ala Glu Asp Thr His Gly Trp
145      150      155      160
Leu Lys Arg Val Cys
      165

```

```

<210> 2487
<211> 339
<212> DNA
<213> Homo sapiens

```

```

<400> 2487
nnccctcag gagagcagcc catggaaggt ccccccaag gggccctga gagccctgac
60
agtctgcaaa gaaaccagaa agagctccag ggccctcctga cccaggtgca agccctggag
120
aaggaggcgc caagcagtgt ggacgtgcag gccctgcgga ggctctttga ggccgtgccc
180
cagctgggag gggctgctcc tcaggctcct gctgcccacc aaaagccccg ggcctcagtg
240
gagcaggcct ttggggagct gacacgggtc agcacggaag ttgtcctaact gaaggaacag
300
accttggtaa ggctgctgga cattgaagag gctgtgcac
339

```

```

<210> 2488
<211> 113
<212> PRT
<213> Homo sapiens

```

```

<400> 2488
Xaa Pro Ser Gly Glu Gln Pro Met Glu Gly Pro Pro Gln Gly Ala Pro
1      5      10      15
Glu Ser Pro Asp Ser Leu Gln Arg Asn Gln Lys Glu Leu Gln Gly Leu
20      25      30
Leu Thr Gln Val Gln Ala Leu Glu Lys Glu Ala Ala Ser Ser Val Asp
35      40      45
Val Gln Ala Leu Arg Arg Leu Phe Glu Ala Val Pro Gln Leu Gly Gly
50      55      60
Ala Ala Pro Gln Ala Pro Ala Ala His Gln Lys Pro Glu Ala Ser Val
65      70      75      80
Glu Gln Ala Phe Gly Glu Leu Thr Arg Val Ser Thr Glu Val Ala Gln
85      90      95
Leu Lys Glu Gln Thr Leu Val Arg Leu Leu Asp Ile Glu Glu Ala Val
100      105      110
His

```

```

<210> 2489

```

<211> 594

<212> DNA

<213> Homo sapiens

<400> 2489

nacgcgttct tcggactggc gacgatgctg atttctatcc cgacgggggt gaagctattt
 60
 aactggctgg tcaccatcta tcacggccgg gtgcgtatca ccagccaggt tctttgacc
 120
 ctgggcttca tggtagcctt cgcgatcgga ggcatgaccg gcgtactgct ggccatcccc
 180
 ggtgctgact tcgtactgca caacagcctg ttcggaattg ctcacttcca caacgtgatc
 240
 atcggcggcg cagtattcgg ctacatcgca ggtttcagct tctacttccc gaaagcgctt
 300
 ggcttcaagc tgcacgaaag ctggggcaag gctgcattct ggttctggat ctcgggcttc
 360
 ttcgctgcgt tcattgccgt ctatgcactg ggtttcattg gcattgacct ttgtttgaac
 420
 gccccccca cccctgagtg ggtcccgta cgtacgttg ccattgctcg tgcactgatg
 480
 atcgtctgct gtatgcctg ccagttgatt cagctgtatg tcacgctgcg tgatcgcaag
 540
 cagaacatgt gcgaatccgg cgacccatgg aatgcacaca ccttgggaatg gtcg
 594

<210> 2490

<211> 198

<212> PRT

<213> Homo sapiens

<400> 2490

Xaa	Ala	Phe	Phe	Gly	Leu	Ala	Thr	Met	Leu	Ile	Ser	Ile	Pro	Thr	Gly
1			5						10					15	
Val	Lys	Leu	Phe	Asn	Trp	Leu	Val	Thr	Ile	Tyr	His	Gly	Arg	Val	Arg
		20						25					30		
Ile	Thr	Ser	Gln	Val	Leu	Trp	Thr	Leu	Gly	Phe	Met	Val	Thr	Phe	Ala
		35					40					45			
Ile	Gly	Gly	Met	Thr	Gly	Val	Leu	Leu	Ala	Ile	Pro	Gly	Ala	Asp	Phe
		50			55					60					
Val	Leu	His	Asn	Ser	Leu	Phe	Gly	Ile	Ala	His	Phe	His	Asn	Val	Ile
		65			70					75				80	
Ile	Gly	Gly	Ala	Val	Phe	Gly	Tyr	Ile	Ala	Gly	Phe	Ser	Phe	Tyr	Phe
			85					90						95	
Pro	Lys	Ala	Phe	Gly	Phe	Lys	Leu	His	Glu	Ser	Trp	Gly	Lys	Ala	Ala
		100						105					110		
Phe	Trp	Phe	Trp	Ile	Ser	Gly	Phe	Phe	Val	Ala	Phe	Met	Pro	Leu	Tyr
		115				120						125			
Ala	Leu	Gly	Phe	Met	Gly	Met	Thr	Arg	Cys	Leu	Asn	Ala	Pro	Pro	Thr
		130				135					140				
Pro	Glu	Trp	Val	Pro	Tyr	Leu	Tyr	Val	Ala	Met	Val	Gly	Ala	Leu	Met
			145			150				155				160	
Ile	Ala	Val	Gly	Ile	Ala	Cys	Gln	Leu	Ile	Gln	Leu	Tyr	Val	Ser	Val
			165					170						175	

Arg Asp Arg Lys Gln Asn Met Cys Glu Ser Gly Asp Pro Trp Asn Ala
 180 185 190
 His Thr Leu Glu Trp Ser
 195

<210> 2491
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 2491
 acgcgtcacg caactgtcaa acttgccaat ccgcttgacg atactcgccc ctacctacgc
 60
 actacgttgt tgcttggtct attccatgca gtaacgacga atatgtcgcg atctcaggat
 120
 gatcttgcag tgttcgaaag cggaactgta ttccgcgccc tcactccggc tgcggcaccg
 180
 cgtcccggtg tcgacgagcg cccctccgat gaagtccttg ccgagatcga cgccgccttg
 240
 ccagcccagc cgcgcgatgt cgcggccgtg atctgtggca gctgggtgcc cgatcgctgg
 300
 gatggagagt cgggtcaaggc tgactggcga cacgctgtgc tggctgcccc gaaggctgct
 360
 gatgctcttg gcgtgaggct ggtgcgcaag gctgaccgtc aggtcccatg gcattccggt
 420
 cgttgtgcgg ctctcatcgt cgatgggaag gtcattggcc atgctgggtga gttgcacccc
 480
 acagtagtgt cgaaggctgg tctgcctcag cgcacctgtg cggctcgagt caatctagat
 540
 gctttggtag cctgcgctcc gagcgggtgt gaggtcatgg ttatttcaag gt
 592

<210> 2492
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 2492
 Thr Arg His Ala Thr Val Lys Leu Ala Asn Pro Leu Asp Asp Thr Arg
 1 5 10 15
 Pro Tyr Leu Arg Thr Thr Leu Leu Pro Gly Leu Phe His Ala Val Thr
 20 25 30
 Thr Asn Met Ser Arg Ser Gln Asp Asp Leu Ala Val Phe Glu Ser Gly
 35 40 45
 Thr Val Phe Arg Ala Val Thr Pro Ala Ala Ala Pro Arg Pro Gly Val
 50 55 60
 Asp Glu Arg Pro Ser Asp Glu Val Leu Ala Glu Ile Asp Ala Ala Leu
 65 70 75 80
 Pro Ala Gln Pro Arg Met Leu Ala Ala Val Ile Cys Gly Ser Trp Leu
 85 90 95
 Pro Asp Arg Trp Asp Gly Glu Ser Val Lys Ala Asp Trp Arg His Ala
 100 105 110
 Val Leu Val Ala Gln Lys Ala Ala Asp Ala Leu Gly Val Arg Leu Val
 115 120 125

```

Arg Lys Ala Asp Arg Gln Ala Pro Trp His Pro Gly Arg Cys Ala Ala
  130                135                140
Leu Ile Val Asp Gly Lys Val Ile Gly His Ala Gly Glu Leu His Pro
 145                150                155                160
Thr Val Val Ser Lys Ala Gly Leu Pro Gln Arg Thr Cys Ala Val Glu
 165                170                175
Phe Asn Leu Asp Ala Leu Val Ala Cys Ala Pro Ser Gly Gly Glu Val
 180                185                190
Met Val Ile Ser Arg
 195

```

```

<210> 2493
<211> 418
<212> DNA
<213> Homo sapiens

```

```

<400> 2493
acgcgtcagg ttgccgtga tcgtgccacc gtcacctcca tgggtgccttc aggagcagac
 60
ccccacacct atgagccgtc gctgcgtgac gttcggaccg tcgtgtattc gagagtcgcg
 120
ctatcgaact acctcatgct cgaacctcat tcggtcatca agaccatcga ctcttcctta
 180
cctacgggat ctatcaatgt ctccctggct gaggaagccc aaaagtacgg cgcacaagtg
 240
atccccgtgg ttgaaatgc caacctagac accgtgtggc tggggttgcg cgctattggc
 300
aaggcgccca ggccggggagc cgaccgctct tcctcggtct acctccagct gacgtcgggt
 360
gagggggcctg gggacttcac tgcctatatc actgggacct ttgggtcgacc tcagatct
 418

```

```

<210> 2494
<211> 139
<212> PRT
<213> Homo sapiens

```

```

<400> 2494
Thr Arg Gln Val Ala Gly Asp Arg Ala Thr Val Thr Ser Met Val Pro
 1         5         10        15
Ser Gly Ala Asp Pro His Thr Tyr Glu Pro Ser Leu Arg Asp Val Arg
 20        25        30
Thr Val Val Tyr Ser Arg Val Ala Leu Ser Asn Tyr Leu Met Leu Glu
 35        40        45
Pro His Ser Val Ile Lys Thr Ile Asp Ser Ser Leu Pro Thr Gly Ser
 50        55        60
Ile Asn Val Ser Leu Ala Glu Glu Ala Gln Lys Tyr Gly Ala Gln Val
 65        70        75        80
Ile Pro Leu Val Glu Asn Ala Asn Leu Asp Thr Val Trp Leu Gly Leu
 85        90        95
Arg Val Ile Gly Lys Gly Ala Arg Arg Gly Ala Asp Arg Ser Ser Ser
 100       105       110
Val Tyr Leu Gln Leu Thr Ser Val Glu Gly Pro Gly Asp Phe Thr Ala
 115       120       125

```

Tyr Ile Thr Gly Thr Phe Gly Arg Pro Gln Ile
 130 135

<210> 2495
 <211> 1478
 <212> DNA
 <213> Homo sapiens

<400> 2495
 nnggcctggc ccagttgcac cagcagcgct gcggacactc ggggcggcag tcggtctgtc
 60
 agtcctcccg ccaggtcccg cggcccgcac ctgccgcccg cacctgcagc tccgcacctg
 120
 cggccagtgc ctactgccct ctcttgccgc cgcacactgc agccccgcac ctgccgcttg
 180
 cacctgcagc cccgcgctct acccgggttc agcatggctg accaggcgcc cttcgacacg
 240
 gacgtcaaca cctgacccg ctctgctcatg gaggagggca ggaaggcccg cggcacgggc
 300
 gagttgaccc agctgctcaa ctgcctctgc acagcagtc aagccatctc ttccggcggtg
 360
 cgcaaggcgg gcctgcgcga cctctatggc attgctgggt ctaccaactg gacaggtgat
 420
 caagttaaag agctggcagt cctctccaac gacctgggta tgaacatgtt aaagtcatcc
 480
 ttggccactg gtgttctcgt gtcagaagaa gataaacacg ccactcatagt ggaaccggag
 540
 aaaaggggta aatatgtggt ctgttttgat ccccttgatg gatcttccaa catcgattgc
 600
 cttgtgtccg ttggaacat ttttggcctc tatagaaaga aatcaactga tgagccttct
 660
 gagaaggatg ctctgcaacc aggcgcgaac ctggtggcag cgggctacgc actgtatggc
 720
 agtgccacca tgctggctct tgccatggac tgtgggggtca actgcttcat gctggaccgg
 780
 gccatcgggg agttcatttt ggtggacaag gatgtgaaga taaaaaaga aggtaaaaac
 840
 tacagcctta acgagggtca gcgcaaggac ttgacctctg ccgtcactga gtacatccag
 900
 aggaagaagt tccccccaga taattcagct ccttatgggg cccgggtatgt gggctccatg
 960
 gtggctgatg ttcctgcac tctggtctac ggagggatat ttctgtaccg cgctaacaag
 1020
 aagagcccca atggaagct gagactgctg tacgaatgca accccatggc ctacgtcatg
 1080
 gagaaggctg ggggaatggc caccactggg aaggaggccg tggtagacgt cattccccca
 1140
 gacattcacc agaggcgcc ggtgatcttg gggcccccg acgacgtgct cgagttcctg
 1200
 aagggtgatg agaagcactc tgcccagtga gcacctgccc tgctgcctac cggagaattg
 1260
 cctctacctg gaccttttgt ctcacacagc agtacctgta cctgctgtgc accttacatt
 1320


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<210> 2496
<211> 338
<212> PRT
<213> Homo sapiens
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1793

325 330 335

Ala Gln

<210> 2497
 <211> 399
 <212> DNA
 <213> Homo sapiens

<400> 2497
 acgcgtgtct tggccggtga aacccttccc gcagcagggt cagtacgtcg caccggcgag
 60
 cttggctacc tgccacagga tccccgcgac ccagacatgg aaatgatcgc gagggcaagg
 120
 atcctgtcag cgcgtggcct ggaccacata ctggaacgga tgcgcaccct ggagtatcag
 180
 atggcgaaac gttccgagga cgaccgtgcc gttgcgatgg acaataacgc gaaggctgaa
 240
 gaccgtctcg tcgcggcccg tggctatggc gcctctgcag aggcagcccg aatcgcgtcg
 300
 aacttggggc ttgacgaccg cgtcctttcc cagccgttga aaaacctctc ggggtggtcag
 360
 cgtcgtcgcg tcgagctggc gcgcatectc ttttccgga
 399

<210> 2498
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 2498
 Thr Arg Val Leu Ala Gly Glu Thr Leu Pro Ala Ala Gly Ser Val Arg
 1 5 10 15
 Arg Thr Gly Glu Leu Gly Tyr Leu Pro Gln Asp Pro Arg Asp Pro Asp
 20 25 30
 Met Glu Met Ile Ala Arg Ala Arg Ile Leu Ser Ala Arg Gly Leu Asp
 35 40 45
 His Ile Leu Glu Arg Met Arg Thr Leu Glu Tyr Gln Met Ala Asn Gly
 50 55 60
 Ser Glu Asp Asp Arg Ala Val Ala Met Asp Lys Tyr Ala Lys Ala Glu
 65 70 75 80
 Asp Arg Leu Val Ala Ala Gly Gly Tyr Gly Ala Ser Ala Glu Ala Ala
 85 90 95
 Arg Ile Ala Ser Asn Leu Gly Leu Asp Asp Arg Val Leu Ser Gln Pro
 100 105 110
 Leu Lys Asn Leu Ser Gly Gly Gln Arg Arg Arg Val Glu Leu Ala Arg
 115 120 125
 Ile Leu Phe Ser Gly
 130

<210> 2499
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 2499
 nggccgggag aagaccggtt ctatatggcc taccacgaca ccgagtgggg cgtgccggaa
 60
 tatgacgacc gcgcattgta cgagaagctc attctcgacg gattccaggc cggcctgtcg
 120
 tggatcacca tctcgcgcaa gcgcgacaac ttctcgaaag ccttcgacga tttccagccc
 180
 gagaagatag cgcgttacaa tgagaagaag gttcacgcgc tgatgaacga tgcggcgatc
 240
 gtgcgcaacc gcgcaagat cgaaggcagc atcgccagcg cgaaggcgta tctcgacatc
 300
 atggaaaaag gcccgggctt ctccaggctg ctgtgggact tcgtcgac
 348

<210> 2500
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 2500
 Xaa Pro Gly Glu Asp Pro Phe Tyr Met Ala Tyr His Asp Thr Glu Trp
 1 5 10 15
 Gly Val Pro Glu Tyr Asp Asp Arg Ala Leu Tyr Glu Lys Leu Ile Leu
 20 25 30
 Asp Gly Phe Gln Ala Gly Leu Ser Trp Ile Thr Ile Leu Arg Lys Arg
 35 40 45
 Asp Asn Phe Arg Lys Ala Phe Asp Asp Phe Gln Pro Glu Lys Ile Ala
 50 55 60
 Arg Tyr Asn Glu Lys Lys Val His Ala Leu Met Asn Asp Ala Gly Ile
 65 70 75 80
 Val Arg Asn Arg Ala Lys Ile Glu Gly Thr Ile Ala Ser Ala Lys Ala
 85 90 95
 Tyr Leu Asp Ile Met Glu Lys Gly Pro Gly Phe Ser Arg Leu Leu Trp
 100 105 110
 Asp Phe Val Asp
 115

<210> 2501
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 2501
 gaattcgatt catttgtggc aaatgcttac aatttgatga ttgtaaccca tcaaatcaca
 60
 taatgcccat taagccatc catacacttc tttaaatagg aaaatatatg taaagtacgt
 120
 acttagcaca gggcctgacc tatagtaatg gtcaagaatg atagcggggg tgagggtatgg
 180
 ctttcaagag tcaaacaatt ttactgggtgc atcatttcca ttattctttt ctcttttgc
 240
 taataaaacc actcttaaga ttctaccttg gttagttaga gacaacagtt ctctggaaa
 300

tagattctat agcttcaact cctgaagag atgtgtgcta atttacatca aaaaaatcct
 360
 taagggtata aaatatgcc aagaactgtca acatcacaga ttaccactgg tagcttctgg
 420
 tatattgtta agtttccact taatttttaa gggacactag agaattagta tgactcacct
 480
 acactaagtt tataactgt atttaacagt gtaattttca aatatgacag gaataaccca
 540
 gatgtgaaat gctgaatcat taatcacag
 569

<210> 2502

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2502

Met	Ile	Ala	Gly	Val	Arg	Tyr	Gly	Phe	Gln	Glu	Ser	Asn	Asn	Phe	Thr
1			5					10						15	
Gly	Ala	Ser	Phe	Pro	Phe	Ile	Leu	Ser	Leu	Leu	His	Asn	Lys	Thr	Thr
		20					25					30			
Leu	Lys	Ile	Leu	Pro	Trp	Leu	Val	Arg	Asp	Asn	Ser	Ser	Leu	Glu	Ser
		35				40					45				
Arg	Phe	Tyr	Ser	Phe	Asn	Ser	Leu	Lys	Arg	Cys	Val	Leu	Ile	Tyr	Ile
	50				55					60					
Lys	Lys	Ile	Leu	Lys	Gly	Ile	Lys	Tyr	Ala	Lys	Asn	Cys	Gln	His	His
65			70					75						80	
Arg	Leu	Pro	Leu	Val	Ala	Ser	Gly	Ile	Leu	Leu	Ser	Phe	His	Leu	Ile
			85					90						95	
Phe	Lys	Gly	His												
			100												

<210> 2503

<211> 419

<212> DNA

<213> Homo sapiens

<400> 2503

gccacgccag ccactctaccc ttctctcgac tcgccaaata agtattcact gaacatgtac
 60
 aaggccttgc tacctcagca gtcctacagc ttggcccagc cgctgtattc tccagtcctg
 120
 accaatgggg agcgctttct ctacctgccg ccacctcact acgtcggtcc ccacatccca
 180
 tcgtctctgg catcaccat gaggtctctg acaccttcgg cctccccagc catccgcct
 240
 ctctgcatt gcgcagacaa aagcctcccg tggaagatgg gcgtcagccc tgggaatcct
 300
 gttgattccc acgcctatcc tcacatccag aacagtaagc agcccagggt tccctctggc
 360
 aaggcgggtca ccagtggcct gccgggggac acagctctcc tgttgcccc ctcacgcgt
 419

<210> 2504

<211> 121
 <212> PRT
 <213> Homo sapiens

<400> 2504
 Met Tyr Lys Ala Leu Leu Pro Gln Gln Ser Tyr Ser Leu Ala Gln Pro
 1 5 10 15
 Leu Tyr Ser Pro Val Cys Thr Asn Gly Glu Arg Phe Leu Tyr Leu Pro
 20 25 30
 Pro Pro His Tyr Val Gly Pro His Ile Pro Ser Ser Leu Ala Ser Pro
 35 40 45
 Met Arg Leu Ser Thr Pro Ser Ala Ser Pro Ala Ile Pro Pro Leu Val
 50 55 60
 His Cys Ala Asp Lys Ser Leu Pro Trp Lys Met Gly Val Ser Pro Gly
 65 70 75 80
 Asn Pro Val Asp Ser His Ala Tyr Pro His Ile Gln Asn Ser Lys Gln
 85 90 95
 Pro Arg Val Pro Ser Ala Lys Ala Val Thr Ser Gly Leu Pro Gly Asp
 100 105 110
 Thr Ala Leu Leu Leu Pro Pro Ser Arg
 115 120

<210> 2505
 <211> 540
 <212> DNA
 <213> Homo sapiens

<400> 2505
 tccggagcca atccgactca ggccctcgtc tggagccagg tgctgttgag catgggggtg
 60
 ccgctcgtgt tgggtccggtt ggctcgggtc accggcgatc ggctcgtgat gggccaatgg
 120
 acgaatgggc gtgtcatggc cgccatcgcg tggatcgtcg tggcagcagt ctcggtcttc
 180
 aacgtgggtc tcgtcgtcga gacgggtcatg ggtgcatgat ccttgagggc agttttctgg
 240
 cgacaatcgt gaaaatgagt gacaaactca agcgggtgac gacgccgaac ccgcgaccga
 300
 cctctgcgcc cgagctagcc aacgatttgg ccaactgcatt tcgcgggtac cctgtcggag
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 420
 cgtcgggtgc agtcgtcccg gctgttgtgt cgggtgtcgtt gggtaaatggt tcgacgacc
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<210> 2506
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 2506
 Ser Gly Ala Asn Pro Thr Gln Ala Leu Val Trp Ser Gln Val Leu Leu

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      20           25           30
Asp Arg Arg Leu Met Gly Gln Trp Thr Asn Gly Arg Val Met Ala Ala
      35           40           45
Ile Ala Trp Ile Val Val Ala Ala Val Ser Ala Leu Asn Val Val Leu
      50           55           60
Val Val Glu Thr Val Met Gly Ala
      65           70

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<210> 2507

<211> 922

<212> DNA

<213> Homo sapiens

<400> 2507

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420
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gacatcaggg agcttcaggc catggaggcc ttgcagaatg gccagaccac ggtagagggg
540
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720
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922

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<210> 2508

<211> 278

<212> PRT

<213> Homo sapiens

<400> 2508

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 20 25 30
 His Trp His Phe Leu Asn Gln Arg Arg Arg Pro Leu Arg Arg Arg
 35 40 45
 Asp Gly Thr Phe Asn Tyr Ser Pro Asp Val Tyr Cys Ser Lys Tyr Asn
 50 55 60
 Glu Ala Thr Gly Val Cys Pro Asp Gly Asp Glu Cys Pro Tyr Leu His
 65 70 75 80
 Arg Thr Thr Gly Asp Thr Glu Arg Lys Tyr His Leu Arg Tyr Tyr Lys
 85 90 95
 Thr Gly Thr Cys Ile His Glu Thr Asp Ala Arg Gly His Cys Val Lys
 100 105 110
 Asn Gly Leu His Cys Ala Phe Ala His Gly Pro His Asp Leu Arg Ser
 115 120 125
 Pro Val Tyr Asp Ile Arg Glu Leu Gln Ala Met Glu Ala Leu Gln Asn
 130 135 140
 Gly Gln Thr Thr Val Glu Gly Ser Ile Glu Gly Gln Ser Ala Gly Ala
 145 150 155 160
 Ala Ser His Ala Met Ile Glu Lys Ile Leu Ser Glu Glu Pro Arg Trp
 165 170 175
 Gln Glu Thr Ala Tyr Val Leu Gly Asn Tyr Lys Thr Glu Pro Cys Lys
 180 185 190
 Lys Pro Pro Arg Leu Cys Arg Gln Gly Tyr Ala Cys Pro Tyr Tyr His
 195 200 205
 Asn Ser Lys Asp Arg Arg Arg Ser Pro Arg Lys His Lys Tyr Arg Ser
 210 215 220
 Ser Pro Cys Pro Asn Val Lys His Gly Asp Glu Trp Gly Asp Pro Gly
 225 230 235 240
 Lys Cys Glu Asn Gly Asp Ala Cys Gln Tyr Cys His Thr Arg Thr Glu
 245 250 255
 Gln Gln Phe His Pro Glu Ile Tyr Lys Ser Thr Lys Cys Asn Gly Arg
 260 265 270
 Gly Gly Gly Val Arg Glu
 275

<210> 2509

<211> 348

<212> DNA

<213> Homo sapiens

<400> 2509

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 120
 gttcatgaac ggggtggagcc cggcaaaacc gaaactcaac caatccttgg gtagctggga
 180
 cggcaggttg ccgagggcaa acacgttgac cacgttcgca ccgacaccac cgaccacggc
 240
 caccgctccc agcggaatct ctagacttta gcgccagggt tggttaaggcg tgtagcggtc
 300

gtaacgacgg gtgacctcga actcggggct tcaaagtctt ctgctgtg
348

<210> 2510

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2510

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Met Ala Pro Arg Gln Gly Pro Ile Leu Arg Ala Leu Val Ala Leu Asp
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Phe Val Asp Ala Arg Glu Val Leu Leu Pro Ala Thr Ile Gly Leu Asp
 20             25             30
Val His Glu Arg Val Glu Pro Gly Lys Thr Glu Thr Gln Pro Ile Leu
 35             40             45
Gly Asp Ala Gly Arg Gln Val Ala Glu Gly Lys His Val Asp His Val
 50             55             60
Arg Thr Asp Thr Thr Asp His Gly His Arg Ser Gln Arg Asn Leu Val
 65             70             75             80
Asp Leu Ala Pro Gly Leu Val Arg Arg Val Ala Val Val Thr Thr Gly
 85             90             95
Asp Leu Glu Leu Gly Ala Ser Lys Ser Ser Ala Val
100             105
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<210> 2511

<211> 663

<212> DNA

<213> Homo sapiens

<400> 2511

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gcattacgcc caggacgcgt tgctggcctg gcggagatcg tcgtcaacgg tcaacctttt
240
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300
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540
atgtccggac agatccccgc tgaggaacac atccccggtc atctagctat gatcattgag
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660
gac
663
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<210> 2512
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 2512
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 20 25 30
 Asn Glu Gln Asp Leu Gln Val Leu Pro Val Ile Ala His Val Gly Tyr
 35 40 45
 Pro Gln Ala Ala Asp Glu Tyr Tyr Gln Leu Leu Leu Ala Leu Arg Pro
 50 55 60
 Gly Arg Val Ala Gly Leu Ala Glu Ile Val Val Asn Gly Gln Pro Phe
 65 70 75 80
 Thr Val Thr Asp Ala Thr Glu Asp Glu Leu Ala Leu Thr Ala Trp Ala
 85 90 95
 Arg Ile Leu Leu Glu Gly Thr Pro Ile Ala Met Asp Gly Ser Trp Gln
 100 105 110
 Leu His Arg Arg Arg Ala Ala Pro Glu Pro Val Arg Phe Ala Lys Arg
 115 120 125
 Phe Gly Gly Glu Gln Ser Asn Thr Ser Ile Met Val Gly Asp Ala Ile
 130 135 140
 Ile Ile Lys Met Phe Arg Arg Leu Glu Pro Gly Asp Asn Leu Asp Ile
 145 150 155 160
 Thr Val His Ser Ala Leu Asn Asp Ala Gly Ile Ser Ser Val Ala Thr
 165 170 175
 Leu Tyr Gly Phe Met Ser Gly Gln Ile Pro Ala Glu Glu His Ile Pro
 180 185 190
 Val Asp Leu Ala Met Ile Ile Glu Arg Leu Pro Gln Pro Arg Asp Gly
 195 200 205
 Trp Glu Leu Ile Thr Ala Lys Ala Val Asp Leu Val Asp
 210 215 220

<210> 2513
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 2513
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 gacctgaagt tctgcatgga tggagttcag actgctttga ggagtgaa ttatgagcag
 180
 gctgcagcac atattcatcg ctacttgtgc ctggacaagt cggctcattga gctcagccga
 240
 cagggcaag agggctcagca tccgaaactg gagcatgatt gatgccaaac tgaattgtgt
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 360

ggaagggtg
368

<210> 2514
<211> 93
<212> PRT
<213> Homo sapiens

<400> 2514
Leu Ala Gly Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser
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Ser Lys Val Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala
20 25 30
Ile Gln Arg Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly
35 40 45
Val Gln Thr Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala His
50 55 60
Ile His Arg Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg
65 70 75 80
Gln Gly Lys Glu Gly Gln His Pro Lys Leu Glu His Asp
85 90

<210> 2515
<211> 351
<212> DNA
<213> Homo sapiens

<400> 2515
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120
tatcagtccta tcctataaag ccaaccaggc tctcccaggg gaggcaggaa atccctgctc
180
ctcccatccc ccaccgggaa tgctgcaggg ggcttgaggg aggcgacaca gtggggagct
240
ctgggtgcag gtgggcagac aatggggcaa cacacccct cagccccgct ccagtatcag
300
cattccagac ccaccacact gggcccttgg tcaccggggag acctcacgcg t
351

<210> 2516
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2516
Met Ala His Pro Gly Pro Asp Pro Ser Tyr Pro Ser Asn Ser Pro Thr
1 5 10 15
Thr Gly Gln Leu Glu Tyr Gln Ser Ile Pro Lys Ser Gln Pro Gly Ser
20 25 30
Pro Glu Gly Gly Arg Lys Ser Leu Leu Pro Pro Ser Pro Thr Gly Asn.
35 40 45
Ala Ala Gly Gly Leu Arg Glu Ala Thr Gln Trp Gly Ala Leu Gly Ala

```

      50              55              60
Gly Gly Gln Thr Met Gly Gln His Thr Pro Ser Ala Pro Leu Gln Tyr
65              70              75              80
Gln His Ser Arg Pro Thr His Leu Gly Pro Trp Ser Pro Gly Asp Leu
      85              90              95
Thr Arg

```

```

<210> 2517
<211> 356
<212> DNA
<213> Homo sapiens

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<400> 2517
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120
cctgtcacca accaaacccc atgggcctat tcagcagccc caacttggct ggtctggccg
180
aggccacaca ttccctgggg actgagctcc aaggtgtctg gtcctgagc aggaagcggc
240
cagtgttgag tgggcagtgt ctactccag cccctcctc ccaggccagt tcttctcate
300
tccctcagtc ttccaagc aggcctcat ctacaggga gacctgactg gctagc
356

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<210> 2518
<211> 103
<212> PRT
<213> Homo sapiens

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<400> 2518
Met Gly Ala Glu Gly Glu Asp Lys Arg Arg Trp Pro Val Ser Gln Glu
1      5      10      15
Ala Gly Gly Gly Ala Arg Ala Ser Pro Gly Val Arg Thr Cys His Gln
20      25      30
Pro Asn Pro Met Gly Leu Phe Ser Ser Pro Asn Leu Ala Gly Leu Ala
35      40      45
Glu Ala Thr His Ser Leu Gly Thr Glu Leu Gln Gly Ala Gly Ser Leu
50      55      60
Ser Arg Lys Arg Pro Val Leu Ser Gly Gln Cys Leu Thr Pro Ala Pro
65      70      75      80
Pro Ser Gln Ala Ser Ser Ser His Leu Pro Gln Ser Phe Pro Ser Arg
85      90      95
Pro Ser Ser Thr Gly Gln Thr
100

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```

<210> 2519
<211> 830
<212> DNA
<213> Homo sapiens

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```

<400> 2519

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120
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240
cacaagacaa ttgcacagca gaccacacct ttctccaaag ttttcagggc ccaaaccagg
300
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360
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420
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540
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660
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720
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780
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830

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<210> 2520

<211> 107

<212> PRT

<213> Homo sapiens

<400> 2520

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Met Ser Pro Ala Arg Arg Cys Leu Gly Leu Gly Pro Glu Asn Phe Gly
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Glu Glu Val Gly Leu Leu Cys Asn Cys Leu Val Pro Phe Lys Val Ile
          20             25             30
Leu Pro Cys Trp Gly Arg Cys Ser Ser Ser Phe Gln Arg Arg Lys Arg
          35             40             45
Gly Trp Gly Val Ala Gly Arg Gly Ser Ser Arg Pro Glu Ser Gln Ser
          50             55             60
Arg Trp Arg Ala Ala Ser Thr Arg Phe Leu Leu Val Gly Leu Arg Gln
65             70             75             80
Gly Leu Ala Pro Gly Leu Ser Gly Lys Arg Glu Glu Glu Leu Arg Leu
          85             90             95
Arg Gly Ala Val Leu Pro Arg Arg Leu Thr Gly
          100             105

```

<210> 2521

<211> 4291

<212> DNA

<213> Homo sapiens

<400> 2521
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<210> 2522

<211> 952

<212> PRT

<213> Homo sapiens

<400> 2522

Leu	Ser	Leu	Phe	Arg	Ala	Glu	Ser	Pro	Thr	Thr	Ala	Ser	Pro	Ala	Leu
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Gly	Gly	Pro	Ala	Pro	Gly	Cys	Ser	Arg	Arg	Thr	Pro	Pro	Pro	Pro	Met
			20					25					30		
Ala	Pro	Leu	Ala	Leu	Val	Gly	Val	Thr	Leu	Leu	Leu	Ala	Ala	Pro	Pro
		35				40						45			
Cys	Ser	Gly	Ala	Ala	Thr	Pro	Thr	Pro	Ser	Leu	Pro	Pro	Pro	Pro	Ala
	50					55				60					
Asn	Asp	Ser	Asp	Thr	Ser	Thr	Gly	Gly	Cys	Gln	Gly	Ser	Tyr	Arg	Cys

65					70					75					80
Gln	Pro	Gly	Val	Leu	Leu	Pro	Val	Trp	Glu	Pro	Asp	Asp	Pro	Ser	Leu
				85					90					95	
Gly	Asp	Lys	Ala	Ala	Arg	Ala	Val	Val	Tyr	Phe	Val	Ala	Met	Val	Tyr
			100					105					110		
Met	Phe	Leu	Gly	Val	Ser	Ile	Ile	Ala	Asp	Arg	Phe	Met	Ala	Ala	Ile
		115				120					125				
Glu	Val	Ile	Thr	Ser	Lys	Glu	Lys	Glu	Ile	Thr	Ile	Thr	Lys	Ala	Asn
		130				135					140				
Gly	Glu	Thr	Ser	Val	Gly	Thr	Val	Arg	Ile	Trp	Asn	Glu	Thr	Val	Ser
		145			150					155				160	
Asn	Leu	Thr	Leu	Met	Ala	Leu	Gly	Ser	Ser	Ala	Pro	Glu	Ile	Leu	Leu
			165					170						175	
Ser	Val	Ile	Glu	Val	Cys	Gly	His	Asn	Phe	Gln	Ala	Gly	Glu	Leu	Gly
		180						185					190		
Pro	Gly	Thr	Ile	Val	Gly	Ser	Ala	Ala	Phe	Asn	Met	Phe	Val	Val	Ile
		195				200						205			
Ala	Val	Cys	Ile	Tyr	Val	Ile	Pro	Ala	Gly	Glu	Ser	Arg	Lys	Ile	Lys
		210				215						220			
His	Leu	Arg	Val	Phe	Phe	Val	Thr	Ala	Ser	Trp	Ser	Ile	Phe	Ala	Tyr
		225			230					235				240	
Val	Trp	Leu	Tyr	Leu	Ile	Leu	Ala	Val	Phe	Ser	Pro	Gly	Val	Val	Gln
			245					250					255		
Val	Trp	Glu	Ala	Leu	Leu	Thr	Leu	Val	Phe	Phe	Pro	Val	Cys	Val	Val
		260					265					270			
Phe	Ala	Trp	Met	Ala	Asp	Lys	Arg	Leu	Leu	Phe	Tyr	Lys	Tyr	Val	Tyr
		275				280						285			
Lys	Arg	Tyr	Arg	Thr	Asp	Pro	Arg	Ser	Gly	Ile	Ile	Ile	Gly	Ala	Glu
		290				295						300			
Gly	Asp	Pro	Pro	Lys	Ser	Ile	Glu	Leu	Asp	Gly	Thr	Phe	Val	Gly	Ala
		305			310					315				320	
Glu	Ala	Pro	Gly	Glu	Leu	Gly	Gly	Leu	Gly	Pro	Gly	Pro	Ala	Glu	Ala
			325						330					335	
Arg	Glu	Leu	Asp	Ala	Ser	Arg	Arg	Glu	Val	Ile	Gln	Ile	Leu	Lys	Asp
		340					345					350			
Leu	Lys	Gln	Lys	His	Pro	Asp	Lys	Asp	Leu	Glu	Gln	Leu	Val	Gly	Ile
		355				360						365			
Ala	Asn	Tyr	Tyr	Ala	Leu	Leu	His	Gln	Gln	Lys	Ser	Arg	Ala	Phe	Tyr
		370				375					380				
Arg	Ile	Gln	Ala	Thr	Arg	Leu	Met	Thr	Gly	Ala	Gly	Asn	Val	Leu	Arg
		385			390					395				400	
Arg	His	Ala	Ala	Asp	Ala	Ser	Arg	Arg	Ala	Ala	Pro	Ala	Glu	Gly	Ala
			405					410						415	
Gly	Glu	Asp	Glu	Asp	Gly	Ala	Ser	Arg	Ile	Phe	Phe	Glu	Pro	Ser	
		420					425					430			
Leu	Tyr	His	Cys	Leu	Glu	Asn	Cys	Gly	Ser	Val	Leu	Leu	Ser	Val	Thr
		435				440						445			
Cys	Gln	Gly	Gly	Glu	Gly	Asn	Ser	Thr	Phe	Tyr	Val	Asp	Tyr	Arg	Thr
		450				455					460				
Glu	Asp	Gly	Ser	Ala	Lys	Ala	Gly	Ser	Asp	Tyr	Glu	Tyr	Ser	Glu	Gly
		465			470					475				480	
Thr	Leu	Val	Phe	Lys	Pro	Gly	Glu	Thr	Gln	Lys	Glu	Leu	Arg	Ile	Gly
			485					490						495	
Ile	Ile	Asp	Asp	Asp	Ile	Phe	Glu	Glu	Asp	Glu	His	Phe	Phe	Val	Arg

[illegible]

930
Ala Tyr Cys His Ile Arg Gly Phe
945 950

940

<210> 2523
<211> 392
<212> DNA
<213> Homo sapiens

<400> 2523
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ttcagccgaa aaattgttgg tgttgtaca cgctcgacga tgcgtaccga tgcgctgccc
120
atggaggctt tggagcatgc gttaacgact gcagggcgaa ttcattggaaa ccagttaatt
180
caccatagcg atcggggcag ccagtacgtg tcaactgaagt attccaccgc gttacgggaa
240
tccggaatcc gtccagtggt gggaacagtc ggcgattctt atgacaatgc tctagcggaa
300
acagtcaacg gtctctacaa ggcggaactg attcatgccc aagggtccgtg gacgtcggtc
360
ggagaagtcg aattggccac cttgcggnnn nn
392

<210> 2524
<211> 130
<212> PRT
<213> Homo sapiens

<400> 2524
Xaa Ile Thr Tyr Val Arg Thr Leu Ser Gly Phe Ala Tyr Thr Ala Phe
1 5 10 15
Val Val Asp Val Phe Ser Arg Lys Ile Val Gly Val Ala Thr Arg Ser
20 25 30
Thr Met Arg Thr Asp Ala Leu Pro Met Glu Ala Leu Glu His Ala Leu
35 40 45
Thr Thr Ala Gly Arg Ile His Gly Asn Gln Leu Ile His His Ser Asp
50 55 60
Arg Gly Ser Gln Tyr Val Ser Leu Lys Tyr Ser Thr Ala Leu Ala Glu
65 70 75 80
Ser Gly Ile Arg Pro Ser Val Gly Thr Val Gly Asp Ser Tyr Asp Asn
85 90 95
Ala Leu Ala Glu Thr Val Asn Gly Leu Tyr Lys Ala Glu Leu Ile His
100 105 110
Ala Gln Gly Pro Trp Thr Ser Val Gly Glu Val Glu Leu Ala Thr Leu
115 120 125
Arg Xaa
130

<210> 2525
<211> 378
<212> DNA
<213> Homo sapiens

<400> 2525
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 60
 tcccccttga atactgtgtg ctgtcaccgc cgcggaatc aagaaccgca cggtgcgcaa
 120
 atcgctgcgc tacgcaccaa cgtggtcggc aagatgttgg tcacgcgcca gccccgnaa
 180
 tgattcatat ctccgatatc agcacgacag gggcgtcatt ccgctctgca catcggcttg
 240
 gaagtcagcg gtgcgccgc acgcctgcga ttctgggtga agacgcgca ctaccattca
 300
 gaactggtgg ccgcaacact cattcgagc gagaagcccg ccgatttgcc caacacctat
 360
 caatacggcg tggaattc
 378

<210> 2526
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 2526
 Met Ala Val Cys Arg Ile Pro Phe Glu Tyr Val Val Leu Ser Pro Pro
 1 5 10 15
 Arg Glu Ser Arg Thr Ala Arg Cys Ala Asn Arg Cys Ala Thr His Gln
 20 25 30
 Arg Gly Arg Gln Asp Val Gly Gln Arg Arg Ala Pro Xaa Met Ile His
 35 40 45
 Ile Ser Asp Ile Ser Thr Thr Gly Ala Ser Phe Arg Ser Ala His Arg
 50 55 60
 Leu Gly Ser Gln Arg Cys Ala Arg Thr Pro Ala Ile Ser Gly Glu Asp
 65 70 75 80
 Ala Arg Leu Pro Phe Arg Thr Gly Gly Arg Asn Thr His Ser Gln Arg
 85 90 95
 Glu Ala Arg Arg Phe Ala Gln His Leu Ser Ile Arg Arg Gly Ile
 100 105 110

<210> 2527
 <211> 305
 <212> DNA
 <213> Homo sapiens

<400> 2527
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 120
 cgctctcccc cccagaagc tcccgcaggg ccacccatct ccacggcctc cgagacctca
 180
 gtgtacgtga cctggattcc ccgtgggaat ggtgggttcc caatccagtc cttccgtgtg
 240
 gagtaacaaga agctaaagaa agtggggagac tggattctgg ccaccagcgc catcccccca
 300

cgcggt
305

<210> 2528
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2528
Xaa Val Thr Phe Arg Met Gly Arg Arg Pro Lys Pro Glu Ile Met Ala
1 5 10 15
Ser Lys Glu Gln Gln Ile Gln Arg Asp Asp Leu Gly Ala Ser Pro Gln
20 25 30
Ser Ser Ser Gln Pro Asp His Gly Arg Leu Ser Pro Pro Glu Ala Pro
35 40 45
Asp Arg Pro Thr Ile Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr
50 55 60
Trp Ile Pro Arg Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val
65 70 75 80
Glu Tyr Lys Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser
85 90 95
Ala Ile Pro Pro Arg
100

<210> 2529
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2529
acgcgtctcc ccgtggtggg tcccgatccc cgggccgget ctgccactga agcctctccc
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tgtgtctctc gtgccccccg agtggcctgc tagccccgctc tcccacacag tctccttgat
120
gtgaagtgct acccggtctg ctgaggcgtg tctccgccgt aacacgtgta taccggctca
180
gccatggcgg cggctgctgg gaaggctcct gcgtatggct ttgccatccg ggaccggggc
240
ttgctctgc aggggtgggc ttctgagcag aggaaggcca gaggtaacca ggtccatgca
300
cgtttgatgct ttccacaat gtcgggcttt tatggatgct tttagtctca gtcacaaaaa
360
ccatgagctc cacaggttcc tgaggga
387

<210> 2530
<211> 121
<212> PRT
<213> Homo sapiens

<400> 2530
Met Ala Phe Val Thr Glu Thr Lys Ser Ile His Lys Ser Pro Thr Leu
1 5 10 15
Trp Lys Asp Thr Asn Val His Gly Pro Gly Tyr Leu Trp Pro Ser Ser

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                20                25                30
Ala Gln Lys Pro Thr Pro Ala Glu Gln Ser Pro Gly Pro Gly Trp Gln
      35                40                45
Ser His Thr Gln Glu Pro Ser Gln Gln Pro Pro Pro Trp Leu Ser Arg
      50                55                60
Tyr Thr Arg Val Thr Ala Glu Thr Arg Arg Ser Lys Pro Gly Asp Thr
      65                70                75                80
Ser His Gln Gly Asp Cys Val Gly Glu Arg Ala Ser Arg Pro Leu Gly
      85                90                95
Gly His Gly Gly His Arg Glu Arg Leu Gln Trp Gln Ser Arg Pro Gly
      100                105                110
Asp Arg Asp Pro Pro Arg Gly Asp Ala
      115                120

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<210> 2531

<211> 396

<212> DNA

<213> Homo sapiens

<400> 2531

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tctagagata caaaaagtac tctatacaact gagagacatc tggataaata caaaggttga
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gctttccaac cagctgaaga tgacaagact aaaccccaag tcgctgcagc tctgtgtcat
120
ctcatcagca gccctggaga tgacaaagat agtgcgtgagg gggaacagac cttcgtcatc
180
agttaaaagt atgctagctt ttctttttct tccagacatt cctgaatcca gagaactttc
240
ctgtaatgcg tcaaatcctt taggtctcaa ttctttccct agagagacaa ggagcacagt
300
tcgtttccaa ggccccccat gcttggcgag ggcgctctctg ctttccaggc agggtcctgc
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396

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<210> 2532

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2532

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Met Thr Arg Leu Asn Pro Lys Ser Leu Gln Leu Cys Val Ile Ser Ser
1      5      10      15
Ala Ala Leu Glu Met Thr Lys Ile Val Leu Arg Gly Asn Arg Pro Ser
      20      25      30
Ser Ser Val Lys Asp Met Leu Ala Phe Leu Phe Leu Pro Asp Ile Pro
      35      40      45
Glu Ser Arg Glu Leu Ser Cys Asn Ala Ser Asn Pro Leu Gly Leu Asn
      50      55      60
Ser Phe Pro Arg Glu Thr Arg Ser Thr Val Arg Ser Gln Gly Pro Pro
      65      70      75      80
Cys Leu Ala Arg Ala Ser Leu Leu Ser Arg Gln Gly Pro Ala Ala Ser
      85      90      95
Thr His Val Gln Gly Lys Glu Gly Arg

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100

105

<210> 2533
 <211> 495
 <212> DNA
 <213> Homo sapiens

<400> 2533
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 gctgtggcan ccccatgga cgtgatcaag tcgagactgc aggcagacgg gcagggccag
 120
 aggcgctacc ggggtctcct gcaactgtatg gtgaccagcg ttcgagagga gggaccccg
 180
 gtccctttca aggggctggt actcaattgc tgccgcgcct tccctgtcaa catgggtggtc
 240
 ttctgcgcct atgaggcagt gctgaggctc gccggggggtc tgcacacata gccggtcccc
 300
 acgcccagcg gccaccac cagcagctgc tggaggctgt agtgggtgga ggaggcaagg
 360
 ggtagtgtgg ctgggttcgg gacccacag ggcattgcc caggagaatg aggagcctcc
 420
 ctgcagtgtt gtcggccgag gcctgagctc gccctgccca gctactgacc tcaggctgag
 480
 gggcccgcca gccat
 495

<210> 2534
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 2534
 Xaa Arg Pro Asp Val Pro Gly Val Leu Val Ala Gly Gly Cys Ala Gly
 1 5 10 15
 Val Leu Ala Trp Ala Val Ala Xaa Pro Met Asp Val Ile Lys Ser Arg
 20 25 30
 Leu Gln Ala Asp Gly Gln Gly Gln Arg Arg Tyr Arg Gly Leu Leu His
 35 40 45
 Cys Met Val Thr Ser Val Arg Glu Gly Pro Arg Val Leu Phe Lys
 50 55 60
 Gly Leu Val Leu Asn Cys Cys Arg Ala Phe Pro Val Asn Met Val Val
 65 70 75 80
 Phe Val Ala Tyr Glu Ala Val Leu Arg Leu Ala Arg Gly Leu Leu Thr
 85 90 95

<210> 2535
 <211> 1904
 <212> DNA
 <213> Homo sapiens

<400> 2535
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cgtcggtggg aggctgctac catgaggttg aatcagaaca ccttgctgct ggggaagaag
120
gtgggtccttg taccctacac ctccggagcat gtgccacga ggtaccacga gtggatgaaa
180
tcagaggagc tgcagcgttt gacagcctcg gagccgctga ccctggagca ggagtatgcc
240
atgcagtgcg gctggcagga agatgcagac aagtgtacct tcattgtgct ggatgccgag
300
aagtggcagg ccagccagg cgcaccgaa gagagctgca tgggtggaga cgtgaacctc
360
ttcctcacag atctagaaga cccacacctg ggggagatcg aggtcatgat tgcagagccc
420
agctgcaggg gtaaggcctt tggcactgag gccgttctcg cgatgctgct ttacggagtg
480
accacgctag gtctgaccaa gtttgaggct aaaattgggc aaggaaatga accaagcatc
540
cggtatgttc agaaacttca ctttgagcag gtggctacga gcagtgtttt tcaggagggtg
600
accctcacag tgacagttag tgagtcagg catcagtggt ttctggagca gaccagccac
660
gtggaagaga agccttacag agatgggtcg gcagagccct gctgatggct gggccttggtg
720
ggcagccact ctgtgtgagc aggggtgttg gccatacac ttcaagacc agagccctgc
780
actgggagag tgctcctggc ccaggctggg aatcaccttt cgaggccctt cagactctgg
840
cggggcttgc tgtggcctcc ctccagctag tgggtgtggt gagcagactc caggggcagg
900
gccagtctcc ttctccctcc ccggccaaac ccagaccag actctaggaa gctggaatgg
960
agggcaggga tccatgggag atgtcgggat gaaggtggga gctggagggt cagggggacc
1020
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1080
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1140
agctaccacg agccccagcc tcacagtgtc cactcaaggg cagcttggtc ctcttgctct
1200
gcagaggcag gctggtgtga ccctgggaac ttgacccggg aacaacagggt ggtccagagt
1260
gagtgtggcc tggccctca acctagtgtc cgtctctctc tctcctggag ccagtcttga
1320
gtttaaggc attagtgtta gatacagctc cttgtggctg gaaaaccccc ctctgctgat
1380
aaagctcagg gggcactgag gaagcagagg ccccttgggg gtgcccctct gaagagagcg
1440
tcaggccatc agctctgtcc ctctgggtgt cccacgtctg ttctcacc cccatctctg
1500
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ggctacctgg caccctatgg cttacaaagt agagtggcc cagtttctct ccacctgagg
1620
ggagcactct gactcctaac agtcttctct gccctgccat catctggggt ggctggctgt
1680

caagaaaggc cgggcatgct ttctaaacac agccacagga ggcttgtagg gcattctcca
 1740
 ggtggggaaa cagtcttaga taagtaaggt gacttgccca aggcctccca gcacccttga
 1800
 tcttggagtc tcacagcaga ctgcatgtga acaactggaa ccgaaaaaat gcctcagtat
 1860
 aaaacaaaca ttataaaacg aaaaaaaaaa aaaaaaaaaa tact
 1904

<210> 2536

<211> 207

<212> PRT

<213> Homo sapiens

<400> 2536

Met	Arg	Leu	Asn	Gln	Asn	Thr	Leu	Leu	Leu	Gly	Lys	Lys	Val	Val	Leu
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Val	Pro	Tyr	Thr	Ser	Glu	His	Val	Pro	Ser	Arg	Tyr	His	Glu	Trp	Met
			20				25						30		
Lys	Ser	Glu	Glu	Leu	Gln	Arg	Leu	Thr	Ala	Ser	Glu	Pro	Leu	Thr	Leu
		35					40					45			
Glu	Gln	Glu	Tyr	Ala	Met	Gln	Cys	Ser	Trp	Gln	Glu	Asp	Ala	Asp	Lys
		50				55					60				
Cys	Thr	Phe	Ile	Val	Leu	Asp	Ala	Glu	Lys	Trp	Gln	Ala	Gln	Pro	Gly
65				70					75						80
Ala	Thr	Glu	Glu	Ser	Cys	Met	Val	Gly	Asp	Val	Asn	Leu	Phe	Leu	Thr
				85					90					95	
Asp	Leu	Glu	Asp	Pro	Thr	Leu	Gly	Glu	Ile	Glu	Val	Met	Ile	Ala	Glu
			100					105					110		
Pro	Ser	Cys	Arg	Gly	Lys	Gly	Leu	Gly	Thr	Glu	Ala	Val	Leu	Ala	Met
			115				120					125			
Leu	Ser	Tyr	Gly	Val	Thr	Thr	Leu	Gly	Leu	Thr	Lys	Phe	Glu	Ala	Lys
			130				135				140				
Ile	Gly	Gln	Gly	Asn	Glu	Pro	Ser	Ile	Arg	Met	Phe	Gln	Lys	Leu	His
145				150						155					160
Phe	Glu	Gln	Val	Ala	Thr	Ser	Ser	Val	Phe	Gln	Glu	Val	Thr	Leu	Arg
				165					170					175	
Leu	Thr	Val	Ser	Glu	Ser	Glu	His	Gln	Trp	Leu	Leu	Glu	Gln	Thr	Ser
			180					185					190		
His	Val	Glu	Glu	Lys	Pro	Tyr	Arg	Asp	Gly	Ser	Ala	Glu	Pro	Cys	
			195				200						205		

<210> 2537

<211> 509

<212> DNA

<213> Homo sapiens

<400> 2537

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 120
 ccgtgctac tgctcggaact ccccgctcatt gcgtggtggc ccttctccgg ccttgacaa
 180

ctcgccctcg accccatcg agcccttgcg gaccgccgca tcaccgactc ggcagctgac
 240
 aaagatccgt gcaaagccct catacgccgt gcggctcacc taaccgaggg tgactccgac
 300
 ctgtgttggg ctgcaccac cagctggaga gccctagctg cagcagcttt ggatcaacat
 360
 ccagcgaccg tcaagttcgc tcgggtagag tcagccgccg gtaatgcgc gccgatgctg
 420
 ctggcagcct ggctaggatt gcgtctcggc gtcccggtcg agcgggtgac aaccgacgcg
 480
 cccggcatct ccgcatcgt catgtcgac
 509

<210> 2538

<211> 169

<212> PRT

<213> Homo sapiens

<400> 2538

Thr	Arg	Ser	Arg	Lys	Asp	Lys	Leu	Asp	Ala	Glu	Val	His	Ala	Gly	Glu
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Gly	Thr	Pro	Gly	Asp	Val	Ile	Val	Leu	Arg	Phe	Ser	Gly	Ala	Met	Ala
			20					25					30		
Lys	Arg	Pro	Ala	Ser	Val	Ile	Leu	Pro	Leu	Leu	Leu	Ser	Asp	Ser	Pro
		35					40					45			
Val	Ile	Ala	Trp	Trp	Pro	Phe	Ser	Gly	Pro	Asn	Leu	Ala	Ser	Asp	
		50				55				60					
Pro	Ile	Gly	Ala	Leu	Ala	Asp	Arg	Arg	Ile	Thr	Asp	Ser	Ala	Ala	Asp
65				70						75				80	
Lys	Asp	Pro	Cys	Lys	Ala	Leu	Ile	Arg	Arg	Ala	Ala	His	Leu	Thr	Glu
			85						90				95		
Gly	Asp	Ser	Asp	Leu	Cys	Trp	Ala	Arg	Thr	Thr	Ser	Trp	Arg	Ala	Leu
			100					105					110		
Ala	Ala	Ala	Ala	Leu	Asp	Gln	His	Pro	Ala	Thr	Val	Lys	Phe	Ala	Arg
			115				120					125			
Val	Glu	Ser	Ala	Ala	Gly	Asn	Ala	Pro	Ala	Met	Leu	Leu	Ala	Ala	Trp
		130				135					140				
Leu	Gly	Leu	Arg	Leu	Gly	Val	Pro	Val	Glu	Arg	Val	Thr	Thr	Asp	Ala
145				150					155					160	
Pro	Gly	Ile	Ser	Ala	Ile	Val	Met	Ser							
					165										

<210> 2539

<211> 453

<212> DNA

<213> Homo sapiens

<400> 2539

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 120
 cagccgaact acgacctgac gtatgacgac gtcttcatgg caccaaacgg ttcctcggtg
 180

gggtcccgc tgaacgtcga cctcacgtca acagacgggc taggcactcc tctgcccctc
 240
 gtagtgccca atatgaccgc aatttccgga cgtcgcatgg cagagaccat cgccaggcgc
 300
 ggaggcattg ctgttctgcc ccaagatata ccggcggatt tcgtcgcccc gtccattcgg
 360
 cgcgtcaaa atgcgcatac tcgattcgac accccagtcg ccgtcaaccc gacaacgact
 420
 gtcggtgagg ccatgaactt gctcaacaag cgc
 453

<210> 2540

<211> 134

<212> PRT

<213> Homo sapiens

<400> 2540

Phe	Ala	Ala	Ser	Arg	His	Asp	Pro	Arg	Ile	Val	Thr	Trp	Asp	Asn	Gly
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Tyr	Val	Arg	Phe	Leu	Asn	Glu	Gln	Pro	Asn	Tyr	Asp	Leu	Thr	Tyr	Asp
			20				25					30			
Asp	Val	Phe	Met	Ala	Pro	Asn	Arg	Ser	Ser	Val	Gly	Ser	Arg	Met	Asn
	35					40					45				
Val	Asp	Leu	Thr	Ser	Thr	Asp	Gly	Leu	Gly	Thr	Pro	Leu	Pro	Leu	Val
	50				55					60					
Val	Ala	Asn	Met	Thr	Ala	Ile	Ser	Gly	Arg	Arg	Met	Ala	Glu	Thr	Ile
65				70					75					80	
Ala	Arg	Arg	Gly	Gly	Ile	Ala	Val	Leu	Pro	Gln	Asp	Ile	Pro	Ala	Asp
			85					90					95		
Phe	Val	Ala	Arg	Ser	Ile	Arg	Arg	Val	Lys	Asp	Ala	His	Thr	Arg	Phe
			100					105					110		
Asp	Thr	Pro	Val	Thr	Val	Asn	Pro	Thr	Thr	Thr	Val	Gly	Glu	Ala	Met
			115				120					125			
Asn	Leu	Leu	Asn	Lys	Arg										
			130												

<210> 2541

<211> 564

<212> DNA

<213> Homo sapiens

<400> 2541

accggtctcc cacggagtgc tggttctctca ggtactgcac tgtatacaac tctaaatgca
 60
 ccctgcattg aacccattgc agggcacacg cagtctacat gtatcccagg ttttatgtct
 120
 acagagcctg caatactccg tgtctggaat acgttatttg ctgcacacct ccagaggaa
 180
 catgtaacgt ctgtgtaaca tgctatcctg cacacatctg aaagaatctg tgtacacaa
 240
 actattatgc tgtgcacaca tttcctcata ttctgtgtag agagcacctc attttgtact
 300
 caaatattgc gttccataa caagttacat tgctcacatc ttaaaatatt cattacacgt
 360

gaaaccaccg catggtaccg acatccttctt ggaatgtccc gcacagaggc tgatatatgt
 420
 gcacagttct cactgttctg cgtgccccagc ccctcacact ggacgcccac ctcacactct
 480
 tctgccaaag gagactttgg ttctcccctt cctgtgtgctg gctgtgcggg ccacagtctt
 540
 ctgcacgcca gcagcatgac gcgt
 564

<210> 2542
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 2542
 Met Leu Cys Thr His Phe Leu Ile Phe Cys Val Glu Ser Thr Ser Phe
 1 5 10 15
 Cys Thr Gln Ile Phe Gly Phe His Asn Lys Leu His Cys Ser His Leu
 20 25 30
 Lys Ile Phe Ile Thr Arg Glu Thr Thr Ala Trp Tyr Arg His Pro Ser
 35 40 45
 Gly Met Ser Arg Thr Glu Ala Asp Ile Cys Ala Gln Phe Ser Leu Phe
 50 55 60
 Cys Val Pro Ser Pro Ser His Trp Thr Pro Thr Ser His Ser Ser Ala
 65 70 75 80
 Lys Gly Asp Phe Gly Ser Pro Leu Pro Cys Ala Gly Cys Ala Gly His
 85 90 95
 Ser Pro Leu His Ala Ser Ser Met Thr Arg
 100 105

<210> 2543
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 2543
 cgctgaaagg gggcggggaa aatggaatgg gggggaaggg cgcgggtggg gacatgctgg
 60
 aacgtgccca tgctttctgc accacactgg atgactgaag gggaagggaac gagcgtctta
 120
 ccgctcctga tgagattttt gtttttgctt aacaaagaaa tgtgtatgaa tgcacgtctg
 180
 ttgtcagggg cagggaggag gagggtcctt ggaatagctg ccgacaacag ctggaactcc
 240
 tgtctgggtc cccagctgg gctagagagg gcagtgatca tctgtccact ggacagggaag
 300
 gtttgcaaag ggctgtttgc ttactgggtc ccaattttta gccttctgaa gccctgtgcc
 360
 aatggggccc agcaggcagc agtgctg
 387

<210> 2544
 <211> 122
 <212> PRT

<213> Homo sapiens

<400> 2544

```

Met Glu Trp Gly Gly Arg Ala Arg Val Gly Thr Cys Trp Asn Val Pro
 1           5           10           15
Met Leu Ser Ala Pro His Trp Met Thr Glu Gly Thr Ser Val
          20           25           30
Leu Pro Leu Leu Met Arg Phe Leu Phe Leu Pro Asn Lys Glu Met Cys
          35           40           45
Met Asn Ala Arg Leu Phe Ala Gly Ala Gly Arg Arg Val Leu Gly
          50           55           60
Ile Ala Ala Asp Asn Ser Trp Asn Ser Cys Leu Gly Pro Pro Ala Gly
65           70           75           80
Leu Glu Arg Ala Val Ile Ile Cys Pro Leu Asp Arg Lys Val Cys Lys
          85           90           95
Gly Leu Phe Ala Tyr Trp Val Pro Ile Phe Ser Leu Leu Lys Pro Leu
          100          105          110
Ser Asn Gly Ala Gln Gln Ala Ala Val Leu
          115          120

```

<210> 2545

<211> 336

<212> DNA

<213> Homo sapiens

<400> 2545

```

gcgattatatt tcgtgctgcc cggaactatc atggctcggc ggtggtcagg tttcccgtag
60
tggaaccaccc tcgctatctg tctagtcggc ggcatcctcg gcgttatgta ctgcattccg
120
ctgcgtcggg ccctcgtgac aggcctcgat cttccctacc cggagggcgt cgcaggagct
180
gaggtgctca aagtaggcga ttccgctggt gccgccgagg ctaacaaggc gggctgcgca
240
gtcatcatcg tcggttctgt ggtctctgca gcgtacgccc tgtgtgcgga tcttaagctt
300
gtgaagtcgg cgctgaccaa gcctttcaag acggggc
336

```

<210> 2546

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2546

```

Ala Ile Ile Phe Val Leu Pro Gly Leu Ile Met Val Gly Trp Trp Ser
 1           5           10           15
Gly Phe Pro Tyr Trp Thr Thr Leu Ala Ile Cys Leu Val Gly Gly Ile
          20           25           30
Leu Gly Val Met Tyr Ser Ile Pro Leu Arg Arg Ala Leu Val Thr Gly
          35           40           45
Ser Asp Leu Pro Tyr Pro Glu Gly Val Ala Gly Ala Glu Val Leu Lys
          50           55           60
Val Gly Asp Ser Ala Gly Ala Ala Glu Ala Asn Lys Val Gly Leu Arg

```

```

65              70              75              80
Val Ile Ile Val Gly Ser Val Val Ser Ala Ala Tyr Ala Leu Leu Ser
            85              90              95
Asp Leu Lys Leu Val Lys Ser Ala Leu Thr Lys Pro Phe Lys Thr Gly
            100              105              110

```

<210> 2547
 <211> 556
 <212> DNA
 <213> Homo sapiens

```

<400> 2547
acgcgtgcac acacacacac gcaggcgtac acgctcaca gtgcacacac acatatgagt
60
ttcccacaca tctcaccata tcactttctc tttacttttt aaagacaggg cacttgcctt
120
tatggccaat aatattatgc ccaagctaca acattccgag tcaatcaca aggttataaa
180
cttcatttga actgaagacc acctgtaagc acgcagctca aatgtttctc cctagaaatt
240
caagtttgtt ttgaaaagt gacttaacgg tcaagaaaaa aggcctggcc aacttcagag
300
agggacaccc agccctgcta cggtgcgtgt cattatgtgg tgctgtgcta tccatagaga
360
aagaggagat gaaaagatt ctacaaagag agatcaaact gcaagaaagc acaagattt
420
catcaccaca atatgaaggc ctccctggta taaatgactt ttttaggtcc caataagaaa
480
taccatctat tctatctgga attattttat tagcttcaaa ttttattcta agattcatat
540
tatcagatca tctaga
556

```

<210> 2548
 <211> 106
 <212> PRT
 <213> Homo sapiens

```

<400> 2548
Met Asn Leu Arg Ile Lys Phe Glu Ala Asn Lys Ile Ile Pro Asp Arg
1          5          10          15
Ile Asp Gly Ile Ser Tyr Trp Asp Leu Lys Lys Ser Phe Ile Pro Arg
20         25         30
Arg Pro Ser Tyr Cys Gly Asp Glu Ile Phe Val Leu Ser Cys Ser Leu
35         40         45
Ile Ser Leu Cys Arg Ile Phe Phe Ile Ser Ser Phe Ser Met Asp Ser
50         55         60
Thr Ala Pro His Asn Asp Thr Gln Arg Ser Arg Ala Gly Cys Pro Ser
65         70         75         80
Leu Lys Leu Ala Arg Pro Phe Ser Leu Thr Val Lys Ser Thr Phe Gln
85         90         95
Thr Gln Leu Glu Phe Leu Gly Glu Asn Ile
100        105

```

<210> 2549
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 2549
 nncacgctc tctccgaccg cgtacgtatt gaatttgata aagaagccaa cacggttgtt
 60
 atcgatgata atggtgtcgg catgtctcgt gaagaagcca ttacaaactt aggtacgatt
 120
 gctaaatcgg gcacctcttc tttcttagag caattgagtg gcgatcagaa aaaagacagc
 180
 caacttattg gtcaattcgg tgtaggcttt tactctgctt tcacgtttgc tgataaagta
 240
 acagtagaaa cacgtcgcgc aggtgcgacg gaaaatgaag cgggtcgtg ggtatctgat
 300
 gggtctggtg aatttactat tgagacgacg gataaagcga ctcgtggtac acgcattact
 360
 ttgcatctga aagcagatga aaaagatttc gcagacaact tccgtctacg ttcattagta
 420
 acaaaatatt ctgat
 435

<210> 2550
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 2550
 Xaa Gln Pro Leu Ser Asp Arg Val Arg Ile Glu Phe Asp Lys Glu Ala
 1 5 10 15
 Asn Thr Val Val Ile Asp Asp Asn Gly Val Gly Met Ser Arg Glu Glu
 20 25 30
 Ala Ile Thr Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Ser Phe
 35 40 45
 Leu Glu Gln Leu Ser Gly Asp Gln Lys Lys Asp Ser Gln Leu Ile Gly
 50 55 60
 Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Ile Val Ala Asp Lys Val
 65 70 75 80
 Thr Val Glu Thr Arg Arg Ala Gly Ala Thr Glu Asn Glu Ala Val Arg
 85 90 95
 Trp Val Ser Asp Gly Ser Gly Glu Phe Thr Ile Glu Thr Ile Asp Lys
 100 105 110
 Ala Thr Arg Gly Thr Arg Ile Thr Leu His Leu Lys Ala Asp Glu Lys
 115 120 125
 Asp Phe Ala Asp Asn Phe Arg Leu Arg Ser Leu Val Thr Lys Tyr Ser
 130 135 140
 Asp
 145

<210> 2551
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 2551
 nngccggcca gcctcacatc agtctctccg ccccggggaa ggctcagcac tttaaatcga
 60
 ggactccact tctggggacg cctgggttcgt tcgcccacca ggcttaggct acgctccatg
 120
 ctccccacgc aatctctgtc tacacctctc gcggcgccct gccctcctcc gacccctttc
 180
 cagccannaa gtccccccac cccctcagag aagcagcctc aaattccaga agtggaggct
 240
 ccagcctccc cgcgaggtag cagccccaca gtcttctggg agccattgtg gccagggagc
 300
 gcctctggag tgccaggctg ggttggggac cagggaaacat cggctctactc aggtgtgagg
 360
 gggcaggtct ggcctgcccc aaagttggct ccatcctgga can
 403

<210> 2552
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 2552
 Xaa Pro Ala Ser Leu Thr Ser Val Ser Pro Pro Arg Gly Arg Leu Ser
 1 5 10 15
 Thr Leu Asn Arg Gly Leu His Phe Trp Gly Arg Leu Val Arg Ser Pro
 20 25 30
 Thr Arg Pro Arg Leu Arg Ser Met Leu Pro Gln Gln Ser Leu Ser Thr
 35 40 45
 Pro Pro Ala Ala Pro Cys Pro Pro Pro Thr Pro Phe Gln Pro Xaa Ser
 50 55 60
 Pro Pro Thr Pro Ser Glu Lys Gln Pro Gln Ile Pro Glu Val Glu Ala
 65 70 75 80
 Pro Ala Ser Pro Arg Gly Thr Ser Pro Thr Val Phe Trp Glu Pro Leu
 85 90 95
 Trp Pro Gly Thr Ala Ser Gly Leu Pro Gly Trp Val Gly Asp Gln Gly
 100 105 110
 Thr Ser Val Tyr Ser Gly Val Arg Gly Gln Val Trp Pro Ala Pro Lys
 115 120 125
 Leu Ala Pro Ser Trp Thr
 130

<210> 2553
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 2553
 actagtgtcc ctataagaaa aggaaaggac caagacacag gaaagatgaa gcagagattg
 60
 gagagatata gcattgggcca aggagcactg ggagccagca gcagctggaa gaggcaggag
 120
 gcctcctccc tagaccgcac aggatgctac tgggtgagcc tgctgtcctg gaaaaggcgt
 180

gaagtctgcc tgagtgggca ggggcttctg cgcagcacc cagcaaggcca aggtggaagg
 240
 gaccctctg gccctctgccc tggtctccacc ctcagctgct ggcaggtggg tcaccaggcc
 300
 tctgccc aaa gaaactcctg caggcagctc tggacccct gtcttacaca ccttctcact
 360
 gagcctgcca gcctccagn
 380

<210> 2554

<211> 111

<212> PRT

<213> Homo sapiens

<400> 2554

Met	Lys	Gln	Arg	Leu	Glu	Arg	Tyr	Ser	Met	Gly	Gln	Gly	Ala	Leu	Gly
1				5					10					15	
Ala	Ser	Ser	Ser	Trp	Lys	Arg	Gln	Glu	Ala	Ser	Ser	Leu	Asp	Arg	Thr
			20				25						30		
Gly	Cys	Tyr	Trp	Val	Ser	Leu	Leu	Ser	Trp	Lys	Arg	Arg	Glu	Val	Cys
	35						40				45				
Leu	Ser	Gly	Gln	Gly	Leu	Leu	Arg	Ser	Thr	Gln	Gln	Gly	Gln	Gly	Gly
	50				55					60					
Arg	Asp	Pro	Pro	Gly	Pro	Cys	Pro	Gly	Ser	Thr	Leu	Ser	Cys	Trp	Gln
65					70				75					80	
Val	Gly	His	Gln	Ala	Ser	Ala	Gln	Arg	Asn	Ser	Cys	Arg	Gln	Leu	Trp
			85					90						95	
Thr	Pro	Cys	Leu	Thr	His	Leu	Leu	Thr	Glu	Pro	Ala	Ser	Ile	Pro	
			100					105					110		

<210> 2555

<211> 368

<212> DNA

<213> Homo sapiens

<400> 2555

ntccgcatgg aaaagtaaag accagcaata gccataaacg ccataaacac ataccatcat
 60
 atgttggttaa tgctgcccgg tagttcgggt gcattcttca tgggcaatag tttaatggga
 120
 gataacgcga ataatggttag tgcgttctta gtgctcacag acctgggtcacc ccaaatagaa
 180
 ggatttatat cctcccatat cctcattttt gtgctcgttg gcctcggcat tgtctttacc
 240
 gttgccactc gaggtgtaca gtccgcctc ttccgggcaca tggggcacct catgctcgat
 300
 tcacggaagc aaaagggcac ctccctctcc agctctcaag cattcacagt gggctctcgat
 360
 cacgcggn
 368

<210> 2556

<211> 102

<212> PRT

<213> Homo sapiens

<400> 2556

```

Met Leu Leu Met Leu Pro Gly Ser Ser Val Ala Phe Phe Met Gly Asn
 1             5             10             15
Ser Leu Met Gly Asp Asn Ala Asn Asn Gly Ser Val Val Leu Val Leu
      20             25             30
Thr Asp Leu Val Thr Gln Ile Glu Gly Phe Ile Ser Ser His Ile Leu
      35             40             45
Ile Phe Val Leu Val Gly Leu Gly Ile Val Phe Thr Val Ala Thr Arg
      50             55             60
Gly Val Gln Phe Arg Leu Phe Gly His Met Trp His Leu Met Leu Asp
      65             70             75             80
Ser Arg Lys Gln Lys Gly Thr Ser Leu Ser Ser Ser Gln Ala Phe Thr
      85             90             95
Val Gly Leu Asp His Ala
      100

```

<210> 2557

<211> 408

<212> DNA

<213> Homo sapiens

<400> 2557

```

atcactactc cagttggtga ggcagttctg ggtcgcatct taaatgtgat cggtagcgccg
60
attgatgaga tgggcccagt taacgcgaaa gaaaaatggg aaattcaccg tccagctcct
120
aaatcgaag accaagctgt taaagctgag atgttgatga ctggtattaa ggtcgttgat
180
cttcttgcac cttacgcaaa gggtaggcaag atcgggtctct tcggtggtgc gggcgtaggt
240
aaaacagatt tgattcaaga gttgattcgt aacatcgcta ctgagcaccg tggatactct
300
gtattcgcag gtgtcggcga gcgtactcgc gaaggtaacg atctttgggt tgagatgaaa
360
gaatcaggcg ttatcgcaaa gaccgcactt gtattcggtc agatgaat
408

```

<210> 2558

<211> 136

<212> PRT

<213> Homo sapiens

<400> 2558

```

Ile Thr Thr Pro Val Gly Glu Ala Val Leu Gly Arg Ile Leu Asn Val
 1             5             10             15
Ile Gly Glu Pro Ile Asp Glu Met Gly Pro Val Asn Ala Lys Glu Lys
      20             25             30
Trp Glu Ile His Arg Pro Ala Pro Lys Phe Glu Asp Gln Ala Val Lys
      35             40             45
Ala Glu Met Leu Met Thr Gly Ile Lys Val Val Asp Leu Leu Ala Pro
      50             55             60
Tyr Ala Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly

```

```

65          70          75          80
Lys Thr Val Leu Ile Gln Glu Leu Ile Arg Asn Ile Ala Thr Glu His
      85          90          95
Gly Gly Tyr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly
      100        105        110
Asn Asp Leu Trp Val Glu Met Lys Glu Ser Gly Val Ile Ala Lys Thr
      115        120        125
Ala Leu Val Phe Gly Gln Met Asn
      130        135

```

<210> 2559

<211> 389

<212> DNA

<213> Homo sapiens

<400> 2559

```

tccttgaaga tgaacatctt tcggctgcaa actgaaaagg atttgaatcc tcagaaaaca
60
gcttttctga aagatcgact gaatgcaata caggaagagc attctaagga cctgaagctg
120
ttgcattctcg aagttatgaa ttgctgccag caactgagag ctgtaaaaga ggaagaagac
180
aaggcacaaag atgaggtgca aaggttgact gccactctga agattgcctc gcagacaaaag
240
aagaatgcagc ccattattga agaggaactg aagaccacaa aacgtaaaaa gaaccttaaa
300
attcaagagc ttctagagat gacctcattt ccaagttggt tgaagaaaaa aagaacctgc
360
aggatatctt tcaacaggaa catgaagaa
389

```

<210> 2560

<211> 129

<212> PRT

<213> Homo sapiens

<400> 2560

```

Ser Leu Lys Met Asn Ile Phe Arg Leu Gln Thr Glu Lys Asp Leu Asn
1      5      10      15
Pro Gln Lys Thr Ala Phe Leu Lys Asp Arg Leu Asn Ala Ile Gln Glu
      20      25      30
Glu His Ser Lys Asp Leu Lys Leu Leu His Leu Glu Val Met Asn Leu
      35      40      45
Arg Gln Gln Leu Arg Ala Val Lys Glu Glu Glu Asp Lys Ala Gln Asp
      50      55      60
Glu Val Gln Arg Leu Thr Ala Thr Leu Lys Ile Ala Ser Gln Thr Lys
65      70      75      80
Lys Asn Ala Ala Ile Ile Glu Glu Glu Leu Lys Thr Thr Lys Arg Lys
      85      90      95
Met Asn Leu Lys Ile Gln Glu Leu Leu Glu Met Thr Ser Phe Pro Ser
      100      105      110
Trp Leu Lys Lys Ile Arg Thr Cys Arg Ile Ser Phe Asn Arg Asn Met
      115      120      125
Lys

```

<210> 2561
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 2561
 nnactcacca ctgtggttct actatgcctt ctgaccccggt cttggacttc aactgggaga
 60
 atgtggagcc atttgaacag gctcctcttc tggagcatat tttcttctgt cacttgtaga
 120
 aaagctgtat tggattgtga ggcaatgaaa acaaatgaat tcccttctcc atgtttggag
 180
 tcaaagacta aggtgggttat gaagggtcaa aatgtatcta tgttttgttc ccataagaac
 240
 aaatcactgc agatcaccta ttcattgttt cgacgtaaga cacacctggg aaccaggat
 300
 ggaaaagggt aacctgcgat ttttaacctc agcatcacag aagcccatga atcaggcccc
 360
 tacaatagca aagcccaagt taccagctgt tcaaaatata gtctgtgactt cagcttcacg
 420
 attgtcgac
 429

<210> 2562
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 2562
 Xaa Leu Thr Thr Val Val Leu Leu Cys Leu Leu Thr Pro Ser Trp Thr
 1 5 10 15
 Ser Thr Gly Arg Met Trp Ser His Leu Asn Arg Leu Leu Phe Trp Ser
 20 25 30
 Ile Phe Ser Ser Val Thr Cys Arg Lys Ala Val Leu Asp Cys Glu Ala
 35 40 45
 Met Lys Thr Asn Glu Phe Pro Ser Pro Cys Leu Asp Ser Lys Thr Lys
 50 55 60
 Val Val Met Lys Gly Gln Asn Val Ser Met Phe Cys Ser His Lys Asn
 65 70 75 80
 Lys Ser Leu Gln Ile Thr Tyr Ser Leu Phe Arg Arg Lys Thr His Leu
 85 90 95
 Gly Thr Gln Asp Gly Lys Gly Glu Pro Ala Ile Phe Asn Leu Ser Ile
 100 105 110
 Thr Glu Ala His Glu Ser Gly Pro Tyr Lys Cys Lys Ala Gln Val Thr
 115 120 125
 Ser Cys Ser Lys Tyr Ser Arg Asp Phe Ser Phe Thr Ile Val Asp
 130 135 140

<210> 2563
 <211> 267
 <212> DNA
 <213> Homo sapiens

<400> 2563

ggatcccaga cgagtgttg cagcagtatg ggggccgtgg gggcgacggc caccgtcagc
 60
 accccgggtca ccatccagaa catgacctcc tcttatgtca ccatcacatc ccatgtcctt
 120
 aaggcccttta ccttttggga acaggcagag gccctcaca ggaagaacaa agaattcttt
 180
 gctcagctca gcacaaaagt gcgcgtgttg gccctcaaca gcagcctggt ggacctgggtg
 240
 cactacacaa ggcagggcct ccagcgg
 267

<210> 2564

<211> 89

<212> PRT

<213> Homo sapiens

<400> 2564

Gly	Ser	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Met	Gly	Ala	Val	Gly	Ala	Thr
1				5					10				15		
Ala	Thr	Val	Ser	Thr	Pro	Val	Thr	Ile	Gln	Asn	Met	Thr	Ser	Ser	Tyr
			20				25					30			
Val	Thr	Ile	Thr	Ser	His	Val	Leu	Lys	Ala	Phe	Thr	Leu	Trp	Glu	Gln
		35				40					45				
Ala	Glu	Ala	Leu	Thr	Arg	Lys	Asn	Lys	Glu	Phe	Phe	Ala	Gln	Leu	Ser
	50				55					60					
Thr	Lys	Val	Arg	Val	Leu	Ala	Leu	Asn	Ser	Ser	Leu	Val	Asp	Leu	Val
65				70				75					80		
His	Tyr	Thr	Arg	Gln	Gly	Leu	Gln	Arg							
				85											

<210> 2565

<211> 333

<212> DNA

<213> Homo sapiens

<400> 2565

cttcgcactg ctccgcgagt tcttggggga gtgagcacag cgcgtaagct cagccacgtg
 60
 tggttcgaat tcgattcctt ggtcaatgcc cgtgacgtgg gcggaatccc caccgccgat
 120
 gggccgggtga aatcccagcg actgatccgc agcgacaacc tgcaggccct caccgaggcc
 180
 gacatgccc agttgcagca actcgggtgc tccgatgtgg tcgatctgcg ttccacctat
 240
 gaggtggcca gcgagggccc ggggccgctg accgggctg gggtgacat ccacccccat
 300
 tccttctgc cgcaccagca cgccaatgtg cac
 333

<210> 2566

<211> 111

<212> PRT

<213> Homo sapiens

<400> 2566

```

Leu Arg Thr Ala Pro Arg Val Leu Gly Gly Val Ser Thr Ala Arg Lys
 1           5           10           15
Leu Ser His Val Trp Phe Glu Phe Asp Ser Leu Val Asn Ala Arg Asp
           20           25           30
Val Gly Gly Ile Pro Thr Pro Asp Gly Pro Val Lys Ser Gln Arg Leu
           35           40           45
Ile Arg Ser Asp Asn Leu Gln Ala Leu Thr Glu Ala Asp Ile Ala Gln
           50           55           60
Leu Gln Gln Leu Gly Val Ser Asp Val Val Asp Leu Arg Ser Thr Tyr
           65           70           75           80
Glu Val Ala Ser Glu Gly Pro Gly Pro Leu Thr Gly Arg Gly Val Thr
           85           90           95
Ile His Pro His Ser Phe Leu Pro Asp Gln His Ala Asn Val His
           100           105           110

```

<210> 2567

<211> 396

<212> DNA

<213> Homo sapiens

<400> 2567

```

ngaattcaaa ctggtgttcg tatgggccat aagcaaggta catatacgat gcgttttaga
60
agccaggttca cagatcaacg tctattcgga accgatcaat ttagtattgg tggggcgtat
120
tctgtacgag gtttttagtgg agaagaaacc ttaagagggtg actcggggcta ttatgtacaa
180
aatggaatggg cattaccatt tagaaaacaa caaattactc catatgtagg gatagatatt
240
ggacatgtat gggggccatc tacagaaact caattaggta ataccttaat tgggtggtgta
300
gttggtgtac gtggtatggt tgggtgacgat gtaaactatg atgtatcact aggaacacca
360
attaagaaac cagaaggttt tgatacagat acgcgt
396

```

<210> 2568

<211> 132

<212> PRT

<213> Homo sapiens

<400> 2568

```

Xaa Ile Gln Thr Gly Val Arg Met Gly His Lys Gln Gly Thr Tyr Thr
 1           5           10           15
Met Arg Phe Arg Ser Gln Phe Thr Asp Gln Arg Leu Phe Gly Thr Asp
           20           25           30
Gln Phe Ser Ile Gly Gly Arg Tyr Ser Val Arg Gly Phe Ser Gly Glu
           35           40           45
Glu Thr Leu Arg Gly Asp Ser Gly Tyr Tyr Val Gln Asn Glu Trp Ala
           50           55           60
Leu Pro Phe Arg Lys Gln Gln Ile Thr Pro Tyr Val Gly Ile Asp Ile

```

```

65              70              75              80
Gly His Val Trp Gly Pro Ser Thr Glu Thr Gln Leu Gly Asn Thr Leu
            85              90              95
Ile Gly Gly Val Val Gly Val Arg Gly Met Val Gly Asp Asp Val Asn
            100             105             110
Tyr Asp Val Ser Leu Gly Thr Pro Ile Lys Lys Pro Glu Gly Phe Asp
            115             120             125
Thr Asp Thr Arg
            130

```

```

<210> 2569
<211> 330
<212> DNA
<213> Homo sapiens

```

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<400> 2569
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tacctcgtcg ccgatagagt tgtcgtgacc accaagcaca acgatgacga gcagtagctg
120
tgggagtgccc aagcggggcgg gtcgttcact gttactcgtg acacgtcagg ggagcagctt
180
ggcagggggca ctaagatcac actgttcctc aaggacgacg agctggagta ccttgaggag
240
cgtcgctcca aggatctggt caagaagcac tctgagttca tcagctaccc catctccctg
300
tggactgaaa agacaacaga gaaggaaatt
330

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```

<210> 2570
<211> 110
<212> PRT
<213> Homo sapiens

```

```

<400> 2570
Leu Ala Ala Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly
1      5      10      15
Phe Tyr Ser Ala Tyr Leu Val Ala Asp Arg Val Val Val Thr Thr Lys
20     25     30
His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly Ser
35     40     45
Phe Thr Val Thr Arg Asp Thr Ser Gly Glu Gln Leu Gly Arg Gly Thr
50     55     60
Lys Ile Thr Leu Phe Leu Lys Asp Asp Gln Leu Glu Tyr Leu Glu Glu
65     70     75     80
Arg Arg Leu Lys Asp Leu Val Lys Lys His Ser Glu Phe Ile Ser Tyr
85     90     95
Pro Ile Ser Leu Trp Thr Glu Lys Thr Thr Glu Lys Glu Ile
100    105    110

```

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<210> 2571
<211> 335
<212> DNA
<213> Homo sapiens

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<400> 2571
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 60
 gtgctcctta aacatctcga taatgaacta tctgagctct ttactgagat cgctcgggag
 120
 aaatgggatg tccgttttagg gcaggggaacg acagctatcg accaggtgga gaagcagcgt
 180
 gaagatgggt cttcctactt cgaaccacc attacatttg aagacggcag cactgttacc
 240
 ggtgacgcgt tcctagtgtc taccggacgt acccctaaca cgcaccgcct tggcctcgac
 300
 aatgggttcg gtgtgaaggt tgaaagggga cgcgt
 335

<210> 2572
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 2572
 Glu Phe Ala Asn Val Phe Ser Gly Met Gly Ser Thr Val Thr Leu Ile
 1 5 10 15
 Gly Arg Ser Pro Val Leu Leu Lys His Leu Asp Asn Glu Leu Ser Glu
 20 25 30
 Leu Phe Thr Glu Ile Ala Arg Glu Lys Trp Asp Val Arg Leu Gly Gln
 35 40 45
 Gly Thr Thr Ala Ile Asp Gln Val Glu Lys Gln Arg Glu Asp Gly Ser
 50 55 60
 Ser Tyr Phe Glu Thr Thr Ile Thr Phe Glu Asp Gly Ser Thr Val Thr
 65 70 75 80
 Gly Asp Ala Phe Leu Val Ala Thr Gly Arg Thr Pro Asn Thr Asp Arg
 85 90 95
 Leu Gly Leu Asp Asn Gly Ser Gly Val Lys Val Glu Arg Gly Arg
 100 105 110

<210> 2573
 <211> 460
 <212> DNA
 <213> Homo sapiens

<400> 2573
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 gccggatcca taccggaccg ttctcgtcagg gtggtcggac atcgacgaca ccgcatgatc
 120
 cgagacgacg ttgatacgtc caccggcgcg gtccgtgatc cagccgctcg tcgccgttgc
 180
 cgccactggc acgatgaggg ccatcaccga gaagagaacg gccaccactc gcagaccacc
 240
 tcgtccca gaagcgagga cgaaggcgat gacggcgatg accagagccg gtacagccaa
 300
 cgatcccacc agaacggagg agatgaaggt gagggcattg tgtgagggga ggatcgcggc
 360

cactgaccac gccagtaccg gcagggtcag gatcagcccc acgagaccgg aagtgatgcg
 420
 tagccaggaa tgacgggagg ttttcgtgtc agccacgcgt
 460

<210> 2574
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 2574
 Met Gly Thr Val Asp Leu Gly Arg Leu Val Arg Ala Gly Ser Ile Pro
 1 5 10 15
 Asp Arg Phe Val Arg Val Val Gly His Arg Arg His Arg Arg Cys Arg
 20 25 30
 Asp Asp Val Asp Thr Ser Thr Gly Ala Val Arg Asp Pro Arg Arg Arg
 35 40 45
 Arg Arg Cys Arg His Trp His Asp Glu Gly His His Arg Glu Glu Asn
 50 55 60
 Gly His His Ser Gln Thr Thr Ser Ser Gln Lys Ser Glu Asp Glu Gly
 65 70 75 80
 Asp Asp Gly Asp Asp Gln Ser Arg Tyr Ser Gln Arg Ser His Gln Asn
 85 90 95
 Gly Gly Asp Glu Gly Glu Gly Ile Val
 100 105

<210> 2575
 <211> 3954
 <212> DNA
 <213> Homo sapiens

<400> 2575
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 ccactctcgc gcctccgaac agccacaggg gcaaagccct gtcaccccca ggatccggtc
 120
 atcaggggaaa gaggacaggg agaccagaag agggccagct gggacgaggg ggcggacggc
 180
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 240
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 300
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 420
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 480
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720
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1260
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3720
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3780
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3840
tccactggcc ctccaggctg attccctggg ctccaggctc ccccgcgcg gcgcgcccc
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3954

<210> 2576

<211> 1016

<212> PRT

<213> Homo sapiens

<400> 2576

Met	Ala	Pro	Arg	Thr	Leu	Trp	Ser	Cys	Tyr	Leu	Cys	Cys	Leu	Leu	Thr
1			5					10					15		
Ala	Ala	Ala	Gly	Ala	Ala	Ser	Tyr	Pro	Pro	Arg	Gly	Phe	Ser	Leu	Tyr
		20						25				30			
Thr	Gly	Ser	Ser	Gly	Ala	Leu	Ser	Pro	Gly	Gly	Pro	Gln	Ala	Gln	Ile
	35					40					45				
Ala	Pro	Arg	Pro	Ala	Ser	Arg	His	Arg	Asn	Trp	Cys	Ala	Tyr	Val	Val
	50				55					60					
Thr	Arg	Thr	Val	Ser	Cys	Val	Leu	Glu	Asp	Gly	Val	Glu	Thr	Tyr	Val
65				70					75				80		
Lys	Tyr	Gln	Pro	Cys	Ala	Trp	Gly	Gln	Pro	Gln	Cys	Pro	Gln	Ser	Ile
		85						90					95		
Met	Tyr	Arg	Arg	Phe	Leu	Arg	Pro	Arg	Tyr	Arg	Val	Ala	Tyr	Lys	Thr
		100						105					110		
Val	Thr	Asp	Met	Glu	Trp	Arg	Cys	Cys	Gln	Gly	Tyr	Gly	Gly	Asp	Asp
	115					120						125			
Cys	Ala	Glu	Ser	Pro	Ala	Pro	Ala	Leu	Gly	Pro	Ala	Ser	Ser	Thr	Pro
	130				135					140					
Arg	Pro	Leu	Ala	Arg	Pro	Ala	Arg	Pro	Asn	Leu	Ser	Gly	Ser	Ser	Ala
145				150					155						160
Gly	Ser	Pro	Leu	Ser	Gly	Leu	Gly	Gly	Glu	Gly	Pro	Gly	Glu	Ser	Glu
			165					170					175		
Lys	Val	Gln	Gln	Leu	Glu	Glu	Gln	Val	Gln	Ser	Leu	Thr	Lys	Glu	Leu
	180						185						190		
Gln	Gly	Leu	Arg	Gly	Val	Leu	Gln	Gly	Leu	Ser	Gly	Arg	Leu	Ala	Glu
	195					200						205			
Asp	Val	Gln	Arg	Ala	Val	Glu	Thr	Ala	Phe	Asn	Gly	Arg	Gln	Gln	Pro
	210				215						220				
Ala	Asp	Ala	Ala	Ala	Arg	Pro	Gly	Val	His	Glu	Thr	Leu	Asn	Glu	Ile
225				230					235					240	
Gln	His	Gln	Leu	Gln	Leu	Leu	Asp	Thr	Arg	Val	Ser	Thr	His	Asp	Gln
		245						250					255		
Glu	Leu	Gly	His	Leu	Asn	Asn	His	His	Gly	Gly	Ser	Ser	Ser	Ser	Gly
	260				265							270			
Gly	Ser	Arg	Ala	Pro	Ala	Pro	Ala	Ser	Ala	Pro	Pro	Gly	Pro	Ser	Glu
	275				280						285				
Glu	Leu	Leu	Arg	Gln	Leu	Glu	Gln	Arg	Leu	Gln	Glu	Ser	Cys	Ser	Val
	290				295					300					
Cys	Leu	Ala	Gly	Leu	Asp	Gly	Phe	Arg	Arg	Gln	Gln	Gln	Glu	Asp	Arg
305				310						315				320	
Glu	Arg	Leu	Arg	Ala	Met	Glu	Lys	Leu	Leu	Ala	Ser	Val	Glu	Glu	Arg
		325						330					335		
Gln	Arg	His	Leu	Ala	Gly	Leu	Ala	Val	Gly	Arg	Arg	Pro	Pro	Gln	Glu
	340					345						350			
Cys	Cys	Ser	Pro	Glu	Leu	Gly	Arg	Arg	Leu	Ala	Glu	Leu	Glu	Arg	Arg

```

355              360              365
Leu Asp Val Val Ala Gly Ser Val Thr Val Leu Ser Gly Arg Arg Gly
370              375              380
Thr Glu Leu Gly Gly Ala Ala Gly Gln Gly Gly His Pro Pro Gly Tyr
385              390              395
Thr Ser Leu Ala Ser Arg Leu Ser Arg Leu Glu Asp Arg Phe Asn Ser
405              410              415
Thr Leu Gly Pro Ser Glu Glu Gln Glu Glu Ser Trp Pro Gly Ala Pro
420              425
Gly Gly Leu Ser His Trp Leu Pro Ala Ala Arg Gly Arg Leu Glu Gln
435              440              445
Leu Gly Gly Leu Leu Ala Asn Val Ser Gly Glu Leu Gly Gly Arg Leu
450              455              460
Asp Leu Leu Glu Glu Gln Val Ala Gly Ala Met Gln Ala Cys Gly Gln
465              470              475
Leu Cys Ser Gly Ala Pro Gly Glu Gln Asp Ser Gln Val Ser Glu Ile
485              490              495
Leu Ser Ala Leu Glu Arg Arg Val Leu Asp Ser Glu Gly Gln Leu Arg
500              505              510
Leu Val Gly Ser Gly Leu His Thr Val Glu Ala Ala Gly Glu Ala Arg
515              520              525
Gln Ala Thr Leu Glu Gly Leu Gln Glu Val Val Gly Arg Leu Gln Asp
530              535              540
Arg Val Asp Ala Gln Asp Glu Thr Ala Ala Glu Phe Thr Leu Arg Leu
545              550              555
Asn Leu Thr Ala Ala Arg Leu Gly Gln Leu Glu Gly Leu Leu Gln Ala
565              570              575
His Gly Asp Glu Gly Cys Gly Ala Cys Gly Gly Val Gln Glu Glu Leu
580              585              590
Gly Arg Leu Arg Asp Gly Val Glu Arg Cys Ser Cys Pro Leu Leu Pro
595              600              605
Pro Arg Gly Pro Gly Ala Gly Pro Gly Val Gly Gly Pro Ser Arg Gly
610              615              620
Pro Leu Asp Gly Phe Ser Val Phe Gly Gly Ser Ser Gly Ser Ala Leu
625              630              635
Gln Ala Leu Gln Gly Glu Leu Ser Glu Val Ile Leu Ser Phe Ser Ser
645              650              655
Leu Asn Asp Ser Leu Asn Glu Leu Gln Thr Thr Val Glu Gly Gln Gly
660              665              670
Ala Asp Leu Ala Asp Leu Gly Ala Thr Lys Asp Arg Ile Ile Ser Glu
675              680              685
Ile Asn Arg Leu Gln Gln Glu Ala Thr Glu His Ala Thr Glu Ser Glu
690              695              700
Glu Arg Phe Arg Gly Leu Glu Glu Gly Gln Ala Gln Ala Gly Gln Cys
705              710              715
Pro Ser Leu Glu Gly Arg Leu Gly Arg Leu Glu Gly Val Cys Glu Arg
725              730              735
Leu Asp Thr Val Ala Gly Gly Leu Gln Gly Leu Arg Glu Gly Leu Ser
740              745              750
Arg His Val Ala Gly Leu Trp Ala Gly Leu Arg Glu Thr Asn Thr Thr
755              760              765
Ser Gln Met Gln Ala Ala Leu Leu Glu Lys Leu Val Gly Gly Gln Ala
770              775              780
Gly Leu Gly Arg Arg Leu Gly Ala Leu Asn Ser Ser Leu Gln Leu Leu

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```

785              790              795              800
Glu Asp Arg Leu His Gln Leu Ser Leu Lys Asp Leu Thr Gly Pro Ala
      805              810              815
Gly Glu Ala Gly Pro Pro Gly Pro Pro Gly Leu Gln Gly Pro Pro Gly
      820              825              830
Pro Ala Gly Pro Pro Gly Ser Pro Gly Lys Asp Gly Gln Glu Gly Pro
      835              840              845
Ile Gly Pro Pro Gly Pro Gln Gly Glu Gln Gly Val Glu Gly Ala Pro
      850              855              860
Ala Ala Pro Val Pro Gln Val Ala Phe Ser Ala Ala Leu Ser Leu Pro
865              870              875              880
Arg Ser Glu Pro Gly Thr Val Pro Phe Asp Arg Val Leu Leu Asn Asp
      885              890              895
Gly Gly Tyr Tyr Asp Pro Glu Thr Gly Val Phe Thr Ala Pro Leu Ala
      900              905              910
Gly Arg Tyr Leu Leu Ser Ala Val Leu Thr Gly His Arg His Glu Lys
      915              920              925
Val Glu Ala Val Leu Ser Arg Ser Asn Gln Gly Val Ala Arg Val Asp
      930              935              940
Ser Gly Gly Tyr Glu Pro Glu Gly Leu Glu Asn Lys Pro Val Ala Glu
945              950              955              960
Ser Gln Pro Ser Pro Gly Thr Leu Gly Val Phe Ser Leu Ile Leu Pro
      965              970              975
Leu Gln Ala Gly Asp Thr Val Cys Val Asp Leu Val Met Gly Gln Leu
      980              985              990
Ala His Ser Glu Glu Pro Leu Thr Ile Phe Ser Gly Ala Leu Leu Tyr
      995              1000              1005
Gly Asp Pro Glu Leu Glu His Ala
      1010              1015

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<210> 2577

<211> 343

<212> DNA

<213> Homo sapiens

<400> 2577

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acgcgtgaag ggggagggtc atggcctcct gggcttcaag gaggagctgg ggctgggggtg
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ggggcgtggt gcattcatcc ccggccgcag ctgatctgga gccatctgta gcaaatgctt
120
tgctgagcaa attacgaggg tcaacaggag cagggcagac gcttctccca cctgctggcc
180
agtgttcctt cggtaccgt gcactcagcc ccacagtgc cctgagtgg ataccggccc
240
tgctgcctt gggctctcaa tgggggctcg gggcctcaca gggccagcac gagccacttg
300
ccagggtctc caacagacc tgagcctggc agtccctggg ccc
343

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<210> 2578

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2578

```

Met Ala Ser Trp Ala Ser Arg Arg Ser Trp Gly Trp Gly Gly Gly Val
 1           5           10           15
Val His Ser Ser Pro Ala Ala Ala Asp Leu Glu Pro Ser Val Ala Lys
           20           25           30
Cys Leu Leu Ser Lys Leu Arg Gly Ser Thr Gly Ala Gly Gln Thr Leu
           35           40           45
Leu Pro Pro Ala Gly Gln Cys Ser Leu Gly Tyr Arg Ala Leu Ser Pro
           50           55           60
Thr Val Thr Pro Glu Trp Ile Pro Ala Leu Pro Ala Leu Gly Ser Gln
           65           70           75           80
Trp Gly Leu Gly Ala Ser Gln Gly Gln His Glu Pro Leu Ala Arg Val
           85           90           95
Ser Asn Arg Pro
           100

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<210> 2579

<211> 420

<212> DNA

<213> Homo sapiens

<400> 2579

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ntcatgatct tcagaagctg tattaatttg gccgcattta tcatcatagt tttttcctat
60
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120
gttaaaaaag agatgatcct tgccaaacgt tttttcctta tagtatttac tgaatgcatta
180
tgctggatac ccatttttgt agtgaaattt ctttcaactgc ttcaggtaga aataccagggt
240
accataacct ctgggtagt gatttttatt ctgccacatta acagtgtctt gaaccaatt
300
ctctatactc tgaccacaag accatttaaa gaaatgattc atcggttttg gtataactac
360
agacaaaagaa aatctatgga cagcaaaggt cagaaaaacag aggctggagt gtgctcgaga
420

```

<210> 2580

<211> 140

<212> PRT

<213> Homo sapiens

<400> 2580

```

Xaa Met Ile Phe Arg Ser Cys Ile Asn Leu Ala Ala Phe Ile Ile Ile
 1           5           10           15
Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His Gln Ser Ala Ile
           20           25           30
Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu Met Ile Leu Ala
           35           40           45
Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu Cys Trp Ile Pro
           50           55           60
Ile Phe Val Val Lys Phe Leu Ser Leu Leu Gln Val Glu Ile Pro Gly
           65           70           75           80
Thr Ile Thr Ser Trp Val Val Ile Phe Ile Leu Pro Ile Asn Ser Ala

```

```

      85              90              95
Leu Asn Pro Ile Leu Tyr Thr Leu Thr Arg Pro Phe Lys Glu Met
      100              105              110
Ile His Arg Phe Trp Tyr Asn Tyr Arg Gln Arg Lys Ser Met Asp Ser
      115              120              125
Lys Gly Gln Lys Thr Glu Ala Gly Val Cys Ser Arg
      130              135              140

```

<210> 2581
 <211> 459
 <212> DNA
 <213> Homo sapiens

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<400> 2581
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cgctccggtgc acgtccgcgc cgaaggagcc gacaccaga ccacggtgcc cgacaccag
120
cagtttgtat accaggccca ttccctcgac aagattgaga tcattggacg cattctgcag
180
gccaacgacg tcgaaaaggc cattatcttc tgccgcacca agcgtgcatg ccagcggctt
240
tctgacgacc tcgacgacgc cgggtttcaa acccgcgcca tccacggtga tctcacgcag
300
gtcgcgcgtg aaaaggcgct caagaaattc cgtcatggcg aggcgaccat cctgggtggcg
360
accgatgctg ctgcccgtgg cattgacgtc accggggtgt ccacgtcat caaccatgaa
420
tgtcccgaag acgagaaaac atacgtccac cgcattggt
459

```

<210> 2582
 <211> 153
 <212> PRT
 <213> Homo sapiens

```

<400> 2582
Met Leu Phe Ser Ala Thr Met Pro Ala Pro Ile Met Ala Leu Ala Arg
1      5      10      15
Ser Gln Leu Arg Arg Pro Val His Val Arg Ala Glu Gly Ala Asp Thr
20      25      30
Gln Thr Thr Val Pro Asp Thr Gln Gln Phe Val Tyr Gln Ala His Ser
35      40      45
Leu Asp Lys Ile Glu Ile Ile Gly Arg Ile Leu Gln Ala Asn Asp Val
50      55      60
Glu Lys Val Ile Ile Phe Cys Arg Thr Lys Arg Ala Cys Gln Arg Leu
65      70      75      80
Ser Asp Asp Leu Asp Asp Arg Gly Phe Lys Thr Arg Ala Ile His Gly
85      90      95
Asp Leu Thr Gln Val Ala Arg Glu Lys Ala Leu Lys Lys Phe Arg His
100      105      110
Gly Glu Ala Thr Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Ile
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      100          105          110
Pro  Ala  Asp  Leu  Leu  Glu  Pro  Glu  Trp  Asp  Gln  Leu  Val  Glu  Gln  Ala
      115          120          125
Lys  Ser  Leu  Glu  Gly  Phe  Asp  Gly  Ser  Asp  Glu  Asp  Val  Leu  Thr  Asn
      130          135          140
Ala
145

```

<210> 2589

<211> 366

<212> DNA

<213> Homo sapiens

<400> 2589

```

ccggcgaaga aggacatggc catggtcttc ggcgcgactc attacgtcga cccgacggcc
60
ggcgatccgg ttgagcagat cagagcgctg accagggggcc gcggcgctga tttcgcgatc
120
gaggtcgctg gcatcgctga ggtcatggag caggcctact gggcgggcgcg acgcggcggc
180
acgatcgctc acgtcggggc gctggggcgc gacgccaagc tggctcctgcc ggcgaaacgac
240
ctgcacggcg gcgccaagac gatcatggc tgccccaacg gattggggcgc agtcgcacc
300
gactatgcca agatgatctc gctggctcgc accggacggc tggacctggg cgggatgatc
360
acgcgt
366

```

<210> 2590

<211> 122

<212> PRT

<213> Homo sapiens

<400> 2590

```

Pro  Ala  Lys  Lys  Asp  Met  Ala  Met  Val  Phe  Gly  Ala  Thr  His  Tyr  Val
      1           5           10           15
Asp  Pro  Thr  Ala  Gly  Asp  Pro  Val  Glu  Gln  Ile  Arg  Ala  Leu  Thr  Arg
      20           25           30
Gly  Arg  Gly  Val  Asp  Phe  Ala  Ile  Glu  Val  Val  Gly  Ile  Val  Glu  Val
      35           40           45
Met  Glu  Gln  Ala  Tyr  Trp  Ala  Ala  Arg  Arg  Gly  Gly  Thr  Ile  Val  Tyr

```

```

      50              55              60
Val Gly Ala Leu Gly Ile Asp Ala Lys Leu Val Leu Pro Ala Asn Asp
65              70              75              80
Leu His Gly Gly Ala Lys Thr Ile Ile Gly Cys Ala Asn Gly Leu Gly
      85              90              95
Ala Val Arg Thr Asp Tyr Ala Lys Met Ile Ser Leu Val Glu Thr Gly
      100              105              110
Arg Leu Asp Leu Gly Gly Met Ile Thr Arg
      115              120

```

<210> 2591
 <211> 341
 <212> DNA
 <213> Homo sapiens

```

<400> 2591
acgcgtaaaag gcatgacctc accttatcat caggggcaca cgtgtgttat tctggggctg
60
agcagccac gagttgtcca gcaccaggcc aggggtcagt cagcaatgag gacagctcct
120
tcctgtctcca gggcaggccc tgggcagggc aatgctgggg acacgggtggg gagtaggcca
180
cagcttctgtt gggggagttc ctatggcagg aggatcatgc ccagcagcgt ggaagacaa
240
ggggtgaccc tgcactcgag gctcctggga agacggggag ggttgaggtt acatgagggga
300
gagggggtcag ttggtgcatt cacagaacag caggggtggcc a
341

```

<210> 2592
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 2592
Met Thr Ser Pro Tyr His Gln Gly His Thr Cys Val Ile Leu Gly Leu
1      5      10      15
Ser Ser Pro Arg Val Val Gln His Gln Ala Arg Gly Gln Ser Ala Met
20      25      30
Arg Thr Ala Pro Ser Cys Ser Arg Ala Gly Pro Gly Gln Gly Asn Ala
35      40      45
Gly Asp Thr Val Gly Ser Arg Pro Gln Leu Leu Trp Gly Ser Ser Tyr
50      55      60
Gly Arg Arg Ile Met Pro Ser Ser Val Glu Glu Gln Gly Val Thr Leu
65      70      75      80
His Ser Arg Leu Leu Gly Arg Arg Gly Gly Leu Arg Leu His Glu Gly
85      90      95
Glu Gly Ser Val Gly Ala Phe Thr Glu Gln Gln Gly Gly
100      105

```

<210> 2593
 <211> 501
 <212> DNA
 <213> Homo sapiens

<400> 2593
 cgcgtaaggc caccagaaga tttttatgca cagattccgt tgcttcgaga gctaatttcg
 60
 gcgcctttcat ggggttttat ggaggtggat gaatatgagg cggatgatat tatcggtacc
 120
 ttggcgcgcc aagcggatga agcgggggat tatatgactt atattgtgtc ttcggacctc
 180
 gatattgtgc aaatcgtaga tgaaaacacc aagatgtatc gaattctgcg gggattttcg
 240
 gatctcgagg agatggatc tccagcgatt gaagaaaaat atggaatctt gaagtcgcaa
 300
 tttttggacc tgaaggcgct gaagggggat aattcggata atattccagg cgtaccaggg
 360
 attggtgaga aaaccgcagt gaaactcttg aatgagtatg gtatcttgga ggggatttat
 420
 aatcatatca aggaatttc gggggcgaca cagaagaaat tgattgtcgg acgcgaatca
 480
 gctgagatgt ctcttaagct t
 501

<210> 2594
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 2594
 Arg Val Arg Pro Pro Glu Asp Phe Tyr Ala Gln Ile Pro Leu Leu Arg
 1 5 10 15
 Glu Leu Ile Ser Ala Leu Ser Trp Gly Phe Met Glu Val Asp Glu Tyr
 20 25 30
 Glu Ala Asp Asp Ile Ile Gly Thr Leu Ala Arg Gln Ala Asp Glu Ala
 35 40 45
 Gly Asp Tyr Met Thr Tyr Ile Val Ser Ser Asp Leu Asp Met Leu Gln
 50 55 60
 Ile Val Asp Glu Asn Thr Lys Met Tyr Arg Ile Leu Arg Gly Phe Ser
 65 70 75 80
 Asp Leu Glu Glu Met Asp Thr Pro Ala Ile Glu Glu Lys Tyr Gly Ile
 85 90 95
 Leu Lys Ser Gln Phe Leu Asp Leu Lys Ala Leu Lys Gly Asp Asn Ser
 100 105 110
 Asp Asn Ile Pro Gly Val Pro Gly Ile Gly Glu Lys Thr Ala Val Lys
 115 120 125
 Leu Leu Asn Glu Tyr Gly Ser Leu Glu Gly Ile Tyr Asn His Ile Lys
 130 135 140
 Glu Ile Ser Gly Ala Thr Gln Lys Lys Leu Ile Ala Gly Arg Glu Ser
 145 150 155 160
 Ala Glu Met Ser Leu Lys Leu
 165

<210> 2595
 <211> 928
 <212> DNA
 <213> Homo sapiens

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<400> 2595
agatcttcca gatgcaacaa tgatcaatta agacacgcgg cgacatgggtg gccctgcct
60
cacccecccg ggatacctgt aatacctgct tcccacttca tgggctacaa tctcatgctg
120
gtcacaaatt ctggggctca ctcatataac accaacaat gggatatttg tgaagaactt
180
cgcttgcggg agcttgaaga agtcaaggcc agagctgctc agatggaaaa gaccatgcgg
240
tgggtggctcg actgcactgc caactggaga gaaaaatgga gtaaagtctg agctgaaagg
300
aacagtgcgg gaaaggaagg aagacaactc agaataaaac tagagatggc gatgaaagaa
360
tcggatccac tgaacagaa acagagtctg ccaactcaga aggaggcatt agaagctaata
420
gttaccggag atctgaagct tctgggcttc gtagaagaat cctgtgaaca tacagaccaa
480
ttcaattga gttcacaat gcatgagctc atcagagagt atttggtaaa aagacaattt
540
tctacaaagg aggacacaaa taataaggaa caagggtgtg tttattgattc tctaaaatta
600
agtgaggaga tgaagcccaa tctagatggg gttgatttat tcaacaatgg tggttctgga
660
aacggtgaaa cgaaaactgg gctgagactg aaagcaataa atctgccttt ggaaaatgaa
720
gtaactgaaa ttacagcttt gcaggtgcat ttggatgaat tccaaaaaat cttatggaag
780
gaaagagaaa tgcgcacagc ttgggaaaaa gaaatagaga gactggagtc ggctttgtct
840
ctgtggaagt ggaagtatga agaactgaaa gaatcaaagc caaaaaatgt gaaagagttt
900
gacattcttc ttggtcaaca taatgatg
928

```

```

<210> 2596
<211> 309
<212> PRT
<213> Homo sapiens

```

```

<400> 2596
Arg Ser Ser Arg Cys Asn Asn Asp Gln Leu Arg His Ala Ala Thr Trp
1      5      10      15
Trp Pro Leu Pro His Pro Pro Gly Ile Pro Val Ile Pro Ala Ser His
20     25     30
Phe Met Gly Tyr Asn Leu Met Leu Val Thr Ile Ser Gly Ala His Ser
35     40     45
Tyr Asn Thr Asn Lys Trp Asp Ile Cys Glu Glu Leu Arg Leu Arg Glu
50     55     60
Leu Glu Glu Val Lys Ala Arg Ala Ala Gln Met Glu Lys Thr Met Arg
65     70     75     80
Trp Trp Ser Asp Cys Thr Ala Asn Trp Arg Glu Lys Trp Ser Lys Val
85     90     95
Arg Ala Glu Arg Asn Ser Ala Gly Lys Glu Gly Arg Gln Leu Arg Ile

```

100 105 110
 Lys Leu Glu Met Ala Met Lys Glu Ser Asp Pro Leu Lys Gln Lys Gln
 115 120 125
 Ser Leu Pro Leu Gln Lys Glu Ala Leu Glu Ala Asn Val Thr Gln Asp
 130 135 140
 Leu Lys Leu Pro Gly Phe Val Glu Glu Ser Cys Glu His Thr Asp Gln
 145 150 155 160
 Phe Gln Leu Ser Ser Gln Met His Glu Ser Ile Arg Glu Tyr Leu Val
 165 170 175
 Lys Arg Gln Phe Ser Thr Lys Glu Asp Thr Asn Asn Lys Glu Gln Gly
 180 185 190
 Val Val Ile Asp Ser Leu Lys Leu Ser Glu Glu Met Lys Pro Asn Leu
 195 200 205
 Asp Gly Val Asp Leu Phe Asn Asn Gly Gly Ser Gly Asn Gly Glu Thr
 210 215 220
 Lys Thr Gly Leu Arg Leu Lys Ala Ile Asn Leu Pro Leu Glu Asn Glu
 225 230 235 240
 Val Thr Glu Ile Ser Ala Leu Gln Val His Leu Asp Glu Phe Gln Lys
 245 250 255
 Ile Leu Trp Lys Glu Arg Glu Met Arg Thr Ala Leu Glu Lys Glu Ile
 260 265 270
 Glu Arg Leu Glu Ser Ala Leu Ser Leu Trp Lys Trp Lys Tyr Glu Glu
 275 280 285
 Leu Lys Glu Ser Lys Pro Lys Asn Val Lys Glu Phe Asp Ile Leu Leu
 290 295 300
 Gly Gln His Asn Asp
 305

<210> 2597

<211> 631

<212> DNA

<213> Homo sapiens

<400> 2597

ccattgggtgg gaattgcaaga gacacactct agacttacta gaggagcaag agcaggactt
 60
 ggctgcacct gcagctgagg gtttagcagga attaggagat aacagtagaa tagggctaga
 120
 ctgaaaaaggc ctttgatgcc aggttaggaa atttaccatt tatccacaaa atccaaatcc
 180
 tcctttaata atgagatgtc ttacaagtt ttgggcaag agtggtatgg ctgacctggg
 240
 gtctctgggaa ggaactgtgt ggggatgggt tgcaggactt acctagggtg ggaaggcacc
 300
 aagcagcatg gggctgtggc agctaccaga ggtaaaaggga catttcaggg aaagacttgg
 360
 caggacaaga ccttccttgg atggatggat gaataccaga aacagggacc caagagaaa
 420
 gccagatttc ataggagag aagatgggtc atgtatgagg catgttgagc ttgtactgat
 480
 ggtgagacgt ccagtcgaca gtactaccca ctggccagtg agaaatgttg gaccaggggt
 540
 caggagaaa ctggggccgg aaatgagcat ttggaaggcg ccaggggtgga agcgggtggt
 600

tcactccacg agtgctattt cacttacgcg t
631

<210> 2598
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2598
Met Gly Leu Trp Gln Leu Pro Glu Val Lys Gly His Phe Arg Glu Arg
1 5 10 15
Leu Gly Arg Thr Arg Pro Ser Leu Asp Gly Trp Met Asn Thr Arg Asn
20 25 30
Arg Asp Pro Arg Glu Arg Pro Ser Phe Ile Gly Arg Glu Asp Gly Ser
35 40 45
Cys Met Arg His Val Glu Leu Val Leu Met Val Arg Arg Pro Val Asp
50 55 60
Ser Thr Thr His Trp Pro Val Arg Asn Val Gly Pro Gly Phe Arg Arg
65 70 75 80
Lys Leu Gly Pro Glu Met Ser Ile Trp Lys Ala Pro Gly Trp Lys Arg
85 90 95
Val Val His Ser Thr Ser Ala Ile Ser Leu Thr Arg
100 105

<210> 2599
<211> 356
<212> DNA
<213> Homo sapiens

<400> 2599
nagatcttat acagggacgt gatgttgag aactactgga acctgtttc tctgggactg
60
tgtcattttg atatgaatat tatctccatg ttggaggaag ggaaagagcc ctggactgtg
120
aagagctgtg tgaataatgc aagaaaacca agaacgcggg aatgtgtcaa aggcgtggtc
180
acagatatcc ctctaaatg tacaatcaag gatttgctac caaaagagaa gagcagtaca
240
gaagcagtagt tccacacagt ggtgttgaa agacacgaaa gccctgacat tgaagacttt
300
tccttcaagg aaccccgaa aaatgtgcat gatattgagt gtcaatggag agatgn
356

<210> 2600
<211> 118
<212> PRT
<213> Homo sapiens

<400> 2600
Xaa Ile Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr Trp Asn Leu Val
1 5 10 15
Ser Leu Gly Leu Cys His Phe Asp Met Asn Ile Ile Ser Met Leu Glu
20 25 30
Glu Gly Lys Glu Pro Trp Thr Val Lys Ser Cys Val Lys Ile Ala Arg

```

      35              40              45
Lys  Pro  Arg  Thr  Arg  Glu  Cys  Val  Lys  Gly  Val  Val  Thr  Asp  Ile  Pro
   50              55              60
Pro  Lys  Cys  Thr  Ile  Lys  Asp  Leu  Leu  Pro  Lys  Glu  Lys  Ser  Ser  Thr
   65              70              75              80
Glu  Ala  Val  Phe  His  Thr  Val  Val  Leu  Glu  Arg  His  Glu  Ser  Pro  Asp
      85              90              95
Ile  Glu  Asp  Phe  Ser  Phe  Lys  Glu  Pro  Gln  Lys  Asn  Val  His  Asp  Phe
      100              105              110
Glu  Cys  Gln  Trp  Arg  Asp
      115

```

<210> 2601

<211> 329

<212> DNA

<213> Homo sapiens

<400> 2601

```

gcgccgatca  tgatctacgg  cgacgacgtc  acccacctgc  tcaccgaaga  aggcacgcgc
   60
tactttgata  aggcgcgttc  cctggaagag  cgccaagcga  tgatcgccgg  cggtggtggg
   120
gtcaccgcct  tcggttcgcg  ccacaacccc  aaggacactg  cgcgcatgcg  ccgcgaaggc
   180
ttgatcgctt  tgcccgaaga  cctcggtatc  cgccgcaccg  acgccaccgc  cgaactgttg
   240
gccgcccaaga  gcgtggccga  cctgggtggag  tggtcgggtg  gcttgtgcaa  cccgcccgcc
   300
aagttcagga  gctggtaaata  gcgcgcctt
   329

```

<210> 2602

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2602

```

Ala  Pro  Ile  Met  Ile  Tyr  Gly  Asp  Asp  Val  Thr  His  Leu  Leu  Thr  Glu
   1              5              10              15
Glu  Gly  Ile  Ala  Tyr  Leu  Tyr  Lys  Ala  Arg  Ser  Leu  Glu  Glu  Arg  Gln
      20              25              30
Ala  Met  Ile  Ala  Gly  Gly  Gly  Gly  Val  Thr  Ala  Phe  Gly  Leu  Arg  His
      35              40              45
Asn  Pro  Lys  Asp  Thr  Ala  Arg  Met  Arg  Arg  Glu  Gly  Leu  Ile  Ala  Leu
      50              55              60
Pro  Glu  Asp  Leu  Gly  Ile  Arg  Arg  Thr  Asp  Ala  Thr  Arg  Glu  Leu  Leu
      65              70              75              80
Ala  Ala  Lys  Ser  Val  Ala  Asp  Leu  Val  Glu  Trp  Ser  Gly  Gly  Leu  Cys
      85              90              95
Asn  Pro  Pro  Ala  Lys  Phe  Arg  Ser  Trp
      100              105

```

<210> 2603

<211> 423

<212> DNA

<213> Homo sapiens

<400> 2603

tcacgatcca ttgctctacc ctttacgggt gtgcacctac gccaggtcg gtggtcagga
 60
 gcatcggttc ggtgttacgg aggtcgagga cttccttcac gccgttgttc gcggagggga
 120
 ggttgttgga agtggtcagg tgggccacga tctgggcact gatcacctcg gtgaaatcga
 180
 agctctgggt accctgagcg gtcgccgaca cgacacgggc cacaccggag accagaccga
 240
 tctcggagat gatcgcgtaa ctttcattgt cgtagaggat cttgcacgca tcgatgatgc
 300
 gcttgatctc cttggcagtg aagatgattt ccacgggggt gttggccgac agatactgac
 360
 cggagctggt ggtcacctgg gtggaatcca ggtcatccgg aaccgggttc aggttggtccg
 420
 cgg
 423

<210> 2604

<211> 103

<212> PRT

<213> Homo sapiens

<400> 2604

Met	Glu	Ile	Ile	Phe	Thr	Ala	Lys	Glu	Ile	Lys	Arg	Ile	Ile	Asp	Ala
1				5				10				15			
Cys	Lys	Ile	Leu	Tyr	Asp	Asn	Glu	Gly	Tyr	Ala	Ile	Ile	Ser	Glu	Ile
		20					25				30				
Gly	Leu	Val	Ser	Gly	Val	Asp	Arg	Val	Val	Ser	Ala	Thr	Ala	Gln	Gly
		35				40					45				
Asn	Gln	Ser	Phe	Asp	Phe	Thr	Glu	Val	Ile	Ser	Ala	Gln	Ile	Val	Ala
	50				55					60					
His	Leu	Thr	Thr	Tyr	His	Asn	Leu	Pro	Ser	Ala	Asn	Asn	Gly	Val	Lys
	65			70					75				80		
Glu	Val	Leu	Asp	Leu	Gly	Thr	Thr	Glu	Pro	Met	Leu	Leu	Thr	Thr	Asp
			85					90					95		
Leu	Gly	Val	Gly	Ala	Gln	Pro									
			100												

<210> 2605

<211> 354

<212> DNA

<213> Homo sapiens

<400> 2605

ngggaggagg ggcacgtcaa aagcgactgt atccagaggg ttgtatttaa acatttttca
 60
 aaacatatgt ggcaaacagc ggggggaggg gatctcacca acgtttttct ccacttcttc
 120
 tttgcatgct gggacctgtt ccactttcaa aatgtgtcat ttggaagga aaggaggaa
 180

caactacttg aaaggaatac acgtcagtat gagccctttc tcctcagcag aagggtgtccc
 240
 caaagtacct cctctgaggc gagagaaagg agagaggagg agagacagct ttcatacaat
 300
 ggggcaccca ggactctagg gagagaggca cgttctcaca aaggcccttt gagc
 354

<210> 2606

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2606

Met	Ser	Lys	Ala	Thr	Val	Ser	Arg	Gly	Phe	Asp	Leu	Asn	Ile	Phe	Gln
1				5					10				15		
Asn	Ile	Cys	Gly	Lys	Gln	Arg	Gly	Glu	Gly	Ile	Ser	Pro	Thr	Phe	Phe
			20					25				30			
Ser	Thr	Ser	Ser	Leu	His	Ala	Gly	Thr	Cys	Ser	Thr	Phe	Lys	Met	Cys
		35				40					45				
His	Phe	Gly	Arg	Lys	Gly	Arg	Asn	Asn	Tyr	Leu	Lys	Gly	Ile	His	Val
	50					55				60					
Ser	Met	Ser	Pro	Phe	Ser	Ser	Ala	Glu	Gly	Cys	Pro	Lys	Val	Pro	Pro
65					70					75				80	
Leu	Arg	Arg	Glu	Lys	Gly	Glu	Arg	Arg	Arg	Asp	Ser	Phe	His	Gln	Met
			85					90						95	
Gly	His	Pro	Gly	Leu											
			100												

<210> 2607

<211> 297

<212> DNA

<213> Homo sapiens

<400> 2607

tgatacaagaa caatgatacg atatacctaac caacagagga agcaacggaa gttgtgtgtg
 60
 tttttatgct gttttttttt ttgagaacg gatcttgccc ctgccccccag gccggaatgg
 120
 atgacatgga cagaaccccg tcggaaaaaa gccggaatgt gcaaacccaa attcccacca
 180
 caccggggggc ctaacaattg gatccatccc cnaaaaaaanc cntnncaaaa aaagntaaaa
 240
 actttttttt ttttaaan nnanacccccaa aaaaacacaa aaaaaaaatt taaaaaa
 297

<210> 2608

<211> 95

<212> PRT

<213> Homo sapiens

<400> 2608

Met	Ile	Arg	Tyr	Pro	Asn	Gln	Gln	Arg	Lys	Gln	Arg	Lys	Leu	Leu	Leu
1				5				10					15		
Phe	Leu	Cys	Cys	Phe	Phe	Phe	Leu	Arg	Thr	Asp	Leu	Ala	Pro	Ala	Pro

```

                20                25                30
Arg Pro Glu Trp Met Thr Trp Thr Glu Pro Arg Arg Lys Lys Ala Gly
      35                40                45
Met Cys Lys Pro Lys Phe Pro Pro His Gly Gly Pro Asn Asn Trp Ile
      50                55                60
His Pro Xaa Lys Xaa Pro Xaa Gln Lys Lys Xaa Lys Thr Phe Phe Phe
      65                70                75                80
Leu Xaa Xaa Xaa Pro Gln Lys Asn Gln Lys Lys Lys Phe Lys Lys
      85                90                95

```

<210> 2609
 <211> 305
 <212> DNA
 <213> Homo sapiens

```

<400> 2609
ncgccatcgg catgatgtca ggcaaagatg atcctggcat ggcaaaggta tacggttttg
60
ttgacacgtc cctgacgac cctatccgct catctggaga cccatgcgtt ccttggaccc
120
caattgccta cgaaaaaatt ttttttttcc cccccaaaaa acaccccccc ctgcgcatctg
180
tgaaagtctt acctcggggg cgtcatctcg gctgtcatcg tcggcaaadc actcagctgg
240
ccgtaccctt cgtcatcgcc cgggccaccg acctcgacgg cncagcgtgc acggcaacga
300
ccacc
305

```

<210> 2610
 <211> 98
 <212> PRT
 <213> Homo sapiens

```

<400> 2610
Met Met Ser Gly Lys Asp Asp Pro Gly Met Ala Lys Val Tyr Gly Phe
1      5      10      15
Val Asp Thr Ser Leu Thr Ile Pro Ile Arg Ser Ser Gly Asp Pro Cys
20      25      30
Val Pro Trp Thr Pro Ile Ala Tyr Glu Lys Ile Phe Phe Phe Pro Pro
35      40      45
Lys Lys His Pro Pro Leu Ala Ser Val Lys Val Leu Pro Arg Gly Arg
50      55      60
His Leu Gly Cys His Arg Arg Gln Ile Thr Gln Leu Ala Val Pro Phe
65      70      75      80
Val Ile Ala Arg Ala Thr Asp Leu Asp Gly Xaa Ala Cys Thr Ala Thr
85      90      95
Thr Thr

```

<210> 2611
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 2611
 gccgccgcga tcgacggcga ctctctcgacc agctgggtgt ccagctcgct gcaaaccgct
 60
 gtgggggcaat ggcttcaggt ggacttcgac catccgggtga ccaacgcgac catcacctg
 120
 acgcccacg cgccacgtgt cggagctcag gtgcgccgcg tcgagggtggc aacagccaac
 180
 ggcaccagca caatctgctt cgaccagccc ggcaagccgc tgacggcggc gctgcccac
 240
 ggcgagacct catgggtccg gttcaccgcg accggcaccg acgacggctc ccccgcggtg
 300
 cagttcggca tcaccgactt ctccgtgacg cagtacgacg cg
 342

<210> 2612
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 2612
 Ala Ala Ala Ile Asp Gly Asp Ser Ser Thr Ser Trp Val Ser Ser Ser
 1 5 10 15
 Leu Gln Thr Ala Val Gly Gln Trp Leu Gln Val Asp Phe Asp His Pro
 20 25 30
 Val Thr Asn Ala Thr Ile Thr Leu Thr Pro Ser Ala Thr Ala Val Gly
 35 40 45
 Ala Gln Val Arg Arg Val Glu Val Ala Thr Ala Asn Gly Thr Ser Thr
 50 55 60
 Ile Arg Phe Asp Gln Pro Gly Lys Pro Leu Thr Ala Ala Leu Pro Tyr
 65 70 75 80
 Gly Glu Thr Ser Trp Val Arg Phe Thr Ala Thr Gly Thr Asp Asp Gly
 85 90 95
 Ser Pro Gly Val Gln Phe Gly Ile Thr Asp Phe Ser Val Thr Gln Tyr
 100 105 110
 Asp Ala

<210> 2613
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 2613
 acgctgtgg gttgtgcaca gggcatggct gctctggaca ggctcggggc ctgggcatca
 60
 ttctctctct ccaaaagggt agggctctgac ctaatggtac tttgtctgat gttttccaga
 120
 tatgccctca ctgggaaggg ccaagtgggc aggacagatc tgggggtggag cgagggtggg
 180
 ctgggaagca ctctctgttt tctgctgccc cagaacgaat gcaagttctg gcagcttctc
 240
 ctctctctgg gaggaggaaa ggagggctcg cctccaggtc tcaggctgag ggagtggtg
 300

ggagaccctc tagatggcca gcagaggctg gcctctgtga gaaggcttcc ttgcgtgact
 360
 ctggggcccc tcccaggctc tcctcgtggc aggcaggggac ttgggccagc atgg
 414

<210> 2614
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 2614
 Met Val Leu Cys Leu Met Phe Ser Arg Tyr Ala Pro Thr Gly Lys Gly
 1 5 10 15
 Gln Val Gly Arg Gln Ser Leu Gly Trp Ser Glu Val Gly Leu Gly Ser
 20 25 30
 Thr Pro Ala Phe Leu Leu Pro Gln Asn Glu Cys Lys Phe Trp Gln Leu
 35 40 45
 Leu Leu Leu Leu Gly Gly Gly Lys Glu Gly Ser Pro Pro Gly Leu Arg
 50 55 60
 Leu Arg Glu Trp Ala Gly Asp Pro Leu Asp Gly Gln Gln Arg Leu Ala
 65 70 75 80
 Ser Val Arg Arg Leu Pro Cys Val Thr Leu Gly Pro Leu Pro Gly Ser
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 Pro Arg Gly Arg Gln Gly Leu Gly Pro Ala Trp
 100 105

<210> 2615
 <211> 394
 <212> DNA
 <213> Homo sapiens

<400> 2615
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 120
 aacaatgcgg gcgtcacgca tgcggccgat ttctcgacg tgtgcgaaga cgatttcgac
 180
 cgggtcatcg gcattaacct gaaatcgatg ttctgtgtcg gccaggccgc gccgcgcgag
 240
 atggtcaacg gcaacagcgg ctgcatcatc aacatgtcca cggtgaatgc ggaactggcc
 300
 attccgaacc aggtgcgcta cgtggtgtcg aaaggcgcca tcaaccagct gaccaaggtc
 360
 atggccttga acctggcgcc gcacgggtcg cgct
 394

<210> 2616
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 2616
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      20           25           30
Phe  Gly  His  Ile  Asp  Ile  Leu  Val  Asn  Asn  Ala  Gly  Val  Thr  His  Ala
      35           40           45
Ala  Asp  Phe  Leu  Asp  Val  Cys  Glu  Asp  Asp  Phe  Asp  Arg  Val  Met  Arg
      50           55           60
Ile  Asn  Leu  Lys  Ser  Met  Phe  Leu  Cys  Gly  Gln  Ala  Ala  Ala  Arg  Glu
      65           70           75           80
Met  Val  Lys  Arg  Asn  Ser  Gly  Cys  Ile  Ile  Asn  Met  Ser  Ser  Val  Asn
      85           90           95
Ala  Glu  Leu  Ala  Ile  Pro  Asn  Gln  Val  Pro  Tyr  Val  Val  Ser  Lys  Gly
      100          105          110
Ala  Ile  Asn  Gln  Leu  Thr  Lys  Val  Met  Ala  Leu  Asn  Leu  Ala  Pro  His
      115          120          125
Gly  Ala  Arg
      130

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<210> 2617

<211> 513

<212> DNA

<213> Homo sapiens

<400> 2617

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120
gtcaccttgg gaaatcacia gattctcaat gacgtctccg tatcattcca agcgggagtt
180
atgcacgcca tacttgcccc caacgggttct gggaagacca ccctggtagc caggttatgc
240
ggagccctct cccccgagtc ggggagcgtc aaattcgtatg gaacggatct atccacgatg
300
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360
gacctcaccg tacgtcacct cgttggctac gggagatatg cccacacacc gtggtggcag
420
ataagggaca ccagcgccga cagccatgtg gaacaagcaa tggagctggc cgatgtcagc
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<210> 2618

<211> 171

<212> PRT

<213> Homo sapiens

<400> 2618

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Xaa  Arg  Leu  Ala  Ser  Cys  Ser  Gln  His  Trp  Gly  Phe  Pro  Ser  Phe  Phe
      1           5           10           15
Ser  Ser  Ser  Glu  Arg  His  Cys  Glu  Met  Gly  Asn  Ile  Met  Glu  Thr  Pro
      20           25           30
Ile  Leu  Ser  Gly  Ser  His  Leu  Asn  Val  Thr  Leu  Gly  Asn  His  Lys  Ile

```

```

      35              40              45
Leu Asn Asp Val Ser Val Ser Phe Gln Ala Gly Val Met His Ala Ile
  50              55              60
Leu Gly Pro Asn Gly Ser Gly Lys Thr Thr Leu Val Arg Thr Leu Cys
  65              70              75
Gly Ala Leu Ser Pro Glu Ser Gly Ser Val Lys Phe Asp Gly Thr Asp
      85              90              95
Leu Ser Thr Met Ser Ala Ser Cys Ile Ala Arg Arg Ile Ala Ile Val
      100              105              110
Trp Gln Ser Ala Thr Ala Pro Ser Asp Leu Thr Val Arg His Leu Val
      115              120              125
Gly Tyr Gly Arg Tyr Ala His Thr Pro Trp Trp Gln Ile Arg Asp Thr
      130              135              140
Ser Ala Asp Ser His Val Val Glu Gln Ala Met Glu Leu Ala Asp Val Thr
      145              150              155
Cys Phe Ala Asp Arg Arg Val Thr Thr Leu Ser
      160              165              170

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<210> 2619

<211> 348

<212> DNA

<213> Homo sapiens

<400> 2619

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cggtatgaacc cgtacaactc ggtgtggagc ggtgtgaccg acggtgacgg gcccgaggaa
120
cagcacgtca ttttccttga taacggtcgt accgacgtgc ttgccgacac cttggtgcg
180
gaagtgttgc ggtgcatccg gtgtgcttcg tgtatcaata tctgcccggt ttacgagcgg
240
gcggggcggt acccttacgg ctccggtgtac cccggggcga ttggtgcggt gctcaatccg
300
cagctgcggg gcgtggagca tcccgctgat cgtggtctgc catacgcg
348

```

<210> 2620

<211> 116

<212> PRT

<213> Homo sapiens

<400> 2620

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Xaa Asn Phe Asp Leu Glu Val Phe Leu Lys Leu Leu Pro Arg Ser
  1              5              10              15
Ala Xaa Gly Glu Arg Met Asn Pro Tyr Asn Ser Val Trp Ser Gly Val
      20              25              30
Thr Asp Gly Asp Gly Pro Gln Glu Gln His Val Ile Phe Leu Asp Asn
      35              40              45
Gly Arg Thr Asp Val Leu Ala Asp Thr Leu Gly Arg Glu Val Leu Arg
      50              55              60
Cys Ile Arg Cys Ala Ser Cys Ile Asn Ile Cys Pro Val Tyr Glu Arg
      65              70              75              80
Ala Gly Gly His Pro Tyr Gly Ser Val Tyr Pro Gly Pro Ile Gly Ala

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	85		90		95										
Val	Leu	Asn	Pro	Gln	Leu	Arg	Gly	Val	Glu	His	Pro	Val	Asp	Arg	Gly
		100					105						110		
Leu	Pro	Tyr	Ala												
		115													

<210> 2621
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 2621
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 120
 ttttcttttc ctgttttgat ttgtctgaag ggagaggtgg tgggtggttag gatcagagct
 180
 ctctggcat ccgtggggag gatttgctgg tgggtggcttc gggctcatgc ccagacacac
 240
 tcactgcccc gtctgtccaa ggctcccttc tcccctttgc tgggtgggagg agctcgtgtg
 300
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 360
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 420
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 480
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 600
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 660
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 720
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 780
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 900
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 960
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 1020
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 1080
 ttctgtacaa ccgtgtgtta tcacagtgc gttttaagtg taacngttga acttaggcac
 1140
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 1200
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 1260

taacttgnta gctatctttg aaatcaactgn actttgcaat ggtgctaagc tgatagattt
 1320
 aaatacacag acgggagagt ggcgcccgtg tcgatgtctt cagccagtgg tgaccctgct
 1380
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 1440
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<210> 2622

<211> 83

<212> PRT

<213> Homo sapiens

<400> 2622

Met	Phe	Ser	Phe	Pro	Val	Leu	Ile	Leu	Leu	Lys	Gly	Glu	Val	Val	Val
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Val	Arg	Ile	Arg	Ala	Leu	Leu	Ala	Ser	Val	Gly	Arg	Ile	Cys	Trp	Trp
			20				25					30			
Trp	Leu	Arg	Ala	His	Ala	Gln	Thr	His	Ser	Leu	Pro	Arg	Leu	Ser	Lys
	35					40					45				
Ala	Ser	Pro	Ser	Pro	Leu	Leu	Val	Gly	Gly	Ala	Arg	Val	Leu	Leu	Gly
	50					55				60					
Arg	Leu	Leu	Glu	Gly	Arg	Phe	Ser	Glu	Leu	Gln	Gly	Gln	Gly	Glu	Gln
65					70					75				80	
Leu	Lys	Gly													

<210> 2623

<211> 3524

<212> DNA

<213> Homo sapiens

<400> 2623

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 120
 agtgggttcc tgagtggcgg cggagggtacc ggcagtagcg gtggttagcg ctccggcgccg
 180
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 240
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 300
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 360
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 420
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 480
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 540
 caccaccacc actatggggg gctgttcgct ggagctgaag agaggtctcc aggcctagga
 600

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660
cagcagcaac cagcccagca ccaccgtgac gtattactca gcagcagtag caggactgat
720
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960
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1020
cagagacatg agaaaattca tagtagagag aagccatttg gatgtgatca gtgcagcatg
1080
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1140
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1260
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1320
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1560
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 3360
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 3420
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<210> 2624

<211> 895

<212> PRT

<213> Homo sapiens

<400> 2624

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		35					40						45						
Gly	Met	Val	Met	Phe	Asn	His	Arg	Leu	Pro	Pro	Pro	Val	Thr	Ser	Phe	Thr			
	50					55						60							
Arg	Pro	Ala	Gly	Ser	Ala	Ala	Pro	Pro	Pro	Gln	Cys	Val	Leu	Ser	Ser				
65					70					75					80				
Ser	Thr	Ser	Ala	Ala	Pro	Ala	Ala	Glu	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Pro			
				85					90						95				
Asp	Met	Thr	Phe	Lys	Lys	Glu	Pro	Ala	Ala	Ser	Ala	Ala	Ala	Phe	Pro				
			100					105					110						
Ser	Gln	Arg	Thr	Ser	Trp	Gly	Phe	Leu	Gln	Ser	Leu	Val	Ser	Ile	Lys				
		115				120						125							
Gln	Glu	Lys	Pro	Ala	Asp	Pro	Glu	Glu	Gln	Gln	Ser	His	His	His	His				
		130				135					140								
His	His	His	His	Tyr	Gly	Gly	Leu	Phe	Ala	Gly	Ala	Glu	Glu	Arg	Ser				
145					150					155					160				
Pro	Gly	Leu	Gly	Gly	Gly	Glu	Gly	Ser	His	Gly	Val	Ile	Gln	Asp					
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Leu	Ser	Ile	Leu	His	Gln	His	Val	Gln	Gln	Pro	Ala	Gln	His	His					
			180					185					190						
Arg	Asp	Val	Leu	Leu	Ser	Ser	Ser	Arg	Thr	Asp	Asp	His	His	Gly					
		195					200				205								
Thr	Glu	Glu	Pro	Lys	Gln	Asp	Thr	Asn	Val	Lys	Lys	Ala	Lys	Arg	Pro				
						215				220									
Lys	Pro	Glu	Ser	Gln	Gly	Ile	Lys	Ala	Lys	Arg	Lys	Pro	Ser	Ala	Ser				
225					230					235					240				
Ser	Lys	Pro	Ser	Leu	Val	Gly	Asp	Gly	Glu	Gly	Ala	Ile	Leu	Ser	Pro				
				245				250					255						
Ser	Gln	Lys	Pro	His	Ile	Cys	Asp	His	Cys	Ser	Ala	Ala	Phe	Arg	Ser				
				260				265					270						
Ser	Tyr	His	Leu	Arg	Arg	His	Val	Leu	Ile	His	Thr	Gly	Glu	Arg	Pro				
		275					280					285							
Phe	Gln	Cys	Ser	Gln	Cys	Ser	Met	Gly	Phe	Ile	Gln	Lys	Tyr	Leu	Leu				
						295				300									
Gln	Arg	His	Glu	Lys	Ile	His	Ser	Arg	Glu	Lys	Pro	Phe	Gly	Cys	Asp				
305					310					315					320				
Gln	Cys	Ser	Met	Lys	Phe	Ile	Gln	Lys	Tyr	His	Met	Glu	Arg	His	Lys				
				325				330					335						
Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asp	Thr	Cys	Gln	Gln				
				340				345					350						
Tyr	Phe	Ser	Arg	Thr	Asp	Arg	Leu	Leu	Lys	His	Arg	Arg	Thr	Cys	Gly				
		355					360					365							
Glu	Val	Ile	Val	Lys	Gly	Ala	Thr	Ser											

450						455						460					
Leu	Ile	Phe	Lys	Lys	Gly	Ser	Arg	Lys	Asn	Thr	Asp	Lys	Asn	Tyr	Leu		
470	475					480					485						
Asn	Phe	Val	Ser	Pro	Leu	Pro	Asp	Ile	Val	Gly	Gln	Lys	Ser	Leu	Ser		
485					490					495							
Gly	Lys	Pro	Ser	Gly	Ser	Leu	Gly	Ile	Val	Ser	Asn	Asn	Ser	Val	Glu		
500					505					510							
Thr	Ile	Gly	Leu	Gln	Ser	Thr	Ser	Gly	Lys	Gln	Gly	Gln	Ile	Ser			
515					520					525							
Ser	Asn	Tyr	Asp	Asp	Ala	Met	Gln	Phe	Ser	Lys	Lys	Arg	Arg	Tyr	Leu		
530	535					540					545						
Pro	Thr	Ala	Ser	Ser	Asn	Ser	Ala	Phe	Ser	Ile	Asn	Val	Gly	His	Met		
545	550					555					560						
Val	Ser	Gln	Gln	Ser	Val	Ile	Gln	Ser	Ala	Gly	Val	Ser	Val	Leu	Asp		
565					570					575							
Asn	Glu	Ala	Pro	Leu	Ser	Leu	Ile	Asp	Ser	Ser	Ala	Leu	Asn	Ala	Glu		
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Ile	Lys	Ser	Cys	His	Asp	Lys	Ser	Gly	Ile	Pro	Asp	Glu	Val	Leu	Gln		
595					600					605							
Ser	Ile	Leu	Asp	Gln	Tyr	Ser	Asn	Lys	Ser	Glu	Ser	Gln	Lys	Glu	Asp		
610	615					620					625						
Pro	Phe	Asn	Ile	Ala	Glu	Pro	Arg	Val	Asp	Leu	His	Thr	Ser	Gly	Glu		
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His	Ser	Glu	Leu	Val	Gln	Glu	Glu	Asn	Leu	Ser	Pro	Gly	Thr	Gln	Thr		
645					650					655							
Pro	Ser	Asn	Asp	Lys	Ala	Ser	Met	Leu	Gln	Glu	Tyr	Ser	Lys	Tyr	Leu		
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675					680					685							
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690					695					700							
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705	710					715					720						
Gly	Gln	Ser	Val	Thr	Ser	Val	Leu	Pro	Ser	Ser	Leu	Pro	Lys	Pro	Thr		
725					730					735							
Phe	Gly	Met	Leu	Phe	Gly	Ser	Gln	Pro	Gly	Leu	Tyr	Leu	Ser	Ala	Leu		
740					745					750							
Asp	Ala	Thr	His	Gln	Gln	Leu	Thr	Pro	Ser	Gln	Glu	Leu	Asp	Asp	Leu		
755					760					765							
Ile	Asp	Ser	Gln	Lys	Asn	Leu	Glu	Thr	Ser	Ser	Ala	Phe	Gln	Ser	Ser		
770	775					780					785						
Ser	Gln	Lys	Leu	Thr	Ser	Gln	Lys	Glu	Gln	Lys	Asn	Leu	Glu	Ser	Ser		
785	790					795					800						
Thr	Gly	Phe	Gln	Ile	Pro	Ser	Gln	Glu	Leu	Ala	Ser	Gln	Ile	Asp	Pro		
805					810					815							
Gln	Lys	Asp	Ile	Glu	Pro	Arg	Thr	Thr	Tyr	Gln	Ile	Glu	Asn	Phe	Ala		
820					825					830							
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Glu Gln Leu Gly Ser Tyr Asp Pro Leu Pro Asn Ser His Gly Glu Lys
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<213> Homo sapiens

<400> 2629

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<211> 550

<212> PRT

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<400> 2632

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Cys	Tyr	Tyr	Lys	Asn	His	Phe	Ser	Arg	Ser	Ser	Val	Ala	Ala	Gly	Gly
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Gln Trp Gln Ser Pro Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala
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<212> DNA

<213> Homo sapiens

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<210> 2635

<211> 1062

<212> DNA

<213> Homo sapiens

<400> 2635

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<210> 2636

<211> 63
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 Gly Asp Gly Ser Ile Arg Arg Tyr Phe Cys Gly Glu Ala Ala Ala
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35 40 45
Leu Gln Glu Ala Gly Thr Phe Arg His Thr Leu Trp Lys Arg Val Gln
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Gly Ala Val Thr Pro Leu Leu Ala Ser Met Ile Ser Phe Ile Asp Arg
65 70 75 80
Asp Gly Asn Leu Glu Leu Leu Thr Arg Pro Asp Thr Pro Pro Trp Ala
85 90 95
Arg Asp Leu Trp Met Phe Ile Phe Ser Asp Thr Met Leu Leu Asn Ile
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Pro Leu Val Met Asn Asn Glu Arg His Lys Gly Glu Met Ala Tyr Ile
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Ala Gln Tyr Ile Thr Asp Ala Glu Gly Leu Pro Lys Lys Phe Val Asp
165 170 175
Ile Phe Gln Gln Thr Pro Leu Gly Arg Phe Leu Ala Gln Leu His Gly
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Glu Pro Gln Gln Glu Leu Leu Gln Cys Tyr Leu Lys Asp Phe Ile Leu
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Ala Leu Trp Ser Cys Thr Arg Lys Leu Lys Ala Ala Ser Glu Ala Pro
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<211> 645

<212> PRT

<213> Homo sapiens

<400> 2640

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Thr	Asp	Leu	Gly	Leu	Gln	Ile	Asp	His	Ile	Gly	His	Asp	Met	Leu	Pro
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Glu	Thr	Glu	Glu	Lys	Ser	Ile	Leu	Leu	Glu	Ser	Asp	Asn	Glu	Asp	Glu
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Lys	Leu	Ser	Arg	Gly	Gln	His	Cys	Ile	Glu	Ile	Ser	Ser	Leu	Pro	Gly
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Asp	Leu	Val	Ile	Val	Glu	Lys	Asp	His	Ser	Ala	Thr	Thr	Glu	Pro	Leu
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Asp	Val	Thr	Lys	Thr	Gln	Thr	Phe	Ser	Val	Val	Pro	Asn	Gln	Asp	Lys
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Val Ser Ser Glu Asn Glu His Gly Ala Pro Thr Arg Lys Asp Met Val Arg
325                330                335
Ser Ser Phe Val Thr Arg His Ser Arg Ile Pro Val Leu Ala Gln Glu
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Ile Asp Ser Thr Leu Glu Ser Ser Ser Pro Val Ser Ala Lys Glu Lys
355                360                365
Leu Leu Gln Lys Lys Ala Tyr Gln Pro Asp Leu Val Lys Leu Leu Val
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Glu Lys Arg Gln Phe Lys Ser Phe Leu Gly Asp Leu Ser Ser Ala Ser
385                390                395                400
Asp Lys Leu Leu Glu Glu Lys Leu Ala Thr Val Pro Ala Pro Phe Cys
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Glu Glu Glu Val Leu Thr Pro Phe Ser Arg Leu Thr Val Asp Ser His
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Ser Arg Lys Ser Lys Ile Pro Arg Pro Val Ser Trp Val Asn Thr Asp
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Gln Val Asn Ser Ser Thr Ser Ser Gln Phe Phe Pro Arg Pro Pro Pro
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Gly Lys Pro Pro Thr Arg Pro Gly Val Glu Ala Arg Leu Arg Arg Tyr
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Lys Val Leu Gly Ser Ser Asn Ser Asp Ser Asp Leu Phe Ser Arg Leu
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Cys Lys Ser Pro Gly Ser Pro His Asn Pro Lys Thr Pro Pro Lys Ser
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545                550                555                560
Leu Pro Arg Thr Ser Ser Ser Ser Pro Ser Arg Ala Gly Arg Pro His
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His Asp Gln Arg Ser Ser Ser Pro His Leu Gly Arg Ser Lys Ser Pro
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Pro Ser His Ser Gly Ser Ser Ser Ser Arg Arg Ser Cys Gln Gln Glu
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His Cys Lys Pro Ser Lys Asn Gly Leu Lys Gly Ser Gly Ser Leu His
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<211> 744

<212> DNA

<213> Homo sapiens

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 <212> PRT
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<400> 2642
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 Val Thr Val Arg Ile His Gly Ser Met Leu Arg Ala His Arg Cys Val
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 Leu Ala Ala Gly Ser Pro Phe Phe Gln Asp Lys Leu Leu Gly Tyr
 50 55 60
 Ser Asp Ile Glu Ile Pro Ser Val Val Ser Val Gln Ser Val Gln Lys
 65 70 75 80
 Leu Ile Asp Phe Met Tyr Ser Gly Val Leu Arg Val Ser Gln Ser Glu
 85 90 95
 Ala Leu Gln Ile Leu Thr Ala Ala Ser Ile Leu Gln Ile Lys Thr Val
 100 105 110
 Ile Asp Glu Cys Thr Arg Ile Val Ser Gln Asn Val Gly Asp Val Phe
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 130 135 140
 Ser Gly Thr Ser Gly Gln Ser Ser Asp Thr Glu Ser Gly Tyr Leu Gln

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ttaatttaag ttttctttt ttacagtttt tctccagcac tttactcttc ttaagtgcct
3420
ggcctttttt tgtcccttta tctctctctg tttttttctt aagcccaga aagccaaaaa
3480
gaacatgtaa actcttcacc tcaactagct acaaccttcc actcctaacc tcccaagctt
3540
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3660
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3780
atgtcatcat tcaccattta tccaggatgg ccgctacca ggcaatttgc taggctcggg
3840
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3900
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3960
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4020
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4380
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4440
tggaaaactg gcagccattg ggtgtggggg cagtctgtaa atcagtcacc tgtgtgtctg
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<210> 2644

<211> 871

<212> PRT

<213> Homo sapiens

<400> 2644

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 20          25          30
Asp Thr Ala Leu Asp Asn Cys Gln Asp Leu Phe Leu Leu Asp Pro Pro
 35          40          45
Arg Pro Asn Leu Thr Ser His Pro Asp Gly Ser Glu Asp Leu Glu Pro
 50          55          60
Leu Ala Gly Gly Ser Pro Glu Ala Thr Ser Pro Asp Val Thr Glu Thr
 65          70          75          80
Lys Asn Ser Pro Leu Met Glu Asp Phe Glu Glu Gly Phe Ser Gln
 85          90          95
Glu Ile Ile Glu Met Leu Ser Lys Asp Gly Phe Trp Asn Ser Asn Phe
100          105          110
Gly Glu Ala Cys Ile Glu Asp Thr Trp Leu Asp Ser Leu Leu Gly Asp
115          120          125
Pro Glu Ser Leu Leu Arg Ser Asp Ile Ala Thr Asn Gly Glu Ser Pro
130          135          140
Thr Glu Cys Lys Ser His Glu Leu Lys Arg Gly Leu Ser Pro Val Ser
145          150          155          160
Thr Val Ser Thr Gly Glu Asp Ser Met Val His Asn Val Ser Glu Lys
165          170          175
Thr Leu Thr Pro Ala Lys Ser Lys Glu Tyr Arg Gly Glu Phe Phe Ser
180          185          190
Tyr Ser Asp His Ser Gln Gln Asp Ser Val Gln Glu Gly Glu Lys Pro
195          200          205
Tyr Gln Cys Ser Glu Cys Gly Lys Ser Phe Ser Gly Ser Tyr Arg Leu
210          215          220
Thr Gln His Trp Ile Thr His Thr Arg Glu Lys Pro Thr Val His Gln
225          230          235          240
Glu Cys Glu Gln Gly Phe Asp Arg Asn Ala Ser Leu Ser Val Tyr Pro
245          250          255
Lys Thr His Thr Gly Tyr Lys Phe Tyr Val Cys Asn Glu Tyr Gly Thr
260          265          270
Thr Phe Ser Gln Ser Thr Tyr Leu Trp His Gln Lys Thr His Thr Gly
275          280          285
Glu Lys Pro Cys Lys Ser Gln Asp Ser Asp His Pro Pro Ser His Asp
290          295          300
Thr Gln Pro Gly Glu His Gln Lys Thr His Thr Asp Ser Lys Ser Tyr
305          310          315          320
Asn Cys Asn Glu Cys Gly Lys Ala Phe Thr Arg Ile Phe His Leu Thr
325          330          335
Arg His Gln Lys Ile His Thr Arg Lys Arg Tyr Glu Cys Ser Lys Cys
340          345          350
Gln Ala Thr Phe Asn Leu Arg Lys His Leu Ile Gln His Gln Lys Thr

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      355              360              365
His Ala Ala Lys Thr Thr Ser Glu Cys Gln Glu Cys Gly Lys Ile Phe
  370              375              380
Arg His Ser Ser Leu Leu Ile Glu His Gln Ala Leu His Ala Gly Glu
  385              390              395
Glu Pro Tyr Lys Cys Asn Glu Arg Gly Lys Ser Phe Arg His Asn Ser
      405              410              415
Thr Leu Lys Ile His Gln Arg Val His Ser Gly Glu Lys Pro Tyr Lys
      420              425              430
Cys Ser Glu Cys Gly Lys Ala Phe His Arg His Thr His Leu Asn Glu
      435              440              445
His Arg Arg Ile His Thr Gly Tyr Arg Pro His Lys Cys Gln Glu Cys
      450              455              460
Val Arg Ser Phe Ser Arg Pro Ser His Leu Met Arg His Gln Ala Ile
      465              470              475
His Thr Ala Glu Lys Pro Tyr Ser Cys Ala Glu Cys Lys Glu Thr Phe
      485              490              495
Ser Asp Asn Asn Arg Leu Val Gln His Gln Lys Met His Thr Val Lys
      500              505              510
Thr Pro Tyr Glu Cys Gln Glu Cys Gly Glu Arg Phe Ile Cys Gly Ser
      515              520              525
Thr Leu Lys Cys His Glu Ser Val His Ala Arg Glu Lys Gln Gly Phe
      530              535              540
Phe Val Ser Gly Lys Ile Leu Asp Gln Asn Pro Glu Gln Lys Glu Lys
      545              550              555
Cys Phe Lys Cys Asn Lys Cys Glu Lys Thr Phe Ser Cys Ser Lys Tyr
      565              570              575
Leu Thr Gln Tyr Glu Arg Ile His Thr Arg Gly Val Lys Pro Phe Glu
      580              585              590
Cys Asp Gln Cys Gly Lys Ala Phe Gly Gln Ser Thr Arg Leu Ile His
      595              600              605
His Gln Arg Ile His Ser Arg Val Arg Leu Tyr Lys Trp Gly Glu Gln
      610              615              620
Gly Lys Ala Ile Ser Ser Ala Ser Leu Ile Lys Leu Gln Ser Phe His
      625              630              635
Thr Lys Glu His Pro Phe Lys Cys Asn Glu Cys Gly Lys Thr Phe Ser
      645              650              655
His Ser Ala His Leu Ser Lys His Gln Leu Ile His Ala Gly Glu Asn
      660              665              670
Pro Phe Lys Cys Ser Lys Cys Asp Arg Val Phe Thr Gln Arg Asn Tyr
      675              680              685
Leu Val Gln His Glu Arg Thr His Ala Arg Lys Lys Pro Leu Val Cys
      690              695              700
Asn Glu Cys Gly Lys Thr Phe Arg Gln Ser Ser Cys Leu Ser Lys His
      705              710              715
Gln Arg Ile His Ser Gly Glu Lys Pro Tyr Val Cys Asp Tyr Cys Gly
      725              730              735
Lys Ala Phe Gly Leu Ser Ala Glu Leu Val Arg His Gln Arg Ile His
      740              745              750
Thr Gly Glu Lys Pro Tyr Val Cys Gln Glu Cys Gly Lys Ala Phe Thr
      755              760              765
Gln Ser Ser Cys Leu Ser Ile His Arg Arg Val His Thr Gly Glu Lys
      770              775              780
Pro Tyr Arg Cys Gly Glu Cys Gly Lys Ala Phe Ala Gln Lys Ala Asn

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```

785              790              795              800
Leu Thr Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ser Cys
              805              810              815
Asn Val Cys Gly Lys Ala Phe Val Leu Ser Ala His Leu Asn Gln His
              820              825              830
Leu Arg Val His Thr Gln Glu Thr Leu Tyr Gln Cys Gln Arg Cys Gln
              835              840              845
Lys Ala Phe Arg Cys His Ser Ser Leu Ser Arg His Gln Arg Val His
              850              855              860
Asn Lys Gln Gln Tyr Cys Leu
865              870

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<210> 2645

<211> 1018

<212> DNA

<213> Homo sapiens

<400> 2645

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agcctcttcc ttacccatgc ttgggggtgt taacagctga ggctattcgt cggtgacctg
120
tgggactcga gctattcctg cagctcagca gacctcctgg ccgtggcaga cttctgcgtt
180
atgaccggcg tgctgggcta cgtggacccc ctggatccca gctttgtggc tgccgtcatc
240
accatcacct tcaatccgct ctactggaat gtggttgac gatgggaaca caagaccgcg
300
aagctgagca gggccttcgg atccccctac ctggcctgct actctctaag catcaccatc
360
ctgctcctga acttctcgcg ctgcactgc ttcacgcagg ccatgctgag ccagcccagg
420
atggagagcc tggacacccc cgcggcctac agcctggggc tcgcgctcct gggactgggc
480
gtcgtgctcg tgctctccag cttcttttga ctgggggttc ctggaacttt cctagtgat
540
tacttcggga tcctcaagga ggcgagagt accgtgttcc ccttcaacat cctggacaac
600
cccatgtact ggggaagcac agccaactac ctgggctggg ccatcatgca cgccagcccc
660
acgggcctcg tcctgacggt gctggtggcc ctacactaca taatggctct cctatacgaa
720
gagcccttca ccgctgagat ctaccggcag aaagcctccg ggtcccacaa gaggagctga
780
ttgagctgca acagctttgc tgaaggcctg gccagcctcc tggcctgccc caagtggcag
840
gccctgcgca gggcgagaat ggtgcctgct gctcagggct cggccccggc gtgggctggc
900
ccagtgcctt ggaacctgct gccttgggga ccctggacgt gccgacatat ggccattgag
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1018

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<210> 2646

<211> 199

<212> PRT

<213> Homo sapiens

<400> 2646

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Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp Pro Ser Phe Val
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Ala Ala Val Ile Thr Phe Asn Pro Leu Tyr Trp Asn Val Val
      20           25           30
Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser
      35           40           45
Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Ile Thr Ile Leu Leu Leu Asn
      50           55           60
Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu Ser Gln Pro Arg
      65           70           75           80
Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu Gly Leu Ala Leu
      85           90           95
Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe Phe Ala Leu Gly
      100          105          110
Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ala
      115          120          125
Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp
      130          135          140
Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
      145          150          155          160
Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Met Ala
      165          170          175
Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Gln Lys Ala
      180          185          190
Ser Gly Ser His Lys Arg Ser
      195

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<210> 2647

<211> 1368

<212> DNA

<213> Homo sapiens

<400> 2647

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catgtgacac caaaaggaat taatggtata gactttaaa ggaagcgat aacttttaaa
120
gcaactactg ctggaatcct tgcaacactt tctcattgta ttgaactaat ggttaaacgt
180
gaggacagct ggcagaagag actggataag gaaactgaga agaaaagaag aacagaggaa
240
gcataataaa atgcaatgac agaacttaag aaaaaatccc actttggagg accagattat
300
gaagaaggcc ctaacagtct gattaatgaa gaagagttct ttgatgctgt tgaagctgct
360
cttgacagac aagataaaat agaagaacag tcacagagtg aaagggtgag attacattgg
420
cctacatcct tgccctctgg agatgccttt tcttctgtgg ggacacatag atttgtccaa
480

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aaggttgaag agatggtgca gaaccacatg acttactcat tacaggatgt aggcggagat
 540
 gccaatggc agttggtgtt agaagaagga gaaatgaagg tatacagaag agaagtagaa
 600
 gaaaatggga ttgttctgga tcctttaaaa gctacccatg cagttaaagg cgtcacagga
 660
 catgaagtct gcaattatct ctggaatggt gacgttcgca atgactggga aacaactata
 720
 gaaaactttc atgtggtgga aacattagct gataatgcaa tcatcattta tcaaacacac
 780
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 840
 ccagccttga ctgaaaaatga ccctgaaact tggatagttt gtaatttttc tgtggatcat
 900
 gacagtgtct ctctaaacaa ccgatgtgtc cgtgccaaaa taaatgtgtc tatgattgtt
 960
 caaaccttgg taagcccacc agaggggaaac caggaaatta gcaggggacaa cattctatgc
 1020
 aagattacat atgtagctaa tgtgaacctt ggaggatggg caccagcctc agtgtaaagg
 1080
 gcagtggtgca agcgagagta tcctaaatct ctaaaacgtt ttactttctta cgtccaagaa
 1140
 aaaactgcag gaaagcctat ttgttcttag tattaacagt gactgaagca aggcgtgtgtg
 1200
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 1260
 atctatagcc ttgtctgtgg cccaagacct tggccttggt tacaaaaatg acaaaatatt
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 1368

<210> 2648

<211> 389

<212> PRT

<213> Homo sapiens

<400> 2648

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 Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe
 20 25 30
 Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala
 35 40 45
 Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp
 50 55 60
 Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu
 65 70 75 80
 Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe Gly
 85 90 95
 Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu
 100 105 110
 Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu
 115 120 125
 Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu

130 135 140
 Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln
 145 150 155 160
 Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp
 165 170 175
 Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met
 180 185 190
 Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro
 195 200 205
 Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys
 210 215 220
 Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile
 225 230 235 240
 Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile
 245 250 255
 Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu
 260 265 270
 Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro
 275 280 285
 Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro
 290 295 300
 Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys
 305 310 315 320
 Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp
 325 330 335
 Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly
 340 345 350
 Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro
 355 360 365
 Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly
 370 375 380
 Lys Pro Ile Leu Phe
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<210> 2649

<211> 1299

<212> DNA

<213> Homo sapiens

<400> 2649

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 120
 gatgcctggg gcccatggag tgaatgctca cgcacctgcg ggggtggggc ctcctactct
 180
 ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata cagaacatgc
 240
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 300
 aatgatgtca agcaccatgg ccagttttat gaatggcttc ctgtgtctaa tgaccctgac
 360
 aacccatggt cactcaagt ccaagccaaa ggaacaaccc tggttgttga actagcacct
 420

aagggtcttag atgggtacgog ttgctataca gaatctttgg atatgtgcat cagtgggtta
 480
 tgccaaattg ttggctgcga tcaccagctg ggaagcacog tcaaggaaga taactgtggg
 540
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 600
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 660
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 720
 ggtgaaaaa gtctcagctc cacaggaact ttcctgtgg acaattctag tgtggacttc
 780
 cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc agatttcatt
 840
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 900
 atcatccacc gatggaggga gacggatttc tttccttgct cagcaacctg tggaggaggt
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 1020
 tactgtcact attaccaga gaacatcaaa cccaaacca agcttcagga gtgcaacttg
 1080
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 1200
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 1260
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 1299

<210> 2650

<211> 428

<212> PRT

<213> Homo sapiens

<400> 2650

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Leu	Leu	Phe	Leu	Ala	Phe	Leu	Leu	Leu	Ser	Arg	Thr	Ala	Arg	Ser	
			20					25				30			
Glu	Glu	Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu
		35				40					45				
Cys	Ser	Arg	Thr	Cys	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys	
	50				55					60					
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr	Cys
65				70					75					80	
Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala	Gln	Gln
				85				90					95		
Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe	Tyr	Glu	Trp
	100						105					110			
Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser	Leu	Lys	Cys	Gln
	115					120					125				
Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala	Pro	Lys	Val	Leu	Asp

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      130              135              140
Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu
145              150              155
Cys Gln Ile Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu
      165              170              175
Asp Asn Cys Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val
      180              185              190
Arg Gly Gln Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr
      195              200              205
Val Val Ala Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys
      210              215              220
Gly Pro Asp His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys
225              230              235
Gly Glu Asn Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser
      245              250              255
Ser Val Asp Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala
      260              265              270
Gly Pro Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser
      275              280              285
Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg
      290              295              300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly
305              310              315
Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val
      325              330              335
Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys
      340              345              350
Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly
      355              360              365
Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp
      370              375              380
Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile
385              390              395
Gln Ser Pro Gly Ser Phe Leu Cys Gly Gly His Pro Gly Ala Cys
      405              410              415
His Phe Ser Gly Arg Val Glu Met His Val His Pro
      420              425

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<210> 2651

<211> 628

<212> DNA

<213> Homo sapiens

<400> 2651

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120
gagacaggcc gagtgaccaa gacaaaggac gggcatgagg ttccggacctg caaagtggcg
180
gacaaaacag gcagcatcaa tatctctgtc tgggacgatg ttggcaatct gatccagcct
240
ggggacatta tccggctcac caaagggtac gcttcagttt tcaaagggtg tctgacacta
300

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tatactggcc gtgggggtga tctgcagaag attggagaat tctgcattga ttattctgag
 360
 gttcctaact tcagttagacc aaaccagag tacagcacc agcaggcacc caacaaggcg
 420
 gtgcagaacg acagcaaccc ttcagcttcc cagcctacca ctggaccctc tgctgcctct
 480
 ccagcctctg agaaccagaa tgggaatgga atgagtgtccc caccagggtt cggggtggg
 540
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 600
 ccaaccacac acctgcaggc ccgcttgg
 628

<210> 2652

<211> 209

<212> PRT

<213> Homo sapiens

<400> 2652

Tyr	Thr	Val	Leu	Pro	Ala	Gly	Leu	Val	Gly	Cys	Arg	Gly	Ser	Gly	Ser
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Met	Thr	Thr	Glu	Thr	Phe	Val	Lys	Gly	Ile	Lys	Pro	Gly	Leu	Lys	Asn
			20					25					30		
Leu	Asn	Leu	Ile	Phe	Ile	Val	Leu	Glu	Thr	Gly	Arg	Val	Thr	Lys	Thr
		35					40					45			
Lys	Asp	Gly	His	Glu	Val	Arg	Thr	Cys	Lys	Val	Ala	Asp	Lys	Thr	Gly
		50				55				60					
Ser	Ile	Asn	Ile	Ser	Val	Trp	Asp	Asp	Val	Gly	Asn	Leu	Ile	Gln	Pro
65					70					75				80	
Gly	Asp	Ile	Ile	Arg	Leu	Thr	Lys	Gly	Tyr	Ala	Ser	Val	Phe	Lys	Gly
				85					90					95	
Cys	Leu	Thr	Leu	Tyr	Thr	Gly	Arg	Gly	Gly	Asp	Leu	Gln	Lys	Ile	Gly
		100						105					110		
Glu	Phe	Cys	Met	Asp	Tyr	Ser	Glu	Val	Pro	Asn	Phe	Ser	Glu	Pro	Asn
		115					120					125			
Pro	Glu	Tyr	Ser	Thr	Gln	Gln	Ala	Pro	Asn	Lys	Ala	Val	Gln	Asn	Asp
		130				135				140					
Ser	Asn	Pro	Ser	Ala	Ser	Gln	Pro	Thr	Thr	Gly	Pro	Ser	Ala	Ala	Ser
145				150						155				160	
Pro	Ala	Ser	Glu	Asn	Gln	Asn	Gly	Asn	Gly	Met	Ser	Ala	Pro	Pro	Gly
				165					170					175	
Phe	Arg	Val	Val	Ala	His	Ile	Pro	Leu	Ile	Leu	Pro	Pro	Thr	His	Pro
		180						185					190		
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<210> 2653

<211> 2103

<212> DNA

<213> Homo sapiens

<400> 2653

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240
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540
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1620

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 1740
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 1920
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 1980
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 2103

<210> 2654

<211> 70

<212> PRT

<213> Homo sapiens

<400> 2654

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Ser	Glu	Val	Asn	Phe	Leu	Arg	Phe	Glu	Cys	Cys	Phe	Lys	Thr	Leu	Ser
			20					25					30		
Ser	Asp	Ser	Lys	Cys	Leu	Leu	Leu	Gly	Ala	Val	Ala	His	Ala	Cys	
			35				40				45				
Asn	Pro	Ser	Thr	Leu	Gly	Gly	Arg	Gly	Gly	Arg	Ile	Thr	Arg	Ser	Gly
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Asp	Arg	Asp	Tyr	Pro	Gly										
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<210> 2655

<211> 1752

<212> DNA

<213> Homo sapiens

<400> 2655

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 120
 tcttctttgt gattgctttt ttagagacgg atttttttcc agatttgtgc ttcttgtgtt
 180
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 240
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 300
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420
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480
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600
tctctaaatt ttcttttaca caatcagttt ttttaatttc acaaggcctg cgaattctaa
660
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1140
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1380
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<210> 2656

<211> 493

<212> PRT

<213> Homo sapiens

<400> 2656

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20      25      30
Arg Cys Leu Leu Met Pro Gln Cys Asn Ala Phe Leu Ser Lys Ile Met
35      40      45
Thr Ser Leu Leu Ser Pro Pro His Arg Arg Pro Thr Leu His Arg Arg
50      55      60
Pro Thr Leu Pro Tyr Arg Thr Trp Glu Ala Ala Leu Arg Gln Lys Val
65      70      75      80
Gln Gln Trp Tyr Thr Ala Val Gly Gln Thr Glu Asn Pro Asp Asn Cys
85      90      95
Ala Glu Lys Leu Gly Leu Cys Pro Gln Phe Phe Lys Val Leu Gly Glu
100      105      110
Val Asn Pro Leu Glu Glu Lys Pro Phe His Glu Leu Pro Phe Tyr Gln
115      120      125
Lys Val Trp Leu Leu Lys Gly Leu Cys Asp Phe Val Tyr Asp Thr His
130      135      140
Lys Glu Val Gln Asp Ala Val Leu Gly Gln Pro Ile His Glu Cys Arg
145      150      155      160
Ala Val Ile Leu Arg Tyr Asp Tyr Leu Glu Thr Ala Tyr Val His Phe
165      170      175
Pro Gln Phe Cys Gly Ala Asp Val Arg Ile Tyr Lys Gln Arg Pro Phe
180      185      190
Gln Ala Pro Glu Phe Pro Ile Pro Pro Ile Lys Ile Gln Arg Val Pro
195      200      205
Arg Ile Lys Leu Glu Lys Leu Lys Cys Asp Tyr Val Ser Thr Ser Asn
210      215      220
Gly Glu His Arg Cys Ser Arg Asp Ser Leu Pro Ser Ser Phe Lys Lys
225      230      235      240
Glu Gln Glu Asn Asn Phe Asp Pro Ala Cys Cys Pro Ala Lys Met Ile
245      250      255
Leu Asp Asn His Asp Ile Ser Val Glu Met Gly Val Lys Ser Asn Tyr
260      265      270
Glu Ile Arg Ile Arg Arg Pro Cys Glu Ile Lys Lys Thr Asp Cys Cys
275      280      285
Lys Glu Asn Leu Glu Lys Pro Arg Ser Pro Gly Glu Val Thr Gly Phe
290      295      300
Gly Glu Pro Leu Ser Pro Gly Glu Ile Arg Phe Ile Glu Asn Gln Glu
305      310      315      320
Lys Tyr Gly Glu Ala Ser Arg Ile Lys Ile Glu Pro Ser Pro Leu Lys
325      330      335
Glu Asn Thr Leu Lys Ser Cys Gln Ile His Val Asn Gly Ser His Ser
340      345      350
Asp His Pro Glu Ile Asn Cys His Lys Val Val Arg Asp Ile Leu Leu
355      360      365
Glu Gln Ser Leu Gln Ser His Lys Lys Leu Lys Leu Thr Lys Met Arg
370      375      380
Ala Lys Lys Lys Lys Lys Lys Lys Lys Leu Lys Asp Val Leu Asn
385      390      395      400
Glu Asn Leu Gln Arg Lys Arg Glu Gly Leu His Ser Leu Ala Phe Lys
405      410      415
Ser Tyr Lys Pro Glu Ile Gln Asn Lys Leu Leu Ile Ile Lys Lys Lys

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	420		425		430										
Ala	Lys	His	Lys	Lys	His	Lys	Ser	Gly	Lys	Lys	Ser	Val	Ser	Lys	Lys
	435		440		445										
Ala	Ile	Thr	Lys	Lys	Arg	Lys	Thr	Val	Ile	Lys	Ser	Pro	Thr	Val	Pro
	450		455		460										
Glu	Phe	Gln	Leu	Ile	Cys	Thr	Asn	Leu	Asp	Glu	Leu	Arg	Glu	Leu	Ile
	465		470		475									480	
Thr	Lys	Ile	Glu	Asn	Glu	Leu	Lys	Asp	Leu	Glu	Lys	Lys			
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<210> 2657

<211> 972

<212> DNA

<213> Homo sapiens

<400> 2657

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780
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<210> 2658

<211> 76

<212> PRT

<213> Homo sapiens

<400> 2658

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          20          25          30
Leu Trp Gly Gly Ala Gly Glu Arg Gly Cys Gln Ala Trp Ala Ala Ala
          35          40          45
Asp Leu Gly Gly His Gly Gly Ser Met Pro Ser Thr Ala Gly Trp Gly
          50          55          60
Ala Leu Pro Gly Pro Ala Pro Ser Met His Gly Trp
65           70           75
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<210> 2659

<211> 691

<212> DNA

<213> Homo sapiens

<400> 2659

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120
aatggagaga acaccttcaa acgcattgga ccccgctgg agaagcctgt ggagaagggtg
180
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691
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<210> 2660

<211> 120

<212> PRT

<213> Homo sapiens

<400> 2660

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Thr Phe Lys Arg Ile Gly Pro Pro Leu Glu Lys Pro Val Glu Lys Val
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<210> 2662

<211> 415

<212> PRT

<213> Homo sapiens

<400> 2662

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			20					25					30		
Lys	Leu	Glu	Met	Lys	Ala	Leu	Arg	Glu	Leu	Asp	Arg	Phe	Ser	Val	Leu
		35				40						45			
Asn	Ser	Gln	His	Met	Phe	Glu	Val	Leu	Ala	Ala	Met	Asn	His	Arg	Ser
		50			55						60				
Leu	Ile	Leu	Leu	Asp	Glu	Cys	Ser	Lys	Val	Val	Leu	Asp	Asn	Ile	His
				70						75				80	
Gly	Cys	Pro	Leu	Arg	Ile	Met	Ile	Asn	Ile	Leu	Gln	Ser	Cys	Lys	Asp
				85					90					95	
Leu	Gln	Tyr	His	Asn	Leu	Asp	Leu	Phe	Lys	Gly	Leu	Ala	Asp	Tyr	Val
				100				105						110	
Ala	Ala	Thr	Phe	Asp	Ile	Trp	Lys	Phe	Arg	Lys	Val	Leu	Phe	Ile	Leu
				115				120						125	
Ile	Leu	Phe	Glu	Asn	Leu	Gly	Phe	Arg	Pro	Val	Gly	Leu	Met	Asp	Leu
				130		135					140				
Phe	Met	Lys	Arg	Ile	Val	Glu	Asp	Pro	Glu	Ser	Leu	Asn	Met	Lys	Asn
				145		150				155				160	
Ile	Leu	Ser	Ile	Leu	His	Thr	Tyr	Ser	Ser	Leu	Asn	His	Val	Tyr	Lys
				165				170						175	
Cys	Gln	Asn	Lys	Glu	Gln	Phe	Val	Glu	Val	Met	Ala	Ser	Ala	Leu	Thr
			180					185						190	
Gly	Tyr	Leu	His	Thr	Ile	Ser	Ser	Glu	Asn	Leu	Leu	Asp	Ala	Val	Tyr
			195			200						205			
Ser	Phe	Cys	Leu	Met	Asn	Tyr	Phe	Pro	Leu	Ala	Pro	Phe	Asn	Gln	Leu
			210			215						220			
Leu	Gln	Lys	Asp	Ile	Ile	Ser	Glu	Leu	Leu	Thr	Ser	Asp	Asp	Met	Lys
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Asn	Ala	Tyr	Lys	Leu	His	Thr	Leu	Asp	Thr	Cys	Leu	Lys	Leu	Asp	Asp
			245					250						255	
Thr	Val	Tyr	Leu	Arg	Asp	Ile	Ala	Leu	Ser	Leu	Pro	Gln	Leu	Pro	Arg

260										265										270																											
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275										280										285																											
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305										310										315																											
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Gln	Arg	Val	Ala	Val	Leu	Cys	Val	Ser	Arg	Ser	Ala	Tyr	Cys	Leu	Gly	Gln	Arg	Val	Ala	Val	Leu	Cys	Val	Ser	Arg	Ser	Ala	Tyr	Cys	Leu	Gly	Gln	Arg	Val	Ala	Val	Leu	Cys	Val	Ser	Arg	Ser	Ala	Tyr	Cys	Leu	Gly
335										340										345																											
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Leu	Glu	Met	Glu	Asp	Ala	Val	Thr	Phe	Leu	Lys	Thr	Lys	Ile	Tyr	Ser	Leu	Glu	Met	Glu	Asp	Ala	Val	Thr	Phe	Leu	Lys	Thr	Lys	Ile	Tyr	Ser	Leu	Glu	Met	Glu	Asp	Ala	Val	Thr	Phe	Leu	Lys	Thr	Lys	Ile	Tyr	Ser
385										390										395																											
Val	Glu	Ala	Leu	Pro	Val	Ala	Ala	Val	Asn	Val	Gln	Ser	Thr	Gln		Val	Glu	Ala	Leu	Pro	Val	Ala	Ala	Val	Asn	Val	Gln	Ser	Thr	Gln		Val	Glu	Ala	Leu	Pro	Val	Ala	Ala	Val	Asn	Val	Gln	Ser	Thr	Gln	
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<210> 2663

<211> 1024

<212> DNA

<213> Homo sapiens

<400> 2663

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420	tcgcactagt	tcacgcaggc	catgctgagc	cagcccgagg	tggagagcct	ggacaccccc
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 <213> Homo sapiens

<400> 2664
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 Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu Ser Gln Pro Arg
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 Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ala
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 Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
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 Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Met Ala
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 Ser Gly Ser His Lys Arg Ser
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 <213> Homo sapiens

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<210> 2666

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2666

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			20					25					30		
Asp	Gln	Ala	Val	Glu	Ala	Phe	Lys	Thr	Ala	Lys	Glu	Pro	Ile	Val	Val
			35					40				45			
Gln	Val	Leu	Arg	Arg	Thr	Pro	Arg	Thr	Lys	Met	Phe	Thr	Pro	Pro	Ser
			50			55					60				
Glu	Ser	Gln	Leu	Val	Asp	Thr	Gly	Thr	Gln	Thr	Asp	Ile	Thr	Phe	Glu
65				70					75					80	
His	Ile	Met	Ala	Leu	Thr	Lys	Met	Ser	Ser	Pro	Ser	Pro	Pro	Val	Leu
			85					90						95	
Asp	Pro	Tyr	Leu	Leu	Pro	Glu	Glu	His	Pro	Ser	Ala	His	Glu	Tyr	Tyr
			100					105					110		
Asp	Pro	Asn	Asp	Tyr	Ile	Gly	Asp	Ile	His	Gln	Glu	Met	Asp	Arg	Glu
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Glu	Leu	Glu	Leu	Glu	Glu	Val	Asp	Leu	Tyr	Arg	Met	Asn	Ser	Gln	Asp
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<210> 2667

<211> 289

<212> DNA

<213> Homo sapiens

<400> 2667

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<210> 2668

<211> 96

<212> PRT

<213> Homo sapiens

<400> 2668

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			20					25					30		
Asn	Pro	Phe	Ser	Val	Cys	Pro	Arg	Trp	Val	Pro	Gly	Leu	Cys	Trp	Arg
			35					40					45		
Thr	Arg	His	Phe	Lys	Glu	Ser	Ile	Lys	Phe	Ile	His	Glu	Cys	Arg	Leu
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Arg	Gly	Glu	Ser	Cys	Leu	Val	His	Cys	Leu	Ala	Gly	Val	Ser	Arg	Ser
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<210> 2669

<211> 4285

<212> DNA

<213> Homo sapiens

<400> 2669

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<211> 979

<212> PRT

<213> Homo sapiens

<400> 2670

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Cys	Met	Glu	Lys	Leu	Arg	Asp	Ala	Arg	Leu	Cys	Pro	His	Cys	Ser	Lys
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Leu	Cys	Cys	Phe	Ser	Cys	Ile	Arg	Arg	Trp	Leu	Thr	Glu	Gln	Arg	Ala
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Gln	Cys	Pro	His	Cys	Arg	Ala	Pro	Leu	Gln	Leu	Arg	Glu	Leu	Val	Asn
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Cys	Arg	Trp	Ala	Glu	Glu	Val	Thr	Gln	Gln	Leu	Asp	Thr	Leu	Gln	Leu
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Cys	Ser	Leu	Thr	Lys	His	Glu	Glu	Asn	Glu	Lys	Asp	Lys	Cys	Glu	Asn
			100					105						110	
His	His	Glu	Lys	Leu	Ser	Val	Phe	Cys	Trp	Thr	Cys	Lys	Lys	Cys	Ile
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			165					170						175	
Gln	Glu	Val	Glu	Arg	Asn	Val	Glu	Ala	Val	Arg	Asn	Ala	Lys	Asp	Glu
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Arg	Val	Arg	Glu	Ile	Arg	Asn	Ala	Val	Glu	Met	Met	Ile	Ala	Arg	Leu
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Ser	Phe	Val	Thr	Thr	Pro	Val	Pro	Pro	Asp	Phe	Thr	Ser	Glu	Leu	Val		
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Pro	Ser	Tyr	Asp	Ser	Ala	Thr	Phe	Val	Leu	Glu	Asn	Phe	Ser	Thr	Leu		
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Arg	Gln	Arg	Ala	Asp	Pro	Val	Tyr	Ser	Pro	Pro	Gln	Val	Ser	Gly			
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Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly Met
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755                760                765
Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val Ala
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Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala Leu
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Asp Ser Asp Ala Val Val Val Ala Val Phe Ser Gly Leu Pro Ala Val
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Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala Asn Ala Lys Gly Gly
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<210> 2671

<211> 814

<212> DNA

<213> Homo sapiens

<400> 2671

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<211> 223

<212> PRT

<213> Homo sapiens

<400> 2672

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 Phe Ala Ile Leu Ser Pro Ser Pro Tyr Leu Arg Pro Arg Gly Arg Ala
 50 55 60
 His His Pro Pro Ser Arg Leu Gly Gly Gly Arg Ala Pro Ser Trp Pro
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<210> 2674

<211> 690

<212> PRT

<213> Homo sapiens

<400> 2674

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Phe	Ile	Arg	Asp	Ser	Leu	Glu	Lys	Ser	Asp	Gln	Leu	Thr	Lys	Asn	Met
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Val	Ser	Ile	Leu	Ser	Ser	Phe	Glu	Ser	Arg	Leu	Met	Lys	Leu	Glu	Asn
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Ser	Ile	Ile	Pro	Val	His	Lys	Gln	Thr	Glu	Asn	Leu	Gln	Arg	Leu	Gln
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Glu	Asn	Val	Glu	Lys	Thr	Leu	Ser	Cys	Leu	Asp	His	Val	Ile	Ser	Tyr
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Tyr	His	Val	Ala	Ser	Asp	Thr	Glu	Lys	Ile	Arg	Glu	Gly	Pro	Thr	
		100					105					110			
Gly	Arg	Leu	Glu	Glu	Tyr	Leu	Gly	Ser	Met	Ala	Lys	Ile	Gln	Lys	Ala
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Val	Glu	Tyr	Phe	Gln	Asp	Asn	Ser	Pro	Asp	Ser	Pro	Glu	Leu	Asn	Lys
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		275						280					285																
Ser	Gln	His	Gly	Leu	Asp	Gly	Lys	Lys	Gly		Gly	Ser	Asn	Leu	Ile	Pro													
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Pro	Gly	Leu	Ile	Thr	Ser	Met	Glu	Thr	Ile	Gly	Ala	Lys	Ala	Leu	Glu														
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<210> 2675

<211> 711

<212> DNA

<213> Homo sapiens

<400> 2675

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<210> 2676

<211> 180

<212> PRT

<213> Homo sapiens

<400> 2676

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35 40 45
Ile Phe Glu Lys Ser Val Val Phe Ile Val Leu Leu Leu Leu Gln Trp
50 55 60
Lys Lys Val Ala Leu Leu Asn Pro Ile Glu Asn Pro Asp Leu Lys Leu
65 70 75 80
Ala Ile Val Met Leu Ile Val Pro Phe Phe Val Asn Ala Leu Met Phe
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Trp Val Val Asp Asn Phe Leu Met Arg Lys Gly Lys Thr Lys Ala Lys
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Leu Glu Glu Arg Gly Ala Asn Gln Asp Ser Arg Asn Gly Ser Lys Val

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<210> 2677

<211> 735

<212> DNA

<213> Homo sapiens

<400> 2677

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<210> 2678

<211> 170

<212> PRT

<213> Homo sapiens

<400> 2678

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Pro	Ala	Cys	Val	Ser	Thr	Pro	Pro	Ser	Ala	Gly	Ala	Phe	Ser	Leu	Leu
			20					25					30		
Arg	Glu	Asn	Phe	Ser	His	Ala	Pro	Ser	Pro	Asp	Met	Ser	Ala	Ala	Ser

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Arg Val Arg Met Gln Gly Val Gly Pro Ser Trp Gly Gln Ser Pro Gly
      100              105              110
Pro Gly Met Arg Glu Leu Ser His Leu Leu Pro Cys Val Ser Ala Pro
      115              120              125
Ser Gln Leu Leu Ser Cys Ser Leu Gly Gly Leu Val Arg Asn Leu Gly
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<210> 2679

<211> 560

<212> DNA

<213> Homo sapiens

<400> 2679

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<210> 2680

<211> 133

<212> PRT

<213> Homo sapiens

<400> 2680

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Arg Glu Thr Cys His Gln Asp Thr Ala Arg Ser Ser Lys Gly Ala Ser

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Val Gly Arg His Arg Gly Cys Thr Arg Thr Gln Pro Asp Leu Gly Gln
   65                70                75                80
Phe Ala Pro Thr Leu Leu His Ser Arg Gly Pro Gly Ser Thr Cys Gln
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Cys Gly Ser Gln Asn Ala Gln Ala Lys Tyr Arg Asp Gln Leu Thr Ile
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<210> 2681

<211> 585

<212> DNA

<213> Homo sapiens

<400> 2681

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gattctctag tagccctaata tctacccatc tgggtactaa ttcaaaacttt ctctcttcac
60
atctgtttgt ggacttctcc aatataacta gtatgctctg gctcattctg ctctctctct
120
tctggaatag tttatttcat gaccatgtgc agaggggggtg atgggggcaag cctcacaagc
180
ccgggaggtc tgtggctgag gtgtacctg gctttgttgc ctggaactgc tctgactctg
240
ctcttcgctc ttctctgggc tgtgtcacta cagctctgac tcctttccac ctggagttt
300
agcttccctg ccaggaaagc taaggagtag gagttgttct tggaacaaa tgccgagcga
360
tgtgtctgtg tcattctggc tcgagaaggt tcttcattct ctgaactcga gagacgtgca
420
ggacaacggt ccagatttgt ttctagtact aatggttcat ctcttttttt ctgttcatcc
480
attttctctt tcctgtttc tgtatcctct ggtaacagct tgtggatttg atcttcagag
540
ggtttttcct ctgttaactt ttctctctct agctttctca agctt
585

```

<210> 2682

<211> 116

<212> PRT

<213> Homo sapiens

<400> 2682

```

Met Asp Glu Gln Lys Lys Arg Asp Glu Pro Leu Val Leu Lys Thr Asn
  1                5                10                15
Leu Glu Arg Cys Pro Ala Arg Leu Ser Asp Ser Glu Asn Glu Glu Pro
  20                25                30
Ser Arg Gly Gln Met Thr Gln Thr His Arg Ser Ala Phe Val Ser Lys

```

```

          35              40              45
Asn Asn Ser Tyr Ser Leu Ala Phe Leu Ala Gly Lys Leu Asn Ser Lys
  50              55              60
Val Glu Arg Ser Gln Ser Cys Ser Asp Thr Ala Gln Glu Arg Ala Lys
  65              70              75              80
Ser Arg Val Arg Ala Val Pro Gly Asn Lys Ala Lys Val His Leu Ser
          85              90              95
His Arg Pro Pro Gly Leu Val Arg Leu Ala Pro Ser Pro Pro Leu His
          100              105              110
Met Val Met Lys
          115

```

<210> 2683

<211> 498

<212> DNA

<213> Homo sapiens

<400> 2683

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naccggttac actgactcca aaactctcct tgggtggccta ggtgaaacct catggccaac
  60
atcacctgga tggccaacca cactggaagg ttggatttca tcctcatggg actcttcaga
  120
cgatccaaac atccagctct acttagtggt gtcactcttg tggtttctct gatggcggtg
  180
tctgaaaatg ctgtcctgat ccttctgata cactgtgaca cctacctcca caccctcatg
  240
tactttttca tcagtcaatt gtctctcatg gacatggcgt acatttctgt cactgtgcc
  300
aagatgctcc tggaccaggt catgggtgtg aataagatct cagcccctga gtgtgggatg
  360
cagatgttcc tctatctgac actagcaggt tcggaatttt tccttctagc caccatggcc
  420
tatgaccgct acgtggccat ctgccatcct ctccgttacc ctgtcctcat gaaccatagg
  480
gtctgtcttt tcctggca
  498

```

<210> 2684

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2684

```

Met Ala Asn Ile Thr Trp Met Ala Asn His Thr Gly Arg Leu Asp Phe
  1              5              10              15
Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser
          20              25              30
Val Val Ile Phe Val Val Phe Leu Met Ala Leu Ser Glu Asn Ala Val
          35              40              45
Leu Ile Leu Leu Ile His Cys Asp Thr Tyr Leu His Thr Pro Met Tyr
          50              55              60
Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val
  65              70              75              80
Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Ile

```

```

      85              90              95
Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala
      100              105              110
Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val
      115              120              125
Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val
      130              135              140
Cys Leu Phe Leu Ala
145

```

<210> 2685

<211> 391

<212> DNA

<213> Homo sapiens

<400> 2685

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ngcgggctgc acacgctgcc acctgggctg cctcgaaatg tccatgtgct gaaggtcaag
60
cgcaatgagc tggctgccct ggcaagaggg gcgctggcgg gcattggctca gcttcgggaa
120
ctctacctca caggcaaccg actgcgaagc cgggccctgg gccccctgct ctgggtggac
180
ctcgcccatc tgcagttgct ggacatcgcc gggaatcagc tcacagagat cccggagggg
240
ctccccccat cgctggagta tctgtacctg cagaataaca agattagcgc tgttctctgc
300
agcgctcttg actctactcc caacctcaag gggatctttc tcaggttcaa caagctggct
360
gtgggctccg tagtagaaag cgccttcagg a
391

```

<210> 2686

<211> 130

<212> PRT

<213> Homo sapiens

<400> 2686

```

Xaa Arg Leu His Thr Leu Pro Pro Gly Leu Pro Arg Asn Val His Val
1      5      10      15
Leu Lys Val Lys Arg Asn Glu Leu Ala Ala Leu Ala Arg Gly Ala Leu
20      25      30
Ala Gly Met Ala Gln Leu Arg Glu Leu Tyr Leu Thr Gly Asn Arg Leu
35      40      45
Arg Ser Arg Ala Leu Gly Pro Arg Ala Trp Val Asp Leu Ala His Leu
50      55      60
Gln Leu Leu Asp Ile Ala Gly Asn Gln Leu Thr Glu Ile Pro Glu Gly
65      70      75      80
Leu Pro Pro Ser Leu Glu Tyr Leu Tyr Leu Gln Asn Asn Lys Ile Ser
85      90      95
Ala Val Pro Ala Ser Ala Phe Asp Ser Thr Pro Asn Leu Lys Gly Ile
100      105      110
Phe Leu Arg Phe Asn Lys Leu Ala Val Gly Ser Val Val Glu Ser Ala
115      120      125
Phe Arg

```

130

<210> 2687

<211> 399

<212> DNA

<213> Homo sapiens

<400> 2687

nagtgcaaga aatgtttaat acaagagatt gaacctacc aaaatgggag gtttagcctc
 60
 caggaatggg agtgcaataa atctctaata caagagattg agcctcacca acctccagga
 120
 tgggaaatga caggttaagac agggactaca aaagaccaag cagacaataa aattccccct
 180
 gacagtcctc taggccttat gttaagatac cggaagata atgaaaggac caaacacaa
 240
 aaaagacagc aaatgataaa atattgctgg ttattttgga ctaaggaacc catcctgaaa
 300
 cctttggctt ttggccaca gttagggttg agcggggact ggatatgcca actcctaata
 360
 cagtatgtaa aggataaaag tccagtttct caagaggag
 399

<210> 2688

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2688

Met	Thr	Gly	Lys	Thr	Gly	Thr	Thr	Lys	Asp	Gln	Ala	Asp	Asn	Lys	Ile
1			5						10				15		
Pro	Pro	Asp	Ser	Pro	Leu	Gly	Leu	Met	Leu	Arg	Tyr	Arg	Lys	Asp	Asn
			20					25					30		
Glu	Arg	Thr	Lys	His	Lys	Lys	Arg	Gln	Gln	Met	Ile	Lys	Tyr	Cys	Trp
			35				40					45			
Phe	Ile	Trp	Thr	Lys	Glu	Pro	Ile	Leu	Lys	Pro	Leu	Val	Phe	Trp	Pro
			50			55				60					
Gln	Leu	Gly	Leu	Ser	Gly	Asp	Trp	Ile	Cys	Gln	Leu	Leu	Ile	Gln	Tyr
65					70				75					80	
Val	Lys	Asp	Lys	Ser	Pro	Val	Ser	Gln	Glu	Glu					
			85						90						

<210> 2689

<211> 560

<212> DNA

<213> Homo sapiens

<400> 2689

gcaccattc aagttgggtt agttggcttc tgtttggtgt ttgctacacc cctgtgtgtg
 60
 gccctgtttc ctcagaaaag atacaaaaat gtgggtctca ccaagttgcc caggtgtgtc
 120
 tcaaacctct ggcctcaaga aatcctcctg gttcagctc acaaagctcc gagattacag
 180

ttgcatgtct gtgacaagct tggaggccga gttgcaagct aagatccaag agagccatcc
 240
 tgaattgcga cgcgtgtact tcaataaggg attgtaaagc agggaggaaa cctctgcagc
 300
 tcattctgcc actgcaaagc tgggtgtagcc atgctggtga gaaaaatcct gttcaacctg
 360
 ggttggtata tcgtctttga aaaacaatga ctataaaagc tacaggaaa gttatttcagg
 420
 acgtttattg aaggcattgg tggagctctc tgtatgtgtt ttgctctgca gggaaactcaa
 480
 agttggcatt cccgtcacgg atgagaatgg gaaccgcttg ggggagtcgg cgaacgctgc
 540
 gaaacaagcc atcacgccag
 560

<210> 2690

<211> 73

<212> PRT

<213> Homo sapiens

<400> 2690

Ala	Pro	Ile	Gln	Val	Gly	Leu	Val	Gly	Phe	Cys	Leu	Val	Phe	Ala	Thr
1			5					10					15		
Pro	Leu	Cys	Cys	Ala	Leu	Phe	Pro	Gln	Lys	Arg	Tyr	Lys	Asn	Val	Gly
			20					25					30		
Leu	Thr	Lys	Leu	Pro	Arg	Leu	Val	Ser	Asn	Ser	Trp	Pro	Gln	Glu	Ile
			35					40					45		
Leu	Leu	Val	Gln	Pro	His	Lys	Ala	Pro	Arg	Leu	Gln	Leu	His	Val	Cys
	50					55					60				
Asp	Lys	Leu	Gly	Gly	Arg	Val	Ala	Ser							
65						70									

<210> 2691

<211> 532

<212> DNA

<213> Homo sapiens

<400> 2691

gatctcatct gtacacactt catggatggc atgaatgagc tggcgattgc ttacatcctg
 60
 caggggggtgc tgaaggccct cgactacatc caccacatgg gatattgtaca caggagtgtc
 120
 aaagccagcc acatcctgat ctctgtggat gggaaggctc acctgtctcg tttgcgcagc
 180
 aacctcagca tgataagcca tgggcagcgg cagcgagtgg tccacgattt tcccaagtc
 240
 agtgtaagg ttctgccgtg gctcagcccc gaggtctctc agcagaatct ccagggttat
 300
 gatgccaaat ctgacatcta cagtgtggga atcacagcct gtgaactggc caacggccat
 360
 gtccccctta aggatatgcc tgcccaccag atgctgctag agaaactgaa cggcacagtg
 420
 ccctgcctgt tggataccag caccatcccc gctgaggagc tgaccatgag cccttcgcgc
 480

tcagtggcca actctggcct gaggtagcagc ctgaccacca gcacaccccc gg
532

<210> 2692

<211> 177

<212> PRT

<213> Homo sapiens

<400> 2692

Asp	Leu	Ile	Cys	Thr	His	Phe	Met	Asp	Gly	Met	Asn	Glu	Leu	Ala	Ile
1			5					10				15			
Ala	Tyr	Ile	Leu	Gln	Gly	Val	Leu	Lys	Ala	Leu	Asp	Tyr	Ile	His	His
		20					25			30					
Met	Gly	Tyr	Val	His	Arg	Ser	Val	Lys	Ala	Ser	His	Ile	Leu	Ile	Ser
	35				40			45							
Val	Asp	Gly	Lys	Val	Tyr	Leu	Ser	Gly	Leu	Arg	Ser	Asn	Leu	Ser	Met
	50			55				60							
Ile	Ser	His	Gly	Gln	Arg	Gln	Arg	Val	Val	His	Asp	Phe	Pro	Lys	Tyr
65			70					75				80			
Ser	Val	Lys	Val	Leu	Pro	Trp	Leu	Ser	Pro	Glu	Val	Leu	Gln	Gln	Asn
	85						90					95			
Leu	Gln	Gly	Tyr	Asp	Ala	Lys	Ser	Asp	Ile	Tyr	Ser	Val	Gly	Ile	Thr
	100						105					110			
Ala	Cys	Glu	Leu	Ala	Asn	Gly	His	Val	Pro	Phe	Lys	Asp	Met	Pro	Ala
	115					120						125			
Thr	Gln	Met	Leu	Leu	Glu	Lys	Leu	Asn	Gly	Thr	Val	Pro	Cys	Leu	Leu
	130					135				140					
Asp	Thr	Ser	Thr	Ile	Pro	Ala	Glu	Glu	Leu	Thr	Met	Ser	Pro	Ser	Arg
145				150					155					160	
Ser	Val	Ala	Asn	Ser	Gly	Leu	Ser	Asp	Ser	Leu	Thr	Thr	Ser	Thr	Pro
			165					170						175	

Arg

<210> 2693

<211> 798

<212> DNA

<213> Homo sapiens

<400> 2693

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ctgggggaccc acagcttcga ggggctgcac aatctggaga cactagacct gaattataac
120
aagctgcagg agttccctgt ggccatccgg accctgggca gactgcagga actgggggttc
180
cataacaaca acatcaaggc catcccagaa aaggccttca tgggggaaccc tctgctacag
240
acgatacact tttatgataa cccaatccag tttgtgggaa gatcggcatt ccagtaacctg
300
cctaaactcc acacactatc tctgaatggt gccatggaca tccaggagtt tccagatctc
360
aaaggcacca ccagcctgga gatcctgacc ctgaccgcg caggcatccg gctgctccca
420

tcggggatgt gccaacagct gccaggctc cgagtcctgg aactgtctca caatcaaatt
 480
 gaggaagctgc ccagcctgca caggtgtcag aaattggagg aaatcggcct ccaacacaac
 540
 cgcctctggg aaattggagc tgacaccttc agccagctga gctccctgca agccttgat
 600
 ttaagggtgga acgccatccg gtccatccac cccgaggcct tctccacctt gcactccttg
 660
 gtcaagctgg acctgacaga caaccagctg accacactgc ccttggtctg acttgggggg
 720
 ttgatgcctc tgaagctcaa agggaaacctt gctctctccc aggcctcttc caaggacagt
 780
 ttcccaaaac tgaggatc
 798

<210> 2694

<211> 266

<212> PRT

<213> Homo sapiens

<400> 2694

Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Val	Val	Leu	His	Leu	His	Asn	Asn
1			5						10					15	
Arg	Ile	Gln	His	Leu	Gly	Thr	His	Ser	Phe	Glu	Gly	Leu	His	Asn	Leu
		20						25					30		
Glu	Thr	Leu	Asp	Leu	Asn	Tyr	Asn	Lys	Leu	Gln	Glu	Phe	Pro	Val	Ala
		35				40					45				
Ile	Arg	Thr	Leu	Gly	Arg	Leu	Gln	Glu	Leu	Gly	Phe	His	Asn	Asn	Asn
50					55					60					
Ile	Lys	Ala	Ile	Pro	Glu	Lys	Ala	Phe	Met	Gly	Asn	Pro	Leu	Leu	Gln
65			70					75						80	
Thr	Ile	His	Phe	Tyr	Asp	Asn	Pro	Ile	Gln	Phe	Val	Gly	Arg	Ser	Ala
		85						90					95		
Phe	Gln	Tyr	Leu	Pro	Lys	Leu	His	Thr	Leu	Ser	Leu	Asn	Gly	Ala	Met
		100					105					110			
Asp	Ile	Gln	Glu	Phe	Pro	Asp	Leu	Lys	Gly	Thr	Thr	Ser	Leu	Glu	Ile
		115				120						125			
Leu	Thr	Leu	Thr	Arg	Ala	Gly	Ile	Arg	Leu	Leu	Pro	Ser	Gly	Met	Cys
		130			135						140				
Gln	Gln	Leu	Pro	Arg	Leu	Arg	Val	Leu	Glu	Leu	Ser	His	Asn	Gln	Ile
145				150					155					160	
Glu	Glu	Leu	Pro	Ser	Leu	His	Arg	Cys	Gln	Lys	Leu	Glu	Glu	Ile	Gly
		165						170					175		
Leu	Gln	His	Asn	Arg	Ile	Trp	Glu	Ile	Gly	Ala	Asp	Thr	Phe	Ser	Gln
		180				185							190		
Leu	Ser	Ser	Leu	Gln	Ala	Leu	Asp	Leu	Arg	Trp	Asn	Ala	Ile	Arg	Ser
		195				200					205				
Ile	His	Pro	Glu	Ala	Phe	Ser	Thr	Leu	His	Ser	Leu	Val	Lys	Leu	Asp
		210			215					220					
Leu	Thr	Asp	Asn	Gln	Leu	Thr	Thr	Leu	Pro	Leu	Ala	Gly	Leu	Gly	Gly
225				230						235				240	
Leu	Met	His	Leu	Lys	Leu	Lys	Gly	Asn	Leu	Ala	Leu	Ser	Gln	Ala	Phe
			245					250						255	
Ser	Lys	Asp	Ser	Phe	Pro	Lys	Leu	Arg	Ile						

260

265

<210> 2695

<211> 2265

<212> DNA

<213> Homo sapiens

<400> 2695

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 gagcagccca cccatgccgt gtgtgtgctg ggcacctga ctcagcttga catctgcagc
 120
 tctgccccctg aggaactgcac gtccttcagc atcaacgcct ccccgagggt ggtcgtggat
 180
 attgcccaca gccctccagc caagaagaaa tccacagggt cctccacatg gccctggag
 240
 cctggggtag aggtgaccct gacgatgaaa gcggccagtg gtacacagc cgaccagaag
 300
 gttcagattt catactacgg acccaagact ccaccagtca aagctctact ctacctcacc
 360
 gcggtggaaa tctccctgtg cgcagacatc acccgacccg gcaaagtga gccaaccaga
 420
 gctgtgaaa atcagaggac ctggacctgg ggccctgtg gacaggggtc catcctgctg
 480
 gtgaactgtg acagagacaa tctcgaatct tctgccatgg actgcgagga tgatgaagtg
 540
 cttgacagc aagacctgca ggacatgtcg ctgatgacct tgagcacgaa gacccccaa
 600
 gactttctca caaacctac actggtgctc cacgtggcca ggtctgagat ggacaaagt
 660
 aggtgtgttc aggcacacg gggcaaacgt tctccaagt gcagcgtagt cttgggtccc
 720
 aagtggccct ctactacct gatggtcccc ggtggaagc acaacatgga cttctacgtg
 780
 gagggccctg ctttcccgga caccgacttc cgggggctca ttacctcacc catctccctg
 840
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 900
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 960
 agtatttttg aaaatgagga cttcctgaag tcagtacta ctctggccat gaaagccaag
 1020
 tgcaagctga ccatctgccc tgaggaggag aacatggatg accagtggat gcaggatgaa
 1080
 atggagatcg gctacatcca agccccacac aaaacgctgc ccgtggtctt cgactctcca
 1140
 aggaacagag gcctgaagga gtttccatc aaacgagtga tgggtccaga ttttggctat
 1200
 gtaactcgag ggcaccaaac aggggggtatc agtggactgg actccttttg gaacctgga
 1260
 gtgagcccc cagtcacagt caggggcaag gaataccgcg tgggcaggat tctcttcggg
 1320
 gacagctggt atcccagcaa tgacagccgg cagatgcacc aggccctgca ggacttcttc
 1380

agtgcccagc aggtgcaggc ccctgtgaag ctctattctg actggctgtc cgtgggcccac
 1440
 gtggacagct tcctgagctt tgtgccagca cccgacagga agggcttccg gctgctcctg
 1500
 gccagcccca ggtcctgcta caaactgttc caggagcagc agaattgagg ccacggggag
 1560
 gcctctgctg tcgaagggat caagaaaaaa aaacagcaga aaataaagaa cattctgtca
 1620
 aacaagacat tgagagaaca taattcattt gtggagagat gcacgcactg gaaccgcgag
 1680
 ctgctgaagc gggagctggg cctggcccag agtgacatca ttgacatccc gcagctcttc
 1740
 aagctcaaaag agttctctaa ggcggaaagct tttttcccca acatggtgaa catgctgggtg
 1800
 ctagggaagc acctgggcat ccccaagccc ttcggggccc tcatcaacgg ccgctgctgc
 1860
 ctggaggaga aggtgtgttc cctgctggag ccaactgggccc tccagtgcac cttcatcaac
 1920
 gacttcttca cctaccacat caggcatggg gaggtgcact gcggcaccaa cgtgcgcaga
 1980
 aagcccttct ccttcaagtg gtggaacatg gtgccctgag cccatcttcc ctggcgctct
 2040
 ctccctcctg gccagatgct gctgggtcct ctgcagtgtg gcaagcaaga gctcttgta
 2100
 atattgtggc tccctggggg cggccagccc tcccagcagt ggcttgcctt cttctcctgt
 2160
 gatgtccagg ttccctcact tgaagatccc aacatggtcc tagcactgca cactcagttc
 2220
 tgctctaaga agctgcaata aagttttttt aagtcacttt gtaca
 2265

<210> 2696

<211> 663

<212> PRT

<213> Homo sapiens

<400> 2696

Met	Ala	Gln	Gly	Thr	Leu	Ile	Arg	Val	Thr	Pro	Glu	Gln	Pro	Thr	His
1				5					10					15	
Ala	Val	Cys	Val	Leu	Gly	Thr	Leu	Thr	Gln	Leu	Asp	Ile	Cys	Ser	Ser
			20					25					30		
Ala	Pro	Glu	Asp	Cys	Thr	Ser	Phe	Ser	Ile	Asn	Ala	Ser	Pro	Gly	Val
			35				40					45			
Val	Val	Asp	Ile	Ala	His	Ser	Pro	Pro	Ala	Lys	Lys	Lys	Ser	Thr	Gly
	50					55				60					
Ser	Ser	Thr	Trp	Pro	Leu	Asp	Pro	Gly	Val	Glu	Val	Thr	Leu	Thr	Met
65				70					75					80	
Lys	Ala	Ala	Ser	Gly	Ser	Thr	Gly	Asp	Gln	Lys	Val	Gln	Ile	Ser	Tyr
			85					90						95	
Tyr	Gly	Pro	Lys	Thr	Pro	Pro	Val	Lys	Ala	Leu	Leu	Tyr	Leu	Thr	Ala
			100				105						110		
Val	Glu	Ile	Ser	Leu	Cys	Ala	Asp	Ile	Thr	Arg	Thr	Gly	Lys	Val	Lys
	115					120						125			
Pro	Thr	Arg	Ala	Val	Lys	Asp	Gln	Arg	Thr	Trp	Thr	Trp	Gly	Pro	Cys

	130					135					140				
Gly	Gln	Gly	Ala	Ile	Leu	Leu	Val	Asn	Cys	Asp	Arg	Asp	Asn	Leu	Glu
145					150					155					160
Ser	Ser	Ala	Met	Asp	Cys	Glu	Asp	Asp	Glu	Val	Leu	Asp	Ser	Glu	Asp
				165					170					175	
Leu	Gln	Asp	Met	Ser	Leu	Met	Thr	Leu	Ser	Thr	Lys	Thr	Pro	Lys	Asp
				180				185					190		
Phe	Phe	Thr	Asn	His	Thr	Leu	Val	Leu	His	Val	Ala	Arg	Ser	Glu	Met
		195					200					205			
Asp	Lys	Val	Arg	Val	Phe	Gln	Ala	Thr	Arg	Gly	Lys	Leu	Ser	Ser	Ly
	210				215					220					
Cys	Ser	Val	Val	Leu	Gly	Pro	Lys	Trp	Pro	Ser	His	Tyr	Leu	Met	Val
225				230						235					240
Pro	Gly	Gly	Lys	His	Asn	Met	Asp	Phe	Tyr	Val	Glu	Ala	Leu	Ala	Phe
				245				250						255	
Pro	Asp	Thr	Asp	Phe	Pro	Gly	Leu	Ile	Thr	Leu	Thr	Ile	Ser	Leu	Leu
			260					265					270		
Asp	Thr	Ser	Asn	Leu	Glu	Leu	Pro	Glu	Ala	Val	Val	Phe	Gln	Asp	Ser
	275						280					285			
Val	Val	Phe	Arg	Val	Ala	Pro	Trp	Ile	Met	Thr	Pro	Asn	Thr	Gln	Pro
	290				295						300				
Pro	Gln	Glu	Val	Tyr	Ala	Cys	Ser	Ile	Phe	Glu	Asn	Glu	Asp	Phe	Leu
305				310						315				320	
Lys	Ser	Val	Thr	Thr	Leu	Ala	Met	Lys	Ala	Lys	Cys	Lys	Leu	Thr	Ile
				325					330					335	
Cys	Pro	Glu	Glu	Glu	Asn	Met	Asp	Asp	Gln	Trp	Met	Gln	Asp	Glu	Met
		340						345					350		
Glu	Ile	Gly	Tyr	Ile	Gln	Ala	Pro	His	Lys	Thr	Leu	Pro	Val	Val	Phe
	355					360					365				
Asp	Ser	Pro	Arg	Asn	Arg	Gly	Leu	Lys	Glu	Phe	Pro	Ile	Lys	Arg	Val
	370				375						380				
Met	Gly	Pro	Asp	Phe	Gly	Tyr	Val	Thr	Arg	Gly	Pro	Gln	Thr	Gly	Glu
385				405	390					395					400
Ile	Ser	Gly	Leu	Asp	Ser	Phe	Gly	Asn	Leu	Glu	Val	Ser	Pro	Pro	Val
								410					415		
Thr	Val	Arg	Gly	Lys	Glu	Tyr	Pro	Leu	Gly	Arg	Ile	Leu	Phe	Gly	Asp
		420						425					430		
Ser	Cys	Tyr	Pro	Ser	Asn	Asp	Ser	Arg	Gln	Met	His	Gln	Ala	Leu	Gln
	435					440					445				
Asp	Phe	Leu	Ser	Ala	Gln	Gln	Val	Gln	Ala	Pro	Val	Lys	Leu	Tyr	Ser
	450				455					460					
Asp	Trp	Leu	Ser	Val	Gly	His	Val	Asp	Glu	Phe	Leu	Ser	Phe	Val	Pro
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[illegible]

<210> 2697

€211> 2468

<212> DNA

<213> Homo sapiens

<400> 2697

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240					
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300					
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<210> 2698

<211> 332

<212> PRT

<213> Homo sapiens

<400> 2698

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          20          25          30
Gly Arg Ala Asn His Phe Phe Thr Val Thr Asp Pro Arg Asn Ile Leu
          35          40          45
Leu Thr Asn Glu Gln Leu Glu Ser Ala Arg Lys Ile Val His Asp Tyr
          50          55          60
Arg Gln Gly Ile Val Pro Pro Gly Leu Thr Glu Asn Glu Leu Trp Arg
          65          70          75          80
Ala Lys Tyr Ile Tyr Asp Ser Ala Phe His Pro Asp Thr Gly Glu Lys
          85          90          95
Met Ile Leu Ile Gly Arg Met Ser Ala Gln Val Pro Met Asn Met Thr
          100          105          110
Ile Thr Gly Cys Met Met Thr Phe Tyr Arg Thr Thr Pro Ala Val Leu
          115          120          125
Phe Trp Gln Trp Ile Asn Gln Ser Phe Asn Ala Val Val Asn Tyr Thr
          130          135          140
Asn Arg Ser Gly Asp Ala Pro Leu Thr Val Asn Glu Leu Gly Thr Ala
          145          150          155          160
Tyr Val Ser Ala Thr Thr Gly Ala Val Ala Thr Ala Leu Gly Leu Asn
          165          170          175
Ala Leu Thr Lys His Val Ser Pro Leu Ile Gly Arg Phe Val Pro Phe
          180          185          190
Ala Ala Val Ala Ala Ala Asn Cys Ile Asn Ile Pro Leu Met Arg Gln
          195          200          205
Arg Glu Leu Lys Val Gly Ile Pro Val Thr Asp Glu Asn Gly Asn Arg
          210          215          220
Leu Gly Glu Ser Ala Asn Ala Ala Lys Gln Ala Ile Thr Gln Val Val
          225          230          235          240
Val Ser Arg Ile Leu Met Ala Ala Pro Gly Met Ala Ile Pro Pro Phe
          245          250          255
Ile Met Asn Thr Leu Glu Lys Lys Ala Phe Leu Lys Arg Phe Pro Trp
          260          265          270
Met Ser Ala Pro Ile Gln Val Gly Leu Val Gly Phe Cys Leu Val Phe
          275          280          285
Ala Thr Pro Leu Cys Cys Ala Leu Phe Pro Gln Lys Ser Ser Met Ser
          290          295          300
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<210> 2699

<211> 974

<212> DNA

<213> Homo sapiens

<400> 2699

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 240
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 360
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 480
 aagtggaga acttgtgcct gccgaaggaa aaattcaaa gcgtcttaca actggatcct
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 840
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<210> 2700

<211> 177

<212> PRT

<213> Homo sapiens

<400> 2700

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Pro	Glu	Leu	Pro	Asp	Ile	Leu	Lys	Gln	Phe	Thr	Lys	Ala	Ala	Ile	Arg
			20					25					30		
Thr	Gln	Pro	Ala	Asp	Val	Leu	Arg	Trp	Ser	Ala	Gly	Tyr	Phe	Ser	Ala
			35				40					45			
Leu	Ser	Arg	Gly	Asp	Pro	Leu	Pro	Val	Lys	Asp	Arg	Met	Glu	Met	Pro
	50			55						60					
Val	Ala	Thr	Gln	Lys	Thr	Asp	Thr	Gly	Leu	Thr	Gln	Gly	Leu	Leu	Lys
	65			70				75					80		
Val	Leu	His	Lys	Gln	Cys	His	His	Lys	Arg	Tyr	Val	Glu	Leu	Thr	Asp
			85					90					95		
Leu	Glu	Gln	Lys	Trp	Lys	Asn	Leu	Cys	Leu	Pro	Lys	Glu	Lys	Phe	Lys
			100				105						110		
Ala	Leu	Leu	Gln	Leu	Asp	Pro	Cys	Glu	Asn	Lys	Ile	Lys	Trp	Ile	Asn

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          115              120              125
Phe Leu Ala Leu Gly Cys Ser Met Leu Gly Gly Ser Leu Asn Thr Ala
   130              135              140
Leu Lys His Leu Cys Glu Ile Leu Thr Asp Asp Pro Glu Ala Gly Pro
   145              150              155              160
Leu Ala Ser Pro Ser Arg Arg Phe Pro Thr Phe Thr Ala Thr Trp Pro
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<210> 2701
 <211> 646
 <212> DNA
 <213> Homo sapiens

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agcacactga gaggatgatt taagaaaaac tggctgggca cgggtgtccca tgcctgtaat
180
cccagcactt tgggaggcca aaatgccagc agctcttcct tgccagagat gatctgacct
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ggtgggggca gctggaaagc aacactggcc cccagctgaa gggcccagct gcagccagac
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360
ccactttcca tgggacttag aacttcggag ttgctgcctt gcaattggag gaaggacctg
420
gggcccggag accaggagag ccgctggaag cagtacctgg aggacgagag gatcgcgctt
480
ttcttcgaga acgaggagtt catgaaggaa ctgcaacgga accgcgactt cctcctcgct
540
ctggagagag atcgattgaa atacgaatcc cagaaatcta aatccagcag cgtggctgtc
600
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<210> 2702
 <211> 92
 <212> PRT
 <213> Homo sapiens

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Glu Arg Ile Ala Leu Phe Leu Gln Asn Glu Glu Phe Met Lys Glu Leu
          35          40          45
Gln Arg Asn Arg Asp Phe Leu Leu Ala Leu Glu Arg Asp Arg Leu Lys
          50          55          60
Tyr Glu Ser Gln Lys Ser Lys Ser Ser Ser Val Ala Val Gly Asn Asp

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65	70										75				80				
Phe	Gly	Phe	Ser	Ser	Pro	Val	Pro	Gly	Thr	Gly	Asp								
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 <210> 2703																			
<211> 610																			
<212> DNA																			
<213> Homo sapiens																			
 <400> 2703																			
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<211> 108																			
<212> PRT																			
<213> Homo sapiens																			
 <400> 2704																			
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1				5				10				15							
Ser	Val	Val	Ser	Leu	Ala	Thr	Gly	Ala	Gly	Ala	Ile	Tyr	Leu	Leu	Tyr				
			20				25				30								
Lys	Ala	Ile	Lys	Ala	Gly	Ile	Lys	Cys	Lys	Pro	Pro	Leu	Cys	Ser	Asn				
			35				40				45								
Ser	Pro	Ile	Cys	Ile	Ala	Arg	Glu	Cys	Ser	Gly	Pro	Trp	Gly	Lys	Gly				
			50				55				60								
Leu	Leu	Pro	Pro	Glu	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Leu	Leu	Gly	Glu				
			70				75				80								
Gly	Pro	Lys	Gly	Glu	Ala	Ser	Lys	Phe	Pro	Leu	Phe	Phe	Asp	Leu	Ser				
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Leu	Val	His	Leu	Pro	Gln	Ala	His	Pro	Ala	Ala	Ser								
			100				105												

<210> 2705

<211> 843

<212> DNA

<213> Homo sapiens

<400> 2705

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<210> 2706

<211> 251

<212> PRT

<213> Homo sapiens

<400> 2706

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Pro Arg Trp Asp Gln Ser Thr Phe Leu Gly Arg Ala Arg His Phe Phe
20          25          30
Thr Val Thr Asp Pro Arg Asn Leu Leu Leu Ser Gly Ala Gln Leu Glu
35          40          45
Ala Ser Arg Asn Ile Val Gln Asn Tyr Arg Ala Gly Val Val Thr Pro
50          55          60
Gly Ile Thr Glu Asp Gln Leu Trp Arg Ala Lys Tyr Val Tyr Asp Ser
65          70          75          80
Ala Phe His Pro Asp Thr Gly Glu Lys Val Val Leu Ile Gly Arg Met

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	85		90		95
Ser Ala Gln Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Leu Thr					
	100		105		110
Phe Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln					
	115		120		125
Ser Phe Asn Ala Ile Val Asn Tyr Ser Asn Arg Ser Gly Asp Thr Pro					
	130		135		140
Ile Thr Val Arg Gln Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly					
	145		150		155
Ala Val Ala Thr Ala Leu Gly Leu Lys Ser Leu Thr Lys His Leu Pro					
	165		170		175
Pro Leu Val Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Ala Asn					
	180		185		190
Cys Ile Asn Ile Pro Leu Met Arg Gln Arg Glu Leu Gln Val Gly Ile					
	195		200		205
Pro Val Thr Asp Glu Ala Gly Gln Arg Leu Gly His Ser Val Thr Ala					
	210		215		220
Ala Lys Gln Gly Ile Phe Gln Val Val Val Ser Arg Ile Gly Met Ala					
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	245		250		

<210> 2707

<211> 2921

<212> DNA

<213> Homo sapiens

<400> 2707

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<211> 337

<212> PRT

<213> Homo sapiens

<400> 2708

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Tyr Thr Glu Arg Arg Gln Pro Leu Tyr Arg Phe Ile Thr Thr Ile Cys
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Ala Ile Ile Gly Gly Thr Phe Thr Val Ala Gly Ile Leu Asp Ser Cys
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<212> DNA
<213> Homo sapiens

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Tyr Gly Ile Val Thr Met Ser Ser Thr Glu Val Ser Arg Cys Ile
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<213> Homo sapiens

<400> 2711

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<212> PRT

<213> Homo sapiens

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				530				535				540			
Tyr	Glu	Arg	Gln	Cys	Arg	Val	Leu	Gln	Asp	Gln	Val	Asp	Glu	Leu	Gln
				545				550				555			
Ser	Glu	Leu	Glu	Glu	Tyr	Arg	Ala	Gln	Gly	Arg	Val	Leu	Arg	Leu	Pro
				565				570				575			
Leu	Lys	Asn	Ser	Pro	Ser	Glu	Glu	Val	Glu	Ala	Asn	Ser	Gly	Gly	Ile
				580				585				590			
Glu	Pro	Glu	His	Gly	Leu	Gly	Ser	Glu	Glu	Cys	Asn	Pro	Leu	Asn	Met
				595				600				605			
Ser	Ile	Glu	Ala	Glu	Leu	Val	Ile	Glu	Gln	Met	Lys	Glu	Gln	His	His
				610				615				620			
Arg	Asp	Ile	Cys	Cys	Leu	Arg	Leu	Glu	Leu	Glu	Asp	Lys	Val	Arg	His
				625				630				635			
Tyr	Glu	Lys	Gln	Leu	Asp	Glu	Thr	Val	Val	Ser	Cys	Lys	Lys	Ala	Gln
				645				650				655			
Glu	Asn	Met	Lys	Gln	Arg	His	Glu	Asn	Glu	Thr	His	Thr	Leu	Glu	Glu
				660				665				670			
Gln	Ile	Ser	Asp	Leu	Lys	Met	Lys	Ile	Ala	Glu	Leu	Gln	Gly	Gln	Ala
				675				680				685			
Ala	Val	Leu	Lys	Glu	Ala	His	His	Glu	Ala	Thr	Cys	Arg	His	Glu	Glu
				690				695				700			
Glu	Lys	Lys	Gln	Leu	Gln	Val	Lys	Leu	Glu	Glu	Lys	Thr	His	Leu	Leu
				705				710				715			
Gln	Glu	Lys	Leu	Arg	Leu	Gln	His	Glu	Met	Glu	Leu	Lys	Ala	Arg	Leu
				725				730				735			
Thr	Gln	Ala	Gln	Ala	Ser	Phe	Gly	Arg	Glu	Arg	Glu	Gly	Leu	Gln	Ser
				740				745				750			
Ser	Ala	Trp	Thr	Glu	Glu	Lys	Val	Arg	Gly	Leu	Thr	Gln	Glu	Leu	Glu
				755				760				765			
Gln	Phe	His	Gln	Glu	Gln	Leu	Thr	Ser	Leu	Val	Glu	Lys	His	Thr	Leu
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				785				790				795			
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Ser	Gln	Ile	Glu	Ala	Gln	Phe	Gln	Ser	Asp	Cys	Gln	Lys	Val	Thr	Glu
				820				825				830			
Arg	Cys	Glu	Ser	Ala	Leu	Gln	Ser	Leu	Glu	Gly	Arg	Tyr	Arg	Gln	Glu

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Leu	Lys	Glu	Thr	Leu	Lys	Arg	Glu	Lys	Thr	Thr	Ser	Leu	Val	Leu	Thr
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Gln	Glu	Arg	Glu	Met	Leu	Glu	Lys	Thr	Tyr	Lys	Asp	His	Leu	Asn	Ser
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Thr	Lys	Gln	Val	Glu	Gly	Val	Thr	Arg	Arg	His	Val	Leu	Ser	Asp	Leu
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Gln	Arg	Gln	Glu	Val	Lys	Ile	Glu	Glu	Ser	Glu	Ala	Ser	Val	Glu	Gly
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Phe	Ser	Glu	Leu	Glu	Asn	Ser	Glu	Glu	Thr	Arg	Thr	Glu	Ser	Trp	Glu
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Val	Ser	Val	Leu	Lys	Lys	Lys	Leu	Lys	Ile	Leu	Glu	Arg	Ile	Pro	Glu
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Ala	Ser	Pro	Arg	Tyr	Lys	Leu	Leu	Tyr	Glu	Asp	Val	Ser	Arg	Glu	Asn
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Asp	Cys	Leu	Gln	Glu	Glu	Leu	Glu	Met	Met	Glu	Thr	Arg	Tyr	Asp	Glu

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 1300 1305 1310
 Glu Lys Ser Tyr Asp Glu Val Lys Ile Glu Asn Glu Glu Leu Asn Val
 1315 1320 1325
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 1330 1335 1340
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 1345 1350 1355 1360
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 1380 1385 1390
 Cys Lys Gln Glu Asn Gln Tyr Leu Glu Gly Asn Thr Gln Leu Leu Glu
 1395 1400 1405
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 1410 1415 1420
 His Gln Glu Arg Pro Arg Val Gln Asn Gln Val Ile Leu Glu Glu Asn
 1425 1430 1435 1440
 Thr Thr Thr Leu Leu Gly Phe Gln Asp Lys His Phe Gln His Gln Ala Thr
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 1475 1480 1485
 Ser Pro Gly Lys Lys Glu Glu Glu Leu Lys Ala Met Met His Asp Leu
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 1650 1655 1660
 Glu Ala Glu Leu Ser Glu Val Lys Ile Gln Thr His Ile Val Gln Gln
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 Ala Ser Leu Lys Thr Gln Leu Val Ala Ser Gln Glu Lys Val Gln Asn
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 1780 1785 1790
 Ser Asp Pro Arg Val Thr Gln Gln Glu Lys Glu Ala Leu Lys Gln Glu
 1795 1800 1805
 Val Met Pro Leu His Lys Gln Leu Gln Asn Ser Val Xaa Lys Ser Trp
 1810 1815 1820
 Ala Pro Glu Ile Ala Thr His Pro Ser Gly Leu His Asn Gln Gln Lys
 1825 1830 1835 1840
 Arg Leu Ser Trp Asp Lys Leu Asp His Leu Met Asn Glu Glu Gln Gln
 1845 1850 1855
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 1860 1865 1870
 Lys Ala Glu Leu Thr His Ser Arg Glu Lys Val Arg Gln Leu Glu Ser
 1875 1880 1885
 Asn Leu Leu Pro Lys His Gln Lys His Leu Asn Pro Ser Gly Thr Met
 1890 1895 1900
 Asn Pro Thr Glu Gln Glu Lys Leu Ser Leu Lys Arg Glu Cys Asp Gln
 1905 1910 1915 1920
 Phe Gln Lys Glu Gln Ser Pro Ala Asn Arg Lys Val Ser Gln Met Asn
 1925 1930 1935
 Ser Leu Glu Gln Glu Leu Glu Thr Ile His Leu Glu Asn Glu Gly Leu
 1940 1945 1950
 Lys Lys Lys Gln Val Lys Leu Asp Glu Gln Leu Met Glu Met Gln His
 1955 1960 1965
 Leu Arg Ser Thr Ala Thr Pro Ser Pro Ser Pro His Ala Trp Asp Leu
 1970 1975 1980
 Gln Leu Leu Gln Gln Gln Ala Cys Pro Met Val Pro Arg Glu Gln Phe
 1985 1990 1995 2000
 Leu Gln Leu Gln Arg Gln Leu Leu Gln Ala Glu Arg Ile Asn Gln His
 2005 2010 2015
 Leu Gln Glu Glu Leu Glu Asn Arg Thr Ser Glu Thr Asn Thr Pro Gln
 2020 2025 2030
 Gly Asn Gln Glu Gln Leu Val Thr Val Met Glu Glu Arg Met Ile Glu
 2035 2040 2045
 Val Glu Gln Lys Leu Lys Leu Val Lys Arg Leu Glu Gln Lys Val
 2050 2055 2060
 Asn Gln Leu Lys Glu Gln Val Ser Leu Pro Gly His Leu Cys Ser Pro
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<210> 2713

<211> 2066

<212> DNA

<213> Homo sapiens

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<211> 214

<212> PRT

<213> Homo sapiens

<400> 2714

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 Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys
 35 40 45
 Thr Gly Leu Tyr Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser
 50 55 60
 Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln
 65 70 75 80
 Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu
 85 90 95
 Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg
 100 105 110
 Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg
 115 120 125
 Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly
 130 135 140
 Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala
 145 150 155 160
 Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe
 165 170 175
 Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala
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<210> 2715
 <211> 378
 <212> DNA
 <213> Homo sapiens

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 180
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 240
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<210> 2716
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 <212> PRT
 <213> Homo sapiens

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 Gln Arg Gly Asp Leu Ser Asp Val Glu Glu Glu Glu Glu Met
 35 40 45
 Asp Val Asp Glu Ala Thr Gly Ala Val Lys Lys His Asn Gly Val Gly
 50 55 60
 Gly Ser Pro Pro Lys Ser Lys Leu Leu Phe Ser Asn Thr Ala Ala Gln
 65 70 75 80
 Lys Leu Arg Gly Met Asp Glu Val Tyr Asn Leu Phe Tyr Val Asn Asn
 85 90 95
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<210> 2717
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 <212> DNA
 <213> Homo sapiens

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 180
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 360
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 420
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 540
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 720
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 1620
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 1860
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 1920
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 1980
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<210> 2718

<211> 110

<212> PRT

<213> Homo sapiens

<400> 2718

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Glu	Gly	Pro	Arg	Pro	Glu	Asn	Thr	Leu	Gly	Leu	Ser	Ser	Pro	Ala	Gln
		35				40					45				
Thr	Thr	Gly	Glu	Gly	Ala	Gly	His	Arg	Pro	Leu	Thr	Ile	Leu	His	Pro
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Lys	Thr	Gly	Gly	Gln	Gly	Ser	Asp	Ala	Thr	Leu	Leu	Phe	Val	Lys	Tyr
		65			70					75				80	
Gly	Thr	Thr	Phe	Phe	Val	Leu	Phe	Glu	Val	Ser	Ser	Gly	Ser	Lys	Leu
			85					90					95		
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<210> 2719

<211> 546

<212> DNA

<213> Homo sapiens

<400> 2719

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<211> 508

<212> PRT

<213> Homo sapiens

<400> 2722

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Ser	Thr	Ser	Phe	Gly	Gly	Gln	Asn	Arg	Gly	Arg	Ser	Asp	Ser	Val	Asp
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Tyr	Gly	Gln	Thr	His	Tyr	Tyr	His	Gln	Arg	Gln	Asn	Ser	Asp	Asp	Lys
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Leu	Asn	Gly	Trp	Gln	Asn	Ser	Arg	Asp	Ser	Gly	Ile	Cys	Ile	Asn	Ala
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Ser	Asn	Trp	Gln	Asp	Lys	Ser	Met	Gly	Cys	Glu	Asn	Gly	His	Val	Pro
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Leu	Tyr	Ser	Ser	Ser	Ser	Val	Pro	Thr	Thr	Ile	Asn	Thr	Ile	Gly	Thr
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Ser	Thr	Ser	Thr	Asn	Val	Pro	Ala	Trp	Leu	Lys	Ser	Leu	Arg	Leu	His
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Lys	Tyr	Ala	Ala	Leu	Phe	Ser	Gln	Met	Thr	Tyr	Glu	Glu	Met	Met	Ala
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Leu	Thr	Glu	Cys	Gln	Leu	Glu	Ala	Gln	Asn	Val	Thr	Lys	Gly	Ala	Arg
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Ser Ser Pro Ser Thr Thr Pro Glu Ala Arg Arg Arg Glu Pro Gln Ala
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225              230              235
Lys Asp Gly Ala Ala Ala Thr Gly Ala Thr Ala Thr Pro Ser Ala Gly
245              250              255
Ala Ser Gly Gly Leu Gln Pro His Gln Leu Ser Ser Cys Asp Gly Glu
260              265              270
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275              280              285
Arg Val Met Gly Lys Val Cys Thr Gln Leu Leu Val Ser Arg Pro Asp
290              295              300
Glu Glu Asn Ile Ser Ser Tyr Leu Gln Leu Ile Asp Lys Cys Leu Ile
305              310              315
His Glu Ala Phe Thr Glu Thr Gln Lys Lys Arg Leu Leu Ser Trp Lys
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Gln Gln Val Gln Lys Leu Phe Arg Ser Phe Pro Arg Lys Thr Leu Leu
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395              400              405
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410              415              420
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425              430              435
Ser Val Gln Arg Thr Arg Ser Leu Pro Val His Thr Ser Pro Gln Asn
440              445              450
Met Leu Met Phe Gln Gln Pro Glu Phe Gln Leu Pro Val Thr Glu Pro
455              460              465
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<210> 2723

<211> 1221

<212> DNA

<213> Homo sapiens

<400> 2723

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<211> 404

<212> PRT

<213> Homo sapiens

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Thr	Ile	His	Met	Phe	Gly	Asp	His	Thr	Asn	Arg	Val	Lys	Arg	Ile	Ala
			20					25					30		
Thr	Ala	Pro	Met	Trp	Pro	Asn	Thr	Phe	Trp	Ser	Ala	Ala	Glu	Asp	Gly
			35				40					45			
Leu	Ile	Arg	Gln	Tyr	Asp	Leu	Arg	Glu	Asn	Ser	Lys	His	Ser	Glu	Val
			50				55				60				
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Gly Pro Phe Val Arg Leu Tyr Asp Ile Arg Met Ile His Asn His Arg
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Lys Ser Met Lys Gln Ser Pro Ser Ala Gly Val His Thr Phe Cys Asp
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Arg Gln Lys Pro Leu Pro Asp Gly Ala Ala Gln Tyr Tyr Val Ala Gly
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His Leu Pro Val Lys Leu Pro Asp Tyr Asn Asn Arg Leu Arg Val Leu
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Val Ala Thr Tyr Val Thr Phe Ser Pro Asn Gly Thr Glu Leu Leu Val
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Asn Met Gly Gly Glu Gln Val Tyr Leu Phe Asp Leu Thr Tyr Lys Gln
180
Arg Pro Tyr Thr Phe Leu Leu Pro Arg Lys Cys His Ser Ser Gly Glu
195
Val Gln Asn Gly Lys Met Ser Thr Asn Gly Val Ser Asn Gly Val Ser
210
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Leu Tyr Gly Asn Arg Ala Ala Ala Tyr Met Lys Arg Lys Trp Asp Gly
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Asp His Tyr Asp Ala Leu Arg Asp Cys Leu Lys Ala Ile Ser Leu Asn
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<210> 2725

<211> 856

<212> DNA

<213> Homo sapiens

<400> 2725

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<211> 148

<212> PRT

<213> Homo sapiens

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 Trp Ser Leu Gln Glu Lys Tyr Asn Ser Arg Ala Ala Ala Leu Phe Arg
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<210> 2728
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 2728
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Thr	Gly	Met	Ser	Arg	Arg	Gln	Met	Ile	Tyr	Ser	Ala	Ala	Arg	Ala	Ile				
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<210> 2729

<211> 393

<212> DNA

<213> Homo sapiens

<400> 2729

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<210> 2730

<211> 92

<212> PRT

<213> Homo sapiens

<400> 2730

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	20	25	30
Leu Asp Gln Cys Ala Glu Asp Phe Arg Glu Pro Pro His Phe Pro Cys			
	35	40	45
Leu Gln Lys Leu Leu Asp Tyr Leu Thr Arg Met Met Pro Gly Ser Asp			
	50	55	60
Pro Glu Arg Arg Ala Gln Asn Leu Leu Glu Gln Phe Gln Lys Gln Glu			
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Val Glu Thr Asp Asn Gly Leu Pro Asn Thr Ile Ser			
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<210> 2731

<211> 447

<212> DNA

<213> Homo sapiens

<400> 2731

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<210> 2732

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2732

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	20	25	30
Gln Asn Gln Gln Asn Gly Gln Arg Val Tyr Thr Ser Met Ser Asp Cys			
	35	40	45
Leu Ile Lys Thr Val Arg Ser Glu Gly Tyr Phe Gly Met Tyr Arg Gly			
	50	55	60
Ala Ala Val Asn Leu Thr Leu Val Thr Pro Glu Lys Ala Ile Lys Leu			
65	70	75	80
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<212> DNA
<213> Homo sapiens

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1320

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<210> 2734

<211> 790

<212> PRT

<213> Homo sapiens

<400> 2734

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			20					25				30			
Val	Met	Asp	Lys	Leu	Arg	Leu	Ala	Glu	Leu	Thr	Val	Asp	Glu	Phe	Leu
		35				40					45				
Ala	Ser	Gly	Phe	Asp	Ser	Glu	Ser	Glu	Ser	Glu	Ser	Glu	Asn	Ser	Pro
	50				55					60					
Gln	Ala	Glu	Thr	Arg	Glu	Ala	Arg	Glu	Ala	Ala	Arg	Ser	Pro	Asp	Lys
65				70				75				80			
Pro	Gly	Gly	Ser	Pro	Ser	Ala	Ser	Arg	Arg	Lys	Gly	Arg	Ala	Ser	Glu
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His	Lys	Asp	Gln	Leu	Ser	Arg	Leu	Lys	Asp	Arg	Asp	Pro	Glu	Phe	Tyr
			100					105				110			
Lys	Phe	Leu	Gln	Glu	Asn	Asp	Gln	Ser	Leu	Leu	Asn	Phe	Ser	Asp	Ser
		115				120						125			
Asp	Ser	Ser	Glu	Glu	Glu	Glu	Gly	Pro	Phe	His	Ser	Leu	Pro	Asp	Val
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Leu	Glu	Glu	Ala	Ser	Glu	Glu	Glu	Asp	Gly	Ala	Glu	Glu	Gly	Glu	Asp
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Gly	Asp	Arg	Val	Pro	Arg	Gly	Leu	Lys	Gly	Lys	Lys	Asn	Ser	Val	Pro
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	645	650
Glu Ile Gln Leu Glu Ile Ser Gly Lys Glu Arg Val Arg Leu Gly Glu		655
	660	665
Gly Thr Trp Leu Glu Asp Leu Asn Phe Pro Glu Ile Lys Arg Arg Lys		670
	675	680
Met Ala Asp Arg Lys Asp Glu Asp Arg Lys Gln Phe Lys Asp Leu Phe		685
	690	695
Asp Leu Asn Ser Ser Glu Glu Asp Asp Thr Glu Gly Phe Leu Glu Arg		700
	705	710
Gly Ile Leu Gly Pro Leu Ser Thr Arg His Gly Val Glu Asp Asp Glu		715
	725	730
Glu Asp Glu Glu Glu Gly Glu Glu Asp Ser Ser Asn Ser Glu Gly Glu		735
	740	745
Trp Ser Trp Asp Gly Asp Pro Asp Ala Glu Ala Gly Leu Ala Pro Gly		750
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<210> 2735

<211> 1666

<212> DNA

<213> Homo sapiens

<400> 2735

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<210> 2736

<211> 218

<212> PRT

<213> Homo sapiens

<400> 2736

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			20					25					30		
Phe	His	Ser	Ser	His	Ile	Ser	Thr	Ile	Gly	Val	Asp	Phe	Lys	Met	Lys
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Gln	His	Ile	Met	Lys	Trp	Val	Ser	Asp	Val	Asp	Glu	Tyr	Ala	Pro	Glu
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Leu	Ala	Lys	Glu	Tyr	Gly	Met
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Asn	Leu	Asn	Ile	Lys	Glu	Ser
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Gln	Ala	His	Arg	Lys	Glu	Leu
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<210> 2737

<211> 898

<212> DNA

<213> Homo sapiens

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<210> 2738

<211> 299

<212> PRT

<213> Homo sapiens

<400> 2738

```

Xaa Pro Val Cys Ala Thr Cys Ala Gly Phe Gly Gly Arg Cys His Arg
 1          5          10          15
His Arg Ile Arg Arg Ala Glu Glu His Ala Glu Glu Leu Arg Asn Lys
      20          25          30
Ile Val Asp Gln Cys Glu Arg Leu Gln Leu Gln Ser Ala Ala Ile Thr
      35          40          45
Lys Tyr Val Ala Asp Val Leu Pro Gly Lys Asn Gln Arg Ala Val Ser
      50          55          60
Met Ala Ser Ala Ala Arg Glu Leu Val Ile Gln Arg Leu Ser Leu Val
      65          70          75
Arg Ser Leu Cys Glu Ser Glu Glu Gln Arg Leu Leu Glu Gln Val His
      85          90          95
Gly Glu Glu Glu Arg Ala His Gln Ser Ile Leu Thr Gln Arg Val His
      100          105          110
Trp Ala Glu Ala Leu Gln Lys Leu Asp Thr Ile Arg Thr Gly Leu Val
      115          120          125
Gly Met Leu Thr His Leu Asp Asp Leu Gln Leu Ile Gln Lys Glu Gln
      130          135          140
Glu Ile Phe Glu Arg Thr Glu Glu Ala Glu Gly Ile Leu Asp Pro Gln
      145          150          155
Glu Ser Glu Met Leu Asn Phe Asn Glu Lys Cys Thr Arg Ser Pro Leu
      165          170          175
Leu Thr Gln Leu Trp Ala Thr Ala Val Leu Gly Ser Leu Ser Gly Thr
      180          185          190
Glu Asp Ile Arg Ile Asp Glu Arg Thr Val Ser Pro Phe Leu Gln Leu
      195          200          205
Ser Asp Asp Arg Lys Thr Leu Thr Ser Ala Pro Arg Ser Gln Arg Cys
      210          215          220
Ala Asp Gly Pro Glu Arg Phe Asp His Trp Pro Asn Ala Leu Ala Ala
      225          230          235
Thr Ser Phe Gln Asn Gly Leu His Ala Trp Met Val Asn Val Gln Asn
      245          250          255
Ser Cys Ala Tyr Lys Val Gly Val Ala Ser Gly His Leu Pro Arg Lys
      260          265          270
Gly Ser Gly Ser Asp Cys Arg Leu Gly His Asn Ala Phe Ser Trp Val
      275          280          285
Phe Ser Arg Tyr Asp Gln Glu Phe Arg Phe Ser
      290          295

```

<210> 2739

<211> 1501

<212> DNA

<213> Homo sapiens

<400> 2739

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gagagccgcc gagagtgggg gccgatggcg aagctccggg tggcttacga gtacacggaa
 60
gccgaggaca agagcatccg gtcggettgt ttctcatca tctccggcgt cgtgtcgctc
 120
ttcattctcg gcttctgctg gctgagtcgc gcgctgcagg atctgcaagc cacggaggcc
 180

```

aattgcacgg tgctgtcggt gcagcagatc ggcgaggtgt tcgagtgcac cttcacctgt
240
ggcgccgact gcaggggcac ctgcagtae cctcgctcc aggtctactg gaacaactct
300
gagtcceact ctaggcgct gctgcacagc gacgagcacc agctcctgac caaccccaag
360
tgctcctata tccctcctg taagagagaa aatcagaaga atttgaaaag tgcattgaat
420
tggcaacagt actggaaga tgagattggt tcccagccat ttacttgcta ttttaataca
480
catcaaagac cagatgatgt gcttctgcat cgcactcatg atgagattgt cctcctgcat
540
tgcttctctt ggcctcctg gacatttgtg gtgggcgttc tcatttggtt cctgaccatc
600
tgtgccaaga gcttggcggt caaggcggaa gccatgaaga agcgaagt ctcttaaaag
660
ggaaggaggc ttgtagaaag caaagtacag aagctgtact catcgccagc cgtccacctg
720
cggaacctgt gtttcttggc gcaggagatg gacagggccca cgacagggtc ctgagaggct
780
catcctctag tggcaacaga aacaggcaca actggaagac ttggaacctc aaagcttgta
840
ttccatctgc tgtagcaatg gctaaagggt caagatctta gctgtatgga gtaactattt
900
cagaaaaacc tataagaagt tcattttctt tcaaaagtaa cagtatatta ttgtacagt
960
gtagtataca aaccattatg atttatgcta cttaaaaaa ttaaaataga gtggtctgtg
1020
ttattttcta tttcctttt tatgcttaga acaccagggt tttaaaaaa aaaaaagggtg
1080
aggacatctg ggtctcattt gcttctgcta ggttaactt ttacttgaca acaaggatct
1140
ctgctgaagt ctgaacctta ctgtgaacc ctgagtttcc actattaaag agtatctttt
1200
gacgtcctgc ttgaaaaatg aatagtatac tggttaactca gtctccagtc acctctgtgt
1260
ctcttaagca agagattcta aaagattggg aaaacatata ctccaaaacc tgcctttgcc
1320
taaccattat ttttcaccag attactttt aagagaggga ggtgattctg aagaaggctt
1380
ctatctcaa aagcactggg cttccttatt catctgttct tgtgtgtttt gacggagtta
1440
aaaaagtttg tgtgcaatac aatataaatg atgtgaagga cactcttaaa aaaaaaaaaa
1500
a
1501

<210> 2740

<211> 218

<212> PRT

<213> Homo sapiens

<400> 2740

Glu Ser Arg Arg Glu Trp Gly Ala Met Ala Lys Leu Arg Val Ala Tyr

1	5	10	15
Glu Tyr Thr Glu Ala Glu Asp Lys Ser Ile Arg Leu Gly Leu Phe Leu			
	20	25	30
Ile Ile Ser Gly Val Val Ser Leu Phe Ile Phe Gly Phe Cys Trp Leu			
	35	40	45
Ser Pro Ala Leu Gln Asp Leu Gln Ala Thr Glu Ala Asn Cys Thr Val			
	50	55	60
Leu Ser Val Gln Gln Ile Gly Glu Val Phe Glu Cys Thr Phe Thr Cys			
	65	70	75
Gly Ala Asp Cys Arg Gly Thr Ser Gln Tyr Pro Cys Val Gln Val Tyr			
	85	90	95
Val Asn Asn Ser Glu Ser Asn Ser Arg Ala Leu Leu His Ser Asp Glu			
	100	105	110
His Gln Leu Leu Thr Asn Pro Lys Cys Ser Tyr Ile Pro Pro Cys Lys			
	115	120	125
Arg Glu Asn Gln Lys Asn Leu Glu Ser Val Met Asn Trp Gln Gln Tyr			
	130	135	140
Trp Lys Asp Glu Ile Gly Ser Gln Pro Phe Thr Cys Tyr Phe Asn Gln			
	145	150	155
His Gln Arg Pro Asp Asp Val Leu Leu His Arg Thr His Asp Glu Ile			
	165	170	175
Val Leu Leu His Cys Phe Leu Trp Pro Leu Val Thr Phe Val Val Gly			
	180	185	190
Val Leu Ile Val Val Leu Thr Ile Cys Ala Lys Ser Leu Ala Val Lys			
	195	200	205
Ala Glu Ala Met Lys Lys Arg Lys Phe Ser			
	210	215	

<210> 2741

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 2741

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120
tcctacaagg actggtctca gaacatgtat ttcaactgct cagaagacaa ccccgatcga
180
gagcgctgct ctgtgcctta ctccgtgtgc ttgcctactc ctgaccaggc agtgcataac
240
actatgtgtg gccaaaggtat gcaggccttt gactacttgg aagctagcaa agtcatctac
300
accaatggct gtattgacaa gttggtcaac tggatacaca gcaacctatt cttacttggt
360
ggtgtggctc taggcctggc catccccag ctggtgggaa ttctgtgtgc ccagatccta
420
gtgaatcaga tcaaagatca gatcaagcta cagctctaca accagcagca ccgggctgac
480
ccatgggtact gagaatccat cctgcacetc ctcccatgg aaactggcaa gcctcataaa
540
cgaacagcag tgggtgctga aagcagcacc aaatggagat ttggattcca gcccccagc
600

```

gacagcccag tgggaagaag caaactccag atgggcagaa ggcaggggtgc acaggtggct
 660
 ccagtctcag gaggatgcgc ctccctctccc ccatcccagc cctcagcatt gtgccagagt
 720
 gataccctta agtgtttggg tttatgtttt cagttttgtt tgggaaacag cagttgcaca
 780
 gagagttggg ggtactgctg ctgccttttc accgaggcac tgccaccacc agctctagca
 840
 gggatgctcc tgagcttggc ggacataact agatcctaac gtgccagtga gacctggctg
 900
 tggagagtag cactggcagc cctgcctgga ctccacttg catgatacca gctccagaag
 960
 ggaagggagt ggagcaggca gtgaggagag agcctggggg tcggctgggg acagccgtat
 1020
 gtgctagtag ggagtggagg gagatatgtt taccaaatgc ctgtcctgcc atcctccca
 1080
 gtagtcagag tgagctacat cctgccccgc cttcatttcc atggaacat ggcagctagg
 1140
 acacggggta tacaacgca gccaaattct tccccacctc ccttacttcg aaaaaaagt
 1200
 tggaaacctg gtcctatac tctgcagtca gaagtgggac tgagccatac atgcccttga
 1260
 attcctccct gtctggccct cctctccag caagcagggt tttctttaac ttggcagtg
 1320
 gcagaggaga agtggttaaca cccccacccc attccctgc atcgagctc agtattccta
 1380
 cagggtaaga ggtaggaatc ttgctgggac gaggggagcc agaagtggca ataaaagcgt
 1440
 gttgacctgg gcaaaaaaaaa aaaaaaaaaa aaagaaaaaa aaaaaaa
 1487

<210> 2742

<211> 163

<212> PRT

<213> Homo sapiens

<400> 2742

Lys Ala Arg Gly Lys Val Ser Glu Ile Ile Asn Asn Ala Ile Val His
 1 5 10 15
 Tyr Arg Asp Asp Leu Asp Leu Gln Asn Leu Ile Asp Phe Gly Gln Lys
 20 25 30
 Lys Phe Ser Cys Cys Gly Gly Ile Ser Tyr Lys Asp Trp Ser Gln Asn
 35 40 45
 Met Tyr Phe Asn Cys Ser Glu Asp Asn Pro Ser Arg Glu Arg Cys Ser
 50 55 60
 Val Pro Tyr Ser Cys Cys Leu Pro Thr Pro Asp Gln Ala Val Ile Asn
 65 70 75 80
 Thr Met Cys Gly Gln Gly Met Gln Ala Phe Asp Tyr Leu Glu Ala Ser
 85 90 95
 Lys Val Ile Tyr Thr Asn Gly Cys Ile Asp Lys Leu Val Asn Trp Ile
 100 105 110
 His Ser Asn Leu Phe Leu Leu Gly Gly Val Ala Leu Gly Leu Ala Ile
 115 120 125
 Pro Gln Leu Val Gly Ile Leu Leu Ser Gln Ile Leu Val Asn Gln Ile

```

      130              135              140
Lys Asp Gln Ile Lys Leu Gln Leu Tyr Asn Gln Gln His Arg Ala Asp
145              150              155              160
Pro Trp Tyr

```

```

<210> 2743
<211> 384
<212> DNA
<213> Homo sapiens

```

```

<400> 2743
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60
gactccgggtg tccagtctcc gcccgagacc tccagagact ggagtgtccc atctccgcc
120
acagcctccc aagactcagg tgtccagtct ccacctggag cctccagaga ctggagtgtc
180
ccatctccgc ccagagccta ccaagactga ggtgtccagt ctccacctgg agcctccga
240
gactggagtg gccatctct acctggagcc tctgggact ggagtgtctc atctctgcc
300
agagcctccc aagactcggg tatctcatct ccacgggag cctcctgaga ctggagtgc
360
tgatctctgc ctggagcctc ccaa
384

```

```

<210> 2744
<211> 69
<212> PRT
<213> Homo sapiens

```

```

<400> 2744
Xaa Ile Leu Pro Ser Ala Ser Arg Asp Ser Gly Val Leu Ser Pro Pro
1      5      10      15
Gly Ala Ser Gln Asp Ser Gly Val Gln Ser Pro Pro Gly Ala Ser Arg
20     25     30
Asp Trp Ser Val Pro Ser Pro Pro Thr Ala Ser Gln Asp Ser Gly Val
35     40     45
Gln Ser Pro Pro Gly Ala Ser Arg Asp Trp Ser Val Pro Ser Pro Pro
50     55     60
Arg Ala Tyr Gln Asp
65

```

```

<210> 2745
<211> 769
<212> DNA
<213> Homo sapiens

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```

<400> 2745
gaattccacc ttcctctctg cagtgtctgag aggcagcgag gacggagagg acagcggcat
60
ctctaggctc ttctgagagg gacagagaaa gaatagaaat gtgccctaaa agcataaatg
120

```

```

agtatcacct gagaaaatta ggcattcccc tcttggaac acgtctctgt gagtttgcac
180
ttcatttggc ttggagccct ggctcgatgc ctcatggatc tttctcccca aggagggacg
240
tcttgagggg tccgagcctc aggccaaagga cccctgatgc agactctgga atccctggcc
300
caaaggcctg tctgggcccc tctggggctg aggacacaca gatacataat gacacctgca
360
gaaatgtatt ctctgaggac acttagaata tgaggaagag ggtgtggccc aacctcact
420
tcacctgggg aggggcttct tccggacagt agacacccctg cccgtgcaga gagatgtcat
480
ggggggcacct gctctccctg atagatgctg agagcatcca gaaacttcca gaccagccct
540
ctcaccacac ccagaagagg cctttcccat ctggagagaa gcttccagac cagcccttca
600
cacaccacag ccaggagggg cctttcccat ctgggagaga aacttccaga ccagccctc
660
ataccacagc caagaggggc ctttctcacc tggagagaaa cttccagacc agccctcac
720
accacagcca agaggggcct tccccccgg gagagaaact tccagacca
769

```

<210> 2746

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2746

```

Met Ser Trp Gly His Leu Leu Ser Leu Ile Asp Ala Glu Ser Ile Gln
  1             5             10            15
Lys Leu Pro Asp Gln Pro Ser His His Thr Gln Lys Arg Pro Phe Pro
      20             25            30
Ser Gly Glu Lys Leu Pro Asp Gln Pro Phe Thr His His Ser Gln Glu
      35             40            45
Gly Pro Phe Pro Pro Gly Arg Glu Thr Ser Arg Pro Ala Pro His Thr
      50             55            60
Thr Ala Lys Arg Gly Leu Ser His Leu Glu Arg Asn Phe Gln Thr Ser
      65             70            75            80
Pro Ser His His Ser Gln Glu Gly Pro Phe Pro Pro Gly Glu Lys Leu
      85             90            95
Pro Asp

```

<210> 2747

<211> 1100

<212> DNA

<213> Homo sapiens

<400> 2747

```

tttttcttct ccaggcccag ggccccggcc agtgcccagc cccgctggga gccccggcca
60
gcaccacgga cggcgcccag gaagcccag tccccctgga cgggggcctt ctggattccg
120

```


agggccccgg cagggttgcg caagggtgcg ttgcttgcg tgtccaagcc cctcgccctg
 180
 cagggtccgg cgccccctgc cctcgagccc tcggcctctc ccccgatggc gccacactg
 240
 ttccccatgg agtccaagag cagcaagacc gacagcgtgc ggggtgccgg cgccccctt
 300
 gctgccaagc acctagccga gaagaagacg atgaccaacc ccacgaccgt catcgaggtc
 360
 taccgggaca ccaccgaggt gaacgactat tacctgtggt ccattcttcaa cttcgtctac
 420
 ctcaactctt gctgcctggg cttcatcgcc ttggcctact cctctaaagt gcgagacaag
 480
 aagcttctca atgacctgaa tggagccgtg gaggatgcaa agacggcccc gctgttcaac
 540
 atcaccagtt ctgcctggc agcctcctgc atcatcctcg tcttcatctt cctgcggtag
 600
 cccctcaccg actactaagg cccgccaggc acggctgctg gcggagacaa gcactgagac
 660
 atgtttatct tcatgggtccc tgaacgcag gatcccatga ggttggggca gggcagggt
 720
 tcttgtctct gggccccctt gagctgtgaa ctgggcagca aggccatcag aagctgagta
 780
 cagcaagggg gcagtgaact tggccctcag tccacccctt ccgctcctg gctccaccc
 840
 tgctgtgtgc tggggcctgg ggggttctcc cctcgtgct gcacctggc ttccagcgtc
 900
 tgtgtccctg cctcactgtg ccccttccca ggctcctggg gcccttgga cctgacacct
 960
 agcaggaagg gcttatgcaa aattgtccca ggttgggagg actcactctg tgctccccga
 1020
 ccctgcctcc tccagatgt gaccccgctc agagcccttg tgtctgtgaa ctttcaatga
 1080
 aatacccatg cagctccaaa
 1100

<210> 2748

<211> 205

<212> PRT

<213> Homo sapiens

<400> 2748

Phe Phe Phe Ser Arg Pro Arg Ala Pro Ala Ser Ala Gln Pro Arg Trp
 1 5 10 15
 Glu Pro Arg Pro Ala Pro Arg Thr Ala Pro Arg Lys Pro Glu Ser Pro
 20 25 30
 Trp Thr Gly Ala Phe Trp Ile Pro Arg Pro Pro Ala Gly Ser Pro Lys
 35 40 45
 Gly Cys Phe Ala Cys Val Ser Lys Pro Pro Ala Leu Gln Ala Pro Ala
 50 55 60
 Ala Pro Ala Pro Glu Pro Ser Ala Ser Pro Pro Met Ala Pro Thr Leu
 65 70 75 80
 Phe Pro Met Glu Ser Lys Ser Ser Lys Thr Asp Ser Val Arg Ala Ala
 85 90 95
 Gly Ala Pro Pro Ala Cys Lys His Leu Ala Glu Lys Lys Thr Met Thr

	100		105		110									
Asn	Pro	Thr	Val	Ile	Glu	Val	Tyr	Pro	Asp	Thr	Thr	Glu	Val	Asn
	115		120		125									
Asp	Tyr	Tyr	Leu	Trp	Ser	Ile	Phe	Asn	Phe	Val	Tyr	Leu	Asn	Phe
	130		135		140									
Cys	Leu	Gly	Phe	Ile	Ala	Leu	Ala	Tyr	Ser	Leu	Lys	Val	Arg	Asp
	145		150		155									
Lys	Leu	Leu	Asn	Asp	Leu	Asn	Gly	Ala	Val	Glu	Asp	Ala	Lys	Thr
	165		170		175									
Arg	Leu	Phe	Asn	Ile	Thr	Ser	Ser	Ala	Leu	Ala	Ala	Ser	Cys	Ile
	180		185		190									
Leu	Val	Phe	Ile	Phe	Leu	Arg	Tyr	Pro	Leu	Thr	Asp	Tyr		
	195		200		205									

<210> 2749

<211> 2050

<212> DNA

<213> Homo sapiens

<400> 2749

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gcgccattcg gcagcgcctt gtgggtctat aatctactta gcacagagag tgtcttctaa
120
gtacttcaca tccttctctg cagatgctct gacctttgac cctgcgcgtt cagctctagg
180
gcccgtagcag gccacacat gaacacctcc ccaggcacgg tgggagctga cccggatcac
240
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300
accgggacgg tgcagcacca ggactccag gtgaatgcct tggaggctac accggacgcg
360
agcatgattg ctgctgcagt tcagcctgtg tccctagggt accagcacat ccgcatgtat
420
gatctcaact ccaataaacc taaccccatc atcagctacg acggcgctca caagaacatc
480
gcgtctgtgg gcttccacga agacggcgcg tggatgtaca cgggcggcga ggactgcaca
540
gccaggatct gggacctcag gtcccggaac ctgcagtgcc agcggatctt ccagggtgaa
600
gcacccatta actgcgtgtg cctgcacccc aaccaggcag agctcatcgt gggtgaccag
660
agcgggggcta tccacatctg ggacttgaaa acagaccaca acgagcagct gatccctgag
720
cccgaggtct ccatcacgtc cgccacatc gatcccgacg ccagctacat ggcagctgtc
780
aatagcaccg gaaactgcta tgtctggaat ctgacggggg gcattgggtga cgaggtgacc
840
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900
agccccgact ccacgctcct cgccacctgc tcggctgac agacgtgcaa gatctggagg
960
acgtccaact tctccctgat gacggagctg agcatcaaga gcggcaaccc cggggagtcc
1020

```

tccccgggct ggatgtgggg ctgcgccttc tggggggact cccagtagat cgtcactgct
 1080
 tctcgggaca acctggcccc gctctggtgt gtggagactg gagagatcaa gagagagtat
 1140
 ggccggccacc agaaggctgt tgtctgectg gccttcaatg acagtgtgct gggctagcct
 1200
 gtgacccttc gggactgcct ggtgcagggtg gtggcagctg gagggaccca tgcagcacc
 1260
 aggtcagagc agaccctccc ctgcggcctc gcgccagctg gacctgatgg cccctgtgg
 1320
 cgccttgacc tgctgggcca ggctgccctg ggaactctcag cccccagttg cttatccaga
 1380
 tgtgacagag ctgcacccaa gccaggctgc acactcctgg actgggctag cctgcactgc
 1440
 ctgggaaaagt cggccgaggg cccaaagctg ctgaggggtc tgaggctggt gccaccccc
 1500
 aagctagtgt gttctctgcc cctccctgcc cgcgtttcag ggctcggtc catagagaac
 1560
 accaccacca tggccagggtg gaaggggtta ttagtccctg ccagcagctg tctccctgg
 1620
 tgcaggtggc ctggccagcc cactggattg gggacgggcc aggtcgggcc aggtcggggg
 1680
 ctacgtctgg gaggaataa aagcagaccg acacgcagat gttgctcggg aagcagatgt
 1740
 cgatgcagag ataaatcagc cgctgtctcc ggggcccttc tgctgcggg gcccagtaga
 1800
 tgggggtcct catgcacagc cgctgcacca aagccccgc ctgggcggta gccacttacg
 1860
 aggtcccttc gcactgccag cagctcctgg gtgtggtggg tgctctggct ggggacccaa
 1920
 gcctcttggg ccttggaggt atccaccagc agccgcaggt ctcccgatca ctgtctcca
 1980
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 2040
 cgtcgaacag
 2050

<210> 2750

<211> 332

<212> PRT

<213> Homo sapiens

<400> 2750

Met Asn Thr Ser Pro Gly Thr Val Gly Ser Asp Pro Val Ile Leu Ala
 1 5 10 15
 Thr Ala Gly Tyr Asp His Thr Val Arg Phe Trp Gln Ala His Ser Gly
 20 25 30
 Ile Cys Thr Arg Thr Val Gln His Gln Asp Ser Gln Val Asn Ala Leu
 35 40 45
 Glu Val Thr Pro Asp Arg Ser Met Ile Ala Ala Ala Val Gln Pro Val
 50 55 60
 Ser Leu Gly Tyr Gln His Ile Arg Met Tyr Asp Leu Asn Ser Asn Asn
 65 70 75 80
 Pro Asn Pro Ile Ile Ser Tyr Asp Gly Val Asn Lys Asn Ile Ala Ser

	85		90		95
Val Gly Phe His Glu Asp Gly Arg Trp Met Tyr Thr Gly Gly Glu Asp					
	100		105		110
Cys Thr Ala Arg Ile Trp Asp Leu Arg Ser Arg Asn Leu Gln Cys Gln					
	115		120		125
Arg Ile Phe Gln Val Asn Ala Pro Ile Asn Cys Val Cys Leu His Pro					
	130		135		140
Asn Gln Ala Glu Leu Ile Val Gly Asp Gln Ser Gly Ala Ile His Ile					
	145		150		155
Trp Asp Leu Lys Thr Asp His Asn Glu Gln Leu Ile Pro Glu Pro Glu					
	165		170		175
Val Ser Ile Thr Ser Ala His Ile Asp Pro Asp Ala Ser Tyr Met Ala					
	180		185		190
Ala Val Asn Ser Thr Gly Asn Cys Tyr Val Trp Asn Leu Thr Gly Gly					
	195		200		205
Ile Gly Asp Glu Val Thr Gln Leu Ile Pro Lys Thr Lys Ile Pro Ala					
	210		215		220
His Thr Arg Tyr Ala Leu Gln Cys Arg Phe Ser Pro Asp Ser Thr Leu					
	225		230		235
Leu Ala Thr Cys Ser Ala Asp Gln Thr Cys Lys Ile Trp Arg Thr Ser					
	245		250		255
Asn Phe Ser Leu Met Thr Glu Leu Ser Ile Lys Ser Gly Asn Pro Gly					
	260		265		270
Glu Ser Ser Arg Gly Trp Met Trp Gly Cys Ala Phe Ser Gly Asp Ser					
	275		280		285
Gln Tyr Ile Val Thr Ala Ser Ser Asp Asn Leu Ala Arg Leu Trp Cys					
	290		295		300
Val Glu Thr Gly Glu Ile Lys Arg Glu Tyr Gly Gly His Gln Lys Ala					
	305		310		315
Val Val Cys Leu Ala Phe Asn Asp Ser Val Leu Gly					320
	325		330		

<210> 2751

<211> 1877

<212> DNA

<213> Homo sapiens

<400> 2751

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nntcatgagc cagcacaact gctccaagga tggccccacc tcgcagccac gcctgcgcac
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gctcccaccn ggccggagac agccaggagc gctcggacag ccccagagatc tgccattacg
120
agaagagcct tcacaagcac tcggccacc ccaactacac gcaactgtggc ctcttcgggg
180
accacacctt caggactttc accgaccgct tccagacctg caaggtgacg ggcgcctggc
240
cgctcatcga caataattac ctgaacgtgc aggtcaccac cagcctctgt ctgccagct
300
cagcggccac tgccaccagc aagetcacca tcatcttcaa gaacttcacg gagtgtgtgg
360
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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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Cys His Thr Val Val Pro Glu Lys Asp Gly Asp Asn Ile Ile Tyr Gln
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Gly Phe Val Phe Thr Ala Arg Thr Pro Phe Ser Val Ile Ile Glu Ala
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Met Gly Gln Glu Gln Thr Phe Gly Ile Leu Asn Val Leu Glu Phe Ser
100           105           110
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Ser Lys Asp Ser Lys Tyr Met Glu Glu Thr Leu Cys His Leu Glu Tyr
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Phe Ala Thr Glu Gly Leu Arg Thr Leu Cys Val Ala Tyr Ala Asp Leu
165           170           175
Ser Glu Gly Asn Glu Tyr Glu Glu Trp Leu Lys Val Tyr Gln Glu Ala
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Ser Thr Ile Leu Lys Asp Arg Ala Gln Arg Leu Glu Glu Cys Tyr Glu
195           200           205
Ile Ile Glu Lys Asn Leu Leu Leu Leu Gly Ala Thr Ala Ile Glu Asp
210           215           220
Arg Leu Gln Ala Gly Val Pro Glu Thr Ile Ala Thr Leu Leu Lys Ala
225           230           235           240
Glu Ile Lys Ile Trp Val Leu Thr Gly Asp Lys Gln Glu Thr Ala Ile
245           250           255
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275           280           285
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<211> 4795

<212> DNA

<213> Homo sapiens

<400> 2755

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<212> PRT

<213> Homo sapiens

<400> 2756

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100      105      110
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          485          490          495
Val Asp Cys Lys Lys Phe Ile Ser Glu Ile Ile Ser Ser Ser Arg Arg
          500          505          510
Ser Leu Val Leu Ala Asn Lys Arg Ala Arg Leu Lys Arg Lys Thr Gln
          515          520          525
Ser Phe Tyr Met Ser Ser Pro Gly Pro Ser Glu Tyr Cys Pro Ser Glu
          530          535          540
Arg Thr Ile Ser Glu Ile
545          550

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<210> 2757

<211> 449

<212> DNA

<213> Homo sapiens

<400> 2757

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120
ggttttaata gttttcagat gtttcaagtg ttgtgaacag agacttggtt ggattatgca
180
ttttctcagct agactaaata aatgctagca atggatacgt gcaaacatgt tgggcagctg
240
cagcttgctc aagaccattc cagcctcaac cctcagaaat ggcaactgtgt ggactgcaac
300
acgaccgagt ccatttgggc ttgccttagc tgctcccatg ttgccttggt aagatatatt
360
gaagagcatg cactcaagca ctttcaagaa agcagtcac ctgttgcatt ggagggtgaat
420
gagatgtacg ttttttgta ctttgtga
449

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<210> 2758

<211> 82

<212> PRT

<213> Homo sapiens

<400> 2758

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Met Leu Ala Met Asp Thr Cys Lys His Val Gly Gln Leu Gln Leu Ala
1          5          10          15
Gln Asp His Ser Ser Leu Asn Pro Gln Lys Trp His Cys Val Asp Cys
          20          25          30
Asn Thr Thr Glu Ser Ile Trp Ala Cys Leu Ser Cys Ser His Val Ala
          35          40          45
Cys Gly Arg Tyr Ile Glu Glu His Ala Leu Lys His Phe Gln Glu Ser

```

```

      50              55              60
Ser His Pro Val Ala Leu Glu Val Asn Glu Met Tyr Val Phe Cys Tyr
65              70              75              80
Leu Cys

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<210> 2759
<211> 688
<212> DNA
<213> Homo sapiens

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<400> 2759
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120
aaccgcccct acttccagcg gagacggcag caggccctcg gcccccagca ggcccctggc
180
ccccggcagc ccgcagcccc tgagacctca gcccctgtca acagtgggga ccccaccacc
240
accatcctgg agtgattcca actcaactca aaggacaccc agagctgcca tctggatatc
300
gccagttttt ccaaagtacc tgtaccctac ccagtaccct gctccccctt tcccataatt
360
catgacatca aaacatcagc ttttcacctt ttccttgaga ctcaggaggg ccaaagcaac
420
agcctttggc ttttttctct ttttcttccc tctcccctag catgggttga aggaagggag
480
ccatccttac tgttcagaga cagcaactcc ctcccgtaac tcaggctgag aaggaaccag
540
ccagctctta cctcctcctg gttgcttttc ttgccccac cccaagtta ttttgtttt
600
ccccggcccc cctacctctg aagccatttt atgatctgtc atgtgccacc tgagcctcca
660
gtaaaaaaca aaacaggaaa aaaaaaaaa
688

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<210> 2760
<211> 84
<212> PRT
<213> Homo sapiens

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<400> 2760
Tyr Arg Ser Pro Phe Arg Pro Arg Pro Arg Gln Gln Pro Thr Thr Glu
1      5      10      15
Gly Gly Asp Gly Glu Thr Lys Pro Ser Gln Gly Pro Ala Asp Gly Ser
20     25     30
Arg Pro Glu Pro Gln Arg Pro Arg Asn Arg Pro Tyr Phe Gln Arg Arg
35     40     45
Arg Gln Gln Ala Pro Gly Pro Gln Gln Ala Pro Gly Pro Arg Gln Pro
50     55     60
Ala Ala Pro Glu Thr Ser Ala Pro Val Asn Ser Gly Asp Pro Thr Thr
65     70     75     80
Thr Ile Leu Glu

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<210> 2761
 <211> 922
 <212> DNA
 <213> Homo sapiens

<400> 2761
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 60
 agtattgaac cagggggaat agacattacc cttagtagtt ctctttccca ggcgggtgat
 120
 cccataactg agggcaataa agagccagat aagacctggg tgaaaaaggg agagccccctc
 180
 ccggtaaaac tgaactcttc tacagaagca aatgtgatta aagaggctct agactcctct
 240
 ttggaatcta ctctggacaa cagctgtcaa ggtgcacaaa tggataataa atctgaagtt
 300
 cagttgtggc tgtaaagag aattcaggta ccattgaag atatacttcc ttcaaaagaa
 360
 gaaaaaagca agacccccacc catgttcctg tgcatacaag tgggaaaacc aatgagaaaa
 420
 tcctttgcc ctcacactgc agccatggtc cagcagtacg gcaaacggag aaagcagcca
 480
 gagtactggt ttgtgttcc tcgggagagg gtggatcatt tgtacacatt ctttgttcag
 540
 tgggtctccg atgtctatgg aaaagatgcc aaagagcaag gctttgtggt ggtggagaa
 600
 gaagaactga acatgattga caacttcttc agtgagccaa caaccaagag ctgggagatc
 660
 atcactgttg aagaggcaaa gcgcaggaag agcacatgca gctactatga agacgaggac
 720
 gaagagggtc tgcctgtcct ccggccccc agggcggtct gggagaataa gccctgaac
 780
 cgctgggccc gccctttcc tgcaagggtg caagggtatc catggagact ggcctatagc
 840
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 900
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 922

<210> 2762
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 2762
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 1 5 10 15
 Ser Asp Gly Lys Ser Ile Glu Pro Gly Gly Ile Asp Ile Thr Leu Ser
 20 25 30
 Ser Ser Leu Ser Gln Ala Gly Asp Pro Ile Thr Glu Gly Asn Lys Glu
 35 40 45
 Pro Asp Lys Thr Trp Val Lys Lys Gly Glu Pro Leu Pro Val Lys Leu


```

      50              55              60
Asn Ser Ser Thr Glu Ala Asn Val Ile Lys Glu Ala Leu Asp Ser Ser
65      70      75      80
Leu Glu Ser Thr Leu Asp Asn Ser Cys Gln Gly Ala Gln Met Asp Asn
      85      90      95
Lys Ser Glu Val Gln Leu Trp Leu Leu Lys Arg Ile Gln Val Pro Ile
      100      105      110
Glu Asp Ile Leu Pro Ser Lys Glu Lys Ser Lys Thr Pro Pro Met
      115      120      125
Phe Leu Cys Ile Lys Val Gly Lys Pro Met Arg Lys Ser Phe Ala Thr
      130      135      140
His Thr Ala Ala Met Val Gln Gln Tyr Gly Lys Arg Arg Lys Gln Pro
      145      150      155
Glu Tyr Trp Phe Ala Val Pro Arg Glu Arg Val Asp His Leu Tyr Thr
      160      165      170      175
Phe Phe Val Gln Trp Ser Pro Asp Val Tyr Gly Lys Asp Ala Lys Glu
      180      185      190
Gln Gly Phe Val Val Val Glu Lys Glu Glu Leu Asn Met Ile Asp Asn
      195      200      205
Phe Phe Ser Glu Pro Thr Thr Lys Ser Trp Glu Ile Ile Thr Val Glu
      210      215      220
Glu Ala Lys Arg Arg Lys Ser Thr Cys Ser Tyr Tyr Glu Asp Glu Asp
      225      230      235      240
Glu Glu Val Leu Pro Val Leu Arg Pro Pro Arg Ala Phe Trp Glu Asn
      245      250      255
Lys Pro Leu Asn Arg Trp Ala Arg Pro Phe Pro Ala Arg Val Gln Gly
      260      265      270
Tyr Pro Trp Arg Leu Ala Tyr Ser Thr Leu Glu His Gly Thr Ser Leu
      275      280      285
Lys Thr Leu Tyr Arg Lys Ser Ala Ser Leu Asp Ser Pro Val Leu Leu
      290      295      300
Val Ile Lys
305

```

<210> 2763

<211> 2210

<212> DNA

<213> Homo sapiens

<400> 2763

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gtgttttttt ttgtgcaaag aaagcttttt atttgagaac acctagatag ttttggaat
60
gttcttgttg gatcacaaac aacctaatgt acagtctatc gccaacatcc acaaacacag
120
caaacagtcg agtctctcag accacacagg gtacatctag aggggttctac ttgcattacc
180
cacacttcca ctctgtgtaa acaactgtct tgggcatgag aagggccagg ataggccagg
240
tgaatggcag gctgcccac aaccccaatc ccaaaccaac ctccaggccc atgggcccac
300
gtccctgcag gaagatgcta ataggtagaa caggtagaac atgtagacac aaacatttag
360
tttatttttt ctgactgtaa ccaaagtcag caaaagaac aacaaaactt cagtgcctta
420

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gaaatcctcc tggattcaat gacaacacat caatggccgg gcacagggtt ggattccttt
480
tatgaaatca ccttataatc tctcatcacc ccaggacagt gcctttttggg actgcatgaa
540
tctttaaatg ctacaccaca ttttctcacc cttaagtta tgacagacag gttatctctc
600
tccaagagca tcagggttaga tgctctttca ctcttaccaa ctgtcagggt gagggagaat
660
cacgacatca ttcataaata actgtggagt ctgggatgct ggctgaaggc atctccagga
720
aggactggag ggcgattttg ctaaagggtt gctcactgct catttcaactg catgccgctt
780
ttctcacttt ggttgggagt ttgaaggacc atgtaatcac agagattaga gctccctgtg
840
aaatcaatca ctgccttttag atctccacaa agacctgttc tccaatagca catgcgtttc
900
tctgtgagct gtattcgcat cagcgccgga gcctcagaaa gaatcgctgt ttacactctg
960
tactctccaa tgggtaatat ttatcataga aatctaatac atattcttca gcttgaatc
1020
caaacttctg gtacagtacc atagcggggt tgcttgctga gacgtgaagg gttacgtcct
1080
tgcccatgca ggtctgaatc agatgataga tcatgaaagt tgcaatccct gctcttctcc
1140
attcagggtg gcgaacaga aatgaaatgt aagcttcatt gtatttcaca tcaggaacca
1200
tgaagccaaa ggcaatgatg acttttttat aaagaacaac aacactgaag tctgggtact
1260
gcagacactc agacaggcca atgccaggcc aaaaaaactc ctgacacatg gagttgatcg
1320
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1380
agtgaagggt gctcctgtgc aggtgggaac gaatctgtga caggagctgc agtttgggtg
1440
gctttgtttc ataatacacc ctgatataag gtttcaagat ccgagaggta taagggtgga
1500
caataactctg gtccacagcc atattctctg atcctaccaa gcgatacaaa aacttggtgg
1560
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1620
agtctgtgca ggtggttctg tacgtggctt gtccagctgg aagtctgga atctcctctt
1680
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1740
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1800
tccgagcttc cggagtcag gcaacagcac cgggacaagc ttccagcctc ttgagcagca
1860
gcttttcttc gtagatgtcc acgggagtat acctgggctc ttctcgcttt gtgtcctctt
1920
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1980
cttcaactgc aatatccatc ctgtcgggtt tttctctctc actctctacc tctgtcttta
2040

tctgttcagc gcctctgacc ttctttctgc ccccaaccac tggcccagaa gctactgacc
 2100
 cagcaggggg tgggacgtac tccatccctg ggtctatgac tccatgcct tccatctcat
 2160
 cgtcatcatg aaacaaggct tgtgggggca tcacatctgg aatcagatct
 2210

<210> 2764

<211> 423

<212> PRT

<213> Homo sapiens

<400> 2764

Met	Pro	Pro	Gln	Ala	Leu	Phe	His	Asp	Asp	Asp	Glu	Met	Glu	Gly	Asp
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Gly	Val	Ile	Asp	Pro	Gly	Met	Glu	Tyr	Val	Pro	Pro	Pro	Ala	Gly	Ser
			20					25					30		
Val	Ala	Ser	Gly	Pro	Val	Val	Gly	Gly	Arg	Lys	Lys	Val	Arg	Gly	Pro
			35				40					45			
Glu	Gln	Ile	Lys	Gln	Glu	Val	Glu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Arg
			50			55					60				
Met	Asp	Ile	Asp	Ser	Glu	Asp	Thr	Asp	Ser	Asn	Thr	Ser	Leu	Gln	Thr
					70					75				80	
Arg	Ala	Arg	Glu	Lys	Arg	Lys	Pro	Gln	Leu	Glu	Lys	Asp	Thr	Lys	Pro
			85					90						95	
Lys	Glu	Pro	Arg	Tyr	Thr	Pro	Val	Ser	Ile	Tyr	Glu	Glu	Lys	Leu	Leu
			100					105					110		
Leu	Lys	Arg	Leu	Glu	Ala	Cys	Pro	Gly	Ala	Val	Ala	Met	Thr	Pro	Glu
			115				120					125			
Ala	Arg	Arg	Leu	Lys	Arg	Lys	Leu	Ile	Val	Arg	Gln	Ala	Lys	Arg	Asp
			130			135					140				
Arg	Gly	Leu	Pro	Leu	Phe	Asp	Leu	Asp	Gln	Val	Val	Asn	Ala	Ala	Leu
					150					155				160	
Leu	Leu	Val	Asp	Gly	Ile	Tyr	Gly	Ala	Lys	Glu	Gly	Gly	Ile	Ser	Arg
			165					170						175	
Leu	Pro	Ala	Gly	Gln	Ala	Thr	Tyr	Arg	Thr	Thr	Cys	Gln	Asp	Phe	Arg
			180					185					190		
Ile	Leu	Asp	Arg	Tyr	Gln	Thr	Ser	Leu	Pro	Ser	Arg	Lys	Gly	Phe	Arg
			195				200					205			
His	Gln	Thr	Thr	Lys	Phe	Leu	Tyr	Arg	Leu	Val	Gly	Ser	Glu	Asp	Met
			210			215					220				
Ala	Val	Asp	Gln	Ser	Ile	Val	Ser	Pro	Tyr	Thr	Ser	Arg	Ile	Leu	Lys
					230					235				240	
Pro	Tyr	Ile	Arg	Arg	Asp	Tyr	Glu	Thr	Lys	Pro	Pro	Lys	Leu	Gln	Leu
			245						250					255	
Leu	Ser	Gln	Ile	Arg	Ser	His	Leu	His	Arg	Ser	Asp	Pro	His	Trp	Thr
			260				265						270		
Pro	Glu	Pro	Asp	Ala	Pro	Leu	Asp	Tyr	Cys	Tyr	Val	Arg	Pro	Asn	His
			275				280					285			
Ile	Pro	Thr	Ile	Asn	Ser	Met	Cys	Gln	Glu	Phe	Phe	Trp	Pro	Gly	Ile
			290			295					300				
Asp	Leu	Ser	Glu	Cys	Leu	Gln	Tyr	Pro	Asp	Phe	Ser	Val	Val	Val	Leu
					310					315				320	
Tyr	Lys	Lys	Val	Ile	Ile	Ala	Phe	Gly	Phe	Met	Val	Pro	Asp	Val	Lys

```

          325          330          335
Tyr Asn Glu Ala Tyr Ile Ser Phe Leu Phe Val His Pro Glu Trp Arg
          340          345          350
Arg Ala Gly Ile Ala Thr Phe Met Ile Tyr His Leu Ile Gln Thr Cys
          355          360          365
Met Gly Lys Asp Val Thr Leu His Val Ser Ala Ser Asn Pro Ala Met
          370          375          380
Leu Leu Tyr Gln Lys Phe Gly Phe Lys Thr Glu Glu Tyr Val Leu Asp
          385          390          395          400
Phe Tyr Asp Lys Tyr Tyr Pro Leu Glu Ser Thr Glu Cys Lys His Ala
          405          410          415
Phe Phe Leu Arg Leu Arg Arg
          420

```

<210> 2765

<211> 582

<212> DNA

<213> Homo sapiens

<400> 2765

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120
agtggagggg caggatggca cggccacttg gggcttgggg gcgctccggc tgccgtaccg
180
tggctcgcaag cctaaaccgg gcttggggccc atcctgagca gccacagggtt tgttcagctc
240
ccggcttctg gccactcggc atcgccagag tctccaggcc agcacagggc cagcgatggc
300
aagtcacaaga agcaggcacc cgctgaccac cactgccccg atagttgcag aggccaggcc
360
agggggcgca ctgacctcca ggaaggcaga gaggttgtgc tgggagctgg ttgtgtccca
420
gcagagcaga ggcttctggc cagagcagtt gtctcggcgg atgtcgtgcc aggactccag
480
ggcacagttg cagtcggcct gcaggtcaag gtcacagcgg gcggccagcg ccccatccac
540
acgagacaag gggttgcgta gcacgttcag gacctcaagc tt
582

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<210> 2766

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2766

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Met Gly Arg Trp Pro Pro Ala Val Thr Leu Thr Cys Arg Pro Thr Ala
1          5          10          15
Thr Val Pro Trp Ser Pro Gly Thr Thr Ser Ala Glu Thr Thr Ala Leu
20          25          30
Ala Arg Ser Leu Cys Ser Ala Gly Thr Gln Pro Ala Pro Ser Thr Thr
35          40          45
Ser Leu Pro Ser Trp Arg Ser Ala Ala Pro Leu Ala Trp Pro Leu Gln

```

50		55		60	
Leu	Ser	Gly	Gln	Trp	Trp
65			70		75
Ser	Leu	Ala	Leu	Cys	Trp
		85		90	
Glu	Ala	Gly	Ser		
		100			

<210> 2767

<211> 1202

<212> DNA

<213> Homo sapiens

<400> 2767

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gaattcctca ttgataactg ctttgaaata ttgggggaga acattccagt gcattccagt
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120
gactcagcct acgacagcaa cgaccctgat gtggaatcca acagcagcag tggcatcagc
180
tctcccagca ggcagcccca ggtgcccatg gccacagctg ctggcttgga tagcgcgggc
240
ccacagagat cccgagaggt cagcccagag ccatttgtga gcaccgtggc caggctgaaa
300
agctccctcg cacagccga taggagatac tcagagccca gcatgccatc ctcccaggag
360
tgccctcgaga gccgggtgac aaaccaaaca ctaacaaaga gtgaagggga cttccccgtg
420
ccccgggtgag gctctcgttt ggaaagttag gaggtgaag acccatttcc agaggaggtc
480
ttccctcgag tgcaaggcaa aaccaagagg ccggtggacc tgaagatcaa gaacttggcc
540
ccgggttcgg tgctcccgcg ggcactgtgt ctcaaagcct tctccagcag ctgcgtggac
600
gcgtctctg acagctcgcc cgtggcttct cttccagtc ccaaaagaaa tttcttcagc
660
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720
cactccatgt ctttcacett tgccctcac aaaaagtgc tgacaaaaa cctcagcgcg
780
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840
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900
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960
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1020
ctagtgccct ccagcaatt tcaatttcta gcttgacact aaaaaggtaa tttttcagta
1080
acggggggag aagtggggag gcagagtgtg aagggaaata aaaccaatta gtaattttta
1140
actatcaaat gcactccagc aatcagtc aaacagggcc aggaacctg ttccaactta
1200

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ag
1202

<210> 2768
<211> 282
<212> PRT
<213> Homo sapiens

<400> 2768
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20 25 30
Ser Leu Ala Gln Pro Asp Arg Arg Tyr Ser Glu Pro Ser Met Pro Ser
35 40 45
Ser Gln Glu Cys Leu Glu Ser Arg Val Thr Asn Gln Thr Leu Thr Lys
50 55 60
Ser Glu Gly Asp Phe Pro Val Pro Arg Val Gly Ser Arg Leu Glu Ser
65 70 75 80
Glu Glu Ala Glu Asp Pro Phe Pro Glu Glu Val Phe Pro Ala Val Gln
85 90 95
Gly Lys Thr Lys Arg Pro Val Asp Leu Lys Ile Lys Asn Leu Ala Pro
100 105 110
Gly Ser Val Leu Pro Arg Ala Leu Val Leu Lys Ala Phe Ser Ser Ser
115 120 125
Ser Leu Asp Ala Ser Ser Asp Ser Ser Pro Val Ala Ser Pro Ser Ser
130 135 140
Pro Lys Arg Asn Phe Phe Ser Arg His Gln Ser Phe Thr Thr Lys Thr
145 150 155 160
Glu Lys Gly Lys Pro Ser Arg Glu Ile Lys Lys His Ser Met Ser Phe
165 170 175
Thr Phe Ala Pro His Lys Lys Val Leu Thr Lys Asn Leu Ser Ala Gly
180 185 190
Ser Gly Lys Ser Gln Asp Phe Thr Arg Asp His Val Pro Arg Gly Val
195 200 205
Arg Lys Glu Ser Gln Leu Ala Gly Arg Ile Val Gln Glu Asn Gly Cys
210 215 220
Glu Thr His Asn Gln Thr Ala Arg Gly Phe Cys Leu Arg Pro His Ala
225 230 235 240
Leu Ser Val Asp Asp Val Phe Gln Gly Ala Asp Trp Glu Arg Pro Gly
245 250 255
Ser Pro Pro Ser Tyr Glu Glu Ala Met Gln Gly Pro Ala Ala Arg Leu
260 265 270
Val Ala Ser Gln Gln Phe Gln Phe Leu Ala
275 280

<210> 2769
<211> 1286
<212> DNA
<213> Homo sapiens

<400> 2769
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 120
 ctggcgtctc tcccggctga acttatcaac cagattggga accgctgcca cccaagctc
 180
 tacgacagg ggcacccctc tgagaagctg gagctggtga caggcaccaa cgtgtacatc
 240
 acaagggcgc agctgatgaa ctgccacgtc agcgcaggca cgcggcacaa ggtctactg
 300
 cggcggctcc tggcctcctt ctttgaccgg aacacgctgg ccaacagctg cggcaccggc
 360
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 420
 gtcaagtact actgccagaa cttcgcccc aacttcaagg agagcgagat gaatgccatc
 480
 gcggccgaca tgtgcaccaa cgcccgccgc gtctgagcga agagctggat gcccaaggtc
 540
 aagggtgctca aggttgagga tgacgctac accaccttca tcagtgaac gggcaagatc
 600
 gagccgggaca tgatgggtgt ggagcatggc ttcgagaccg ccagccacga gggcgaggcg
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 720
 cctcccaaca cacacacaca cctgccatct tggctcatgag ctactgtctg tccctcccca
 780
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 1080
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 1140
 cttccacgtc tccaaaagcg ccttctctgc accctcgtct atccctgcgc ctgggggctg
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 1260
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 1286

<210> 2770

<211> 228

<212> PRT

<213> Homo sapiens

<400> 2770

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 1 5 10 15
 Ala Glu Lys Val Glu Ala Leu Pro Glu Gln Val Ala Pro Glu Ser Arg
 20 25 30
 Asn Arg Ile Arg Val Arg Gln Asp Leu Ala Ser Leu Pro Ala Glu Leu

```

      35              40              45
Ile Asn Gln Ile Gly Asn Arg Cys His Pro Lys Leu Tyr Asp Glu Gly
  50              55              60
Asp Pro Ser Glu Lys Leu Glu Leu Val Thr Gly Thr Asn Val Tyr Ile
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Thr Arg Ala Gln Leu Met Asn Cys His Val Ser Ala Gly Thr Arg His
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Lys Val Leu Leu Arg Arg Leu Leu Ala Ser Phe Phe Asp Arg Asn Thr
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Leu Ala Asn Ser Cys Gly Thr Gly Ile Arg Ser Ser Thr Asn Asp Pro
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Arg Arg Lys Pro Leu Asp Ser Arg Val Leu His Ala Val Lys Tyr Tyr
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Cys Gln Asn Phe Ala Pro Asn Phe Lys Glu Ser Glu Met Asn Ala Ile
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Ala Ala Asp Met Cys Thr Asn Ala Arg Arg Val Val Arg Lys Ser Trp
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Met Pro Lys Val Lys Val Leu Lys Ala Glu Asp Asp Ala Tyr Thr Thr
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Phe Ile Ser Glu Thr Gly Lys Ile Glu Pro Asp Met Met Gly Val Glu
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<210> 2771

<211> 1668

<212> DNA

<213> Homo sapiens

<400> 2771

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<211> 258

<212> PRT

<213> Homo sapiens

<400> 2772

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Phe	Ile	Asp	Arg	Pro	Ser	Thr	Tyr	Phe	Arg	Pro	Ile	Leu	Asp	Tyr	Leu
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Glu Thr Glu Glu Gln Asp Ala Tyr Tyr Ser Glu Val Leu Cys Phe Leu
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Gln Asp Lys Lys Met Phe Lys Ser Val Val Lys Phe Gly Pro Trp Lys
      195              200              205
Ala Val Leu Asp Asn Ser Asp Leu Met His Cys Leu Glu Met Asp Ile
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Lys Ala Gln Gly Tyr Lys Val Phe Ser Lys Phe Tyr Leu Thr Tyr Pro
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<210> 2773

<211> 593

<212> DNA

<213> Homo sapiens

<400> 2773

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<210> 2774

<211> 157

<212> PRT

<213> Homo sapiens

<400> 2774

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Glu Asp Ala Glu Glu Ser Leu Glu Glu Glu Glu Ala Leu Asp Pro Leu
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Lys Ala Lys Pro Ser Pro Arg Leu Thr Ile Phe Asp Glu Glu Val Asp
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Pro Asp Glu Gly Leu Phe Gly Pro Gly Arg Lys Leu Ser Pro Gln Asp
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Pro Asp Leu Gly Gly Ala Ile Pro Leu Gly Asp Ser Leu Leu Leu Pro
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<212> DNA

<213> Homo sapiens

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<211> 370

<212> PRT

<213> Homo sapiens

<400> 2776

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<211> 8625

<212> DNA

<213> Homo sapiens

<400> 2777

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<212> PRT

<213> Homo sapiens

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Asp Ser Cys Cys Ile Cys Ala Cys Asn Met Asn Ile Lys Gly Ala Asp
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Val Gly Leu Tyr Ile Pro Asp Ser Ser Asn Glu Asp Gln Tyr Arg Cys
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Gly Leu Phe Leu Glu Asp Glu Leu Asp Ile Phe Gly Lys Asn Ser Asp
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Leu Pro Gln Val Glu Gly Thr Lys Lys Pro Gln Glu Pro Pro Ile Ser
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	645	650	655	
Gly Pro Asp Asp Pro Leu His Lys Gln Pro Arg Phe Trp Ala Ser				
	660	665	670	
Met Met Glu Ala Ala Ser Cys Pro Pro Asp Tyr Val Pro Pro Glu Ile				
	675	680	685	
Phe His Phe His Thr Arg Ser Asp Val Arg Leu Tyr Gly Met Ile Tyr				
	690	695	700	
Lys Pro His Ala Leu Gln His Ile Thr Lys Lys Ser Thr Val Phe Glu				
705	710	715	720	

<210> 2781

<211> 1268

<212> DNA

<213> Homo sapiens

<400> 2781

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120
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180
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240
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300
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360
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420
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480
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540
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660
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720
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780
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840
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1020

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 1080
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 1140
 aattatattc aaaatgagcc aaagtgtcga gagaccttct atgacacatt agtgtcacat
 1200
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 1260
 aaaaaaaa
 1268

<210> 2782

<211> 314

<212> PRT

<213> Homo sapiens

<400> 2782

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Ile	Gly	Thr	Thr	Lys	Lys	Gly	Ile	Gly	Pro	Thr	Tyr	Ser	Ser	Lys	Ala
			20					25					30		
Ala	Arg	Thr	Gly	Leu	Arg	Ile	Cys	Asp	Leu	Leu	Ser	Asp	Phe	Asp	Glu
			35				40					45			
Phe	Ser	Ser	Arg	Phe	Lys	Asn	Leu	Ala	His	Gln	His	Gln	Ser	Met	Phe
			50			55				60					
Pro	Thr	Leu	Glu	Ile	Asp	Ile	Glu	Gly	Gln	Leu	Lys	Arg	Leu	Lys	Gly
65				70					75					80	
Phe	Ala	Glu	Arg	Ile	Arg	Pro	Met	Val	Arg	Asp	Gly	Val	Tyr	Phe	Met
			85					90						95	
Tyr	Glu	Ala	Leu	His	Gly	Pro	Pro	Lys	Lys	Ile	Leu	Val	Glu	Gly	Ala
			100					105					110		
Asn	Ala	Ala	Leu	Leu	Asp	Ile	Asp	Phe	Gly	Thr	Tyr	Pro	Phe	Val	Thr
			115			120						125			
Ser	Ser	Asn	Cys	Thr	Val	Gly	Gly	Val	Cys	Thr	Gly	Leu	Gly	Ile	Pro
			130			135				140					
Pro	Gln	Asn	Ile	Gly	Asp	Val	Tyr	Gly	Val	Val	Lys	Ala	Tyr	Thr	Thr
145				150				155						160	
Arg	Val	Gly	Ile	Gly	Ala	Phe	Pro	Thr	Glu	Gln	Ile	Asn	Glu	Ile	Gly
			165					170					175		
Gly	Leu	Leu	Gln	Thr	Arg	Gly	His	Glu	Trp	Gly	Val	Thr	Thr	Gly	Arg
			180					185					190		
Lys	Arg	Arg	Cys	Gly	Trp	Leu	Asp	Leu	Met	Ile	Leu	Arg	Tyr	Ala	His
			195			200						205			
Met	Val	Asn	Gly	Phe	Thr	Ala	Leu	Ala	Leu	Thr	Lys	Leu	Asp	Ile	Leu
			210			215				220					
Asp	Val	Leu	Gly	Glu	Val	Lys	Val	Gly	Val	Ser	Tyr	Lys	Leu	Asn	Gly
225				230				235						240	
Lys	Arg	Ile	Pro	Tyr	Phe	Pro	Ala	Asn	Gln	Glu	Met	Leu	Gln	Lys	Val
			245					250					255		
Glu	Val	Glu	Tyr	Glu	Thr	Leu	Pro	Gly	Trp	Lys	Ala	Asp	Thr	Thr	Gly
			260					265					270		
Ala	Arg	Arg	Trp	Glu	Asp	Leu	Pro	Pro	Gln	Ala	Gln	Asn	Tyr	Ile	Arg
			275			280							285		
Phe	Val	Glu	Asn	His	Val	Gly	Val	Ala	Val	Lys	Trp	Val	Gly	Val	Gly

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 Lys Ser Arg Glu Ser Met Ile Gln Leu Phe
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<210> 2783

<211> 2376

<212> DNA

<213> Homo sapiens

<400> 2783

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 120
 gttgatgtag aagattatta cccagctttc ctggacatgg tgcggagcct gctggatggc
 180
 aacatagact catcacagta tgaagattca ctgagagaga tgttcacat tcatgcctac
 240
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 300
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 420
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 480
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 1020
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 1380
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 1860
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 1920
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 1980
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 2040
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 2160
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 2280
 gaatacttaa gtcttttagt acgtgttttt ttcccttggt caaataatct gaaaatattt
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 2376

<210> 2784

<211> 361

<212> PRT

<213> Homo sapiens

<400> 2784

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 20 25 30
 Leu Arg Leu Lys Glu Pro Met Asp Val Asp Val Glu Asp Tyr Tyr Pro
 35 40 45
 Ala Phe Leu Asp Met Val Arg Ser Leu Leu Asp Gly Asn Ile Asp Ser
 50 55 60
 Ser Gln Tyr Glu Asp Ser Leu Arg Glu Met Phe Thr Ile His Ala Tyr
 65 70 75 80
 Ile Ala Phe Thr Met Asp Lys Leu Ile Gln Ser Ile Val Arg Gln Leu

85										90										95													
Gln	His	Ile	Val	Ser	Asp	Glu	Ile	Cys	Val	Gln	Val	Thr	Asp	Leu	Tyr																		
			100					105					110																				
Leu	Ala	Glu	Asn	Asn	Asn	Gly	Ala	Thr	Gly	Gly	Gln	Leu	Asn	Thr	Gln																		
		115					120					125																					
Asn	Ser	Arg	Ser	Leu	Leu	Glu	Ser	Thr	Tyr	Gln	Arg	Lys	Ala	Glu	Gln																		
		130				135					140																						
Leu	Met	Ser	Asp	Glu	Asn	Cys	Phe	Lys	Leu	Met	Phe	Ile	Gln	Ser	Gln																		
145				150					155				160																				
Gly	Gln	Val	Gln	Leu	Thr	Ile	Glu	Leu	Leu	Asp	Thr	Glu	Glu	Glu	Asn																		
			165					170					175																				
Ser	Asp	Asp	Pro	Val	Glu	Ala	Glu	Arg	Trp	Ser	Asp	Tyr	Val	Glu	Arg																		
		180						185					190																				
Tyr	Met	Asn	Ser	Asp	Thr	Thr	Ser	Pro	Glu	Leu	Arg	Glu	His	Leu	Ala																		
		195					200					205																					
Gln	Lys	Pro	Val	Phe	Leu	Pro	Arg	Asn	Leu	Arg	Arg	Ile	Arg	Lys	Cys																		
	210				215					220																							
Gln	Arg	Gly	Arg	Glu	Gln	Gln	Glu	Lys	Glu	Gly	Lys	Glu	Gly	Asn	Ser																		
225				230				235					240																				
Lys	Lys	Thr	Met	Glu	Asn	Val	Asp	Ser	Leu	Asp	Lys	Leu	Glu	Cys	Arg																		
		245						250					255																				
Phe	Lys	Leu	Asn	Ser	Tyr	Lys	Met	Val	Tyr	Val	Ile	Lys	Ser	Glu	Asp																		
		260					265					270																					
Tyr	Met	Tyr	Arg	Arg	Thr	Ala	Leu	Leu	Arg	Ala	His	Gln	Ser	His	Glu																		
	275					280					285																						
Arg	Val	Ser	Lys	Arg	Leu	His	Gln	Arg	Phe	Gln	Ala	Trp	Val	Asp	Lys																		
	290				295					300																							
Trp	Thr	Lys	Glu	His	Val	Pro	Arg	Glu	Met	Ala	Ala	Glu	Thr	Ser	Lys																		
305				310					315				320																				
Trp	Leu	Met	Gly	Glu	Gly	Leu	Glu	Gly	Leu	Val	Pro	Cys	Thr	Thr	Thr																		
		325						330					335																				
Cys	Asp	Thr	Glu	Thr	Leu	His	Phe	Val	Ser	Ile	Asn	Lys	Tyr	Arg	Val																		
		340					345					350																					
Lys	Tyr	Gly	Thr	Val	Phe	Lys	Ala	Pro																									
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<210> 2785

<211> 492

<212> DNA

<213> Homo sapiens

<400> 2785

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 120
 tgatgagatc ctccttcaca tcttgagtca cgtccccagc acagatctga tctgaaacgt
 180
 ccggcgtacc tgtcggaagc ttgcagccct gtgccttgac aagagcctca tccacaccgt
 240
 gttgctgcga aaggactatc aggcgagcga ggacaaagtg aggcagctgg tgaaggagat
 300
 cggccgggag atccagcagc tgagcatggc tggctgctac tggctgctgt gctccaccgt
 360

ggaacacgtg gcccgctgcc cgcagcctgg tgaaggtgaa cctctcgggc tgccacctca
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 480
 acgtgagccc cg
 492

<210> 2786
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 2786
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 Pro Ala Ala Ala Gly Met Ala Asp Gly Val His Leu Leu Gly Phe Ser
 20 25 30
 Asp Glu Ile Leu Leu His Ile Leu Ser His Val Pro Ser Thr Asp Leu
 35 40 45
 Ile Leu Asn Val Arg Arg Thr Cys Arg Lys Leu Ala Ala Leu Cys Leu
 50 55 60
 Asp Lys Ser Leu Ile His Thr Val Leu Leu Gln Lys Asp Tyr Gln Ala
 65 70 75 80
 Ser Glu Asp Lys Val Arg Gln Leu Val Lys Glu Ile Gly Arg Glu Ile
 85 90 95
 Gln Gln Leu Ser Met Ala Gly Cys Tyr Trp Leu Pro Gly Ser Thr Val
 100 105 110
 Glu His Val Ala Arg Cys Pro Gln Pro Gly Glu Gly Glu Pro Leu Gly
 115 120 125
 Leu Pro Pro His Phe Pro Ala Pro Leu Gln Asp Ala Leu Gly Pro Ala
 130 135 140
 Ala Pro Ala Leu Ala Gly His Arg Arg Glu Pro
 145 150 155

<210> 2787
 <211> 299
 <212> DNA
 <213> Homo sapiens

<400> 2787
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 120
 acaatgcaca gacatggcag tatcctctcg gtgggaggga gtcaccattt gctctgccct
 180
 gccctctgct ggggtgctctt acaggtgcta ctgcatccag cgcttgaaac aattctgtgg
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 299

<210> 2788
 <211> 95
 <212> PRT

<213> Homo sapiens

<400> 2788

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Met Thr Arg Asp Ser Gly Met Lys Gln Lys His Ala Ala Ser Thr Ser
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Met Trp Gly Glu Glu Pro Tyr Ser Asp Ile Ser Val Ala Lys Thr Arg
           20           25           30
Ala Gly His Ala Thr Met His Arg His Gly Ser Ile Leu Leu Val Gly
           35           40           45
Gly Ser His His Leu Leu Cys Pro Ala Leu Cys Trp Val Leu Leu Gln
           50           55           60
Val Leu Leu His Pro Ala Leu Glu Thr Ile Leu Trp Gly Ile Asp Ser
           65           70           75           80
Glu Glu Ile Thr Asp Gly Arg Asp Phe Leu Pro Gln Leu Thr Gln
           85           90           95

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<210> 2789

<211> 492

<212> DNA

<213> Homo sapiens

<400> 2789

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120
gcgaggccag gctgtgcagt ggggccagca ccagctgcag cttctcctcc agcagggtcca
180
ccctggactg cagcctctgc acttcttctc tcattgcact gtccactcct gcgggcagag
240
ccaggcgctg ggtcacggcc ggccggctcc ccaccacac cccagggtct cctcctgtc
300
cccagggaga ggcagagcca gaagactcag gcccaggcct ctgccacccc cgctgcctgc
360
ctggcgctgg ccagaggtct caggctatgc cgcctaagta cgctggggcg ggtggctctg
420
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tcggtccgaa tt
492

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<210> 2790

<211> 141

<212> PRT

<213> Homo sapiens

<400> 2790

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Arg Lys Ser Ala Arg Ser Gly Ser Arg Cys Gly Arg Ala Ala Gly Arg
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Ser Ala Pro Gly Gly Cys Arg Gly Pro Gly Ala His Ala Pro Val Pro
           20           25           30
Ala Arg Pro Gly Cys Ala Val Gly Pro Ala Pro Ala Ala Ser Pro
           35           40           45
Pro Ala Gly Pro Pro Trp Thr Ala Ala Ser Ala Leu Leu Pro Ser Leu

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50		55		60
His Cys Pro Leu Leu Arg Ala Glu Pro Gly Ala Gly Ser Arg Pro Ala				
65	70	75	80	
Gly Ser Pro Pro Thr Pro Pro Gly Leu Pro Pro Val Pro Arg Glu Arg				
	85	90	95	
Gln Ser Gln Lys Thr Gln Ala Gln Ala Ser Ala Thr Pro Ala Ala Cys				
	100	105	110	
Leu Ala Leu Ala Arg Gly Leu Arg Leu Cys Arg Leu Ser Thr Ser Gly				
	115	120	125	
Arg Val Ala Leu Arg Arg Gly Ser Gly Ser Arg Pro Arg				
130	135	140		

<210> 2791

<211> 1271

<212> DNA

<213> Homo sapiens

<400> 2791

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 120
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 180
 gtaagattat atccaaatat ttactcctgg ttgctcctct tgggcaagct gtgaatatga
 240
 tcaaaatatt taaagaagga agaaggtaaa gatctaaat atgacatgaa aatacccgaa
 300
 gaagtgtgcc taaattagca ttagggtttg agggatccta aggatgacaa aaagggactc
 360
 ttctattgaa ttcgtggttg atgctcagcg atagtaaciaa tcttgctccc cctaacatct
 420
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 480
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 540
 taatgttcac ttcactctgt gcttcttttc ctagatgtga actatgaaga ctttactttc
 600
 accataccag atgtagagga ctcaagtacg agaccagatc agggaccacca gagacctctc
 660
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 720
 cagagaccac caaaaccagg aggccatcac cgccatctc cccacctcc ttttcaaaat
 780
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 840
 agcctcgagg aagcatcatc attcttccgg agggacagac cagcaagaca tccccaggag
 900
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 1020
 attaatagca tgcggaagaa agaattggtt gcattccacat ggagagtgtg ccatttagag
 1080

gtaacaggga gaggagaggg tgtgccatca agaggcaaca tggaggtgtt tcaaacctat
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 gcatcttgtt ataaatatat ctttgctcac atgaatttta cttgttaatt agcctggctg
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 1271

<210> 2792
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 2792
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 20 25 30
 Gln Gly Pro Gln Arg Pro Pro Pro Glu Gly Leu Leu Pro Arg Pro Pro
 35 40 45
 Gly Asp Ser Gly Asn Gln Asp Asp Gly Pro Gln Gln Arg Pro Pro Lys
 50 55 60
 Pro Gly Gly His His Arg His Pro Pro Pro Pro Phe Gln Asn Gln
 65 70 75 80
 Gln Arg Pro Pro Gln Arg Gly His Arg Gln Leu Ser Leu Pro Arg Phe
 85 90 95
 Pro Ser Val Ser Leu Gln Glu Ala Ser Ser Phe Phe Arg Arg Asp Arg
 100 105 110
 Pro Ala Arg His Pro Gln Glu Gln Pro Leu Trp
 115 120

<210> 2793
 <211> 847
 <212> DNA
 <213> Homo sapiens

<400> 2793
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 120
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 180
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 240
 gaggcgccag aggagccgcc ttctgctca gaacggcggtg actcggagaa ttggagcgtt
 300
 attcagtata ttaatgtctt attgataatg gcagaacatc caccactact ggatacaact
 360
 cagatcttaa gtatgatat ttctcttttg tctgccctta ttgtaagtgc agatggaaca
 420
 caacaggtta ttctggtaca agttaaccca ggagaagcat ttacaataag aagagaagat
 480

ggacagtttc agtgcattac aggtcctgct cagggttccaa tgatgtcccc aaatggttct
 540
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 600
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 660
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 720
 caccacgtca tatgtactca cccgtgactg gagctggaga catgacaaca cagtatatgc
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 840
 cacgcgt
 847

<210> 2794
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 2794
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 1 5 10 15
 Asp Ile Ser Leu Leu Ser Ala Pro Ile Val Ser Ala Asp Gly Thr Gln
 20 25 30
 Gln Val Ile Leu Val Gln Val Asn Pro Gly Glu Ala Phe Thr Ile Arg
 35 40 45
 Arg Glu Asp Gly Gln Phe Gln Cys Ile Thr Gly Pro Ala Gln Val Pro
 50 55 60
 Met Met Ser Pro Asn Gly Ser Val Pro Pro Ile Tyr Val Pro Pro Gly
 65 70 75 80
 Tyr Ala Pro Gln Val Ile Glu Asp Asn Gly Val Arg Arg Val Val Val
 85 90 95
 Val Pro Gln Ala Pro Glu Phe His Pro Gly Ser His Thr Val Leu His
 100 105 110
 Arg Ser Pro His Pro Pro Leu Pro Gly Phe Ile Pro Val Pro Thr Met
 115 120 125
 Met Pro Pro His His Val Ile Cys Thr His Pro
 130 135

<210> 2795
 <211> 1022
 <212> DNA
 <213> Homo sapiens

<400> 2795
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 120
 gcctggcagc tgctggttgt ggaatagttc tggatgccaa tctctccag gctcctgcgg
 180
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 240

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 360
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 420
 ttcccagcca gattgctcca gtccttgtag atcacctgag tagaatccca gggatcctg
 480
 gattgagctt cagctgcctg cctctctagg agctgctggt tgagatcttc ttgtcccaag
 540
 gtagcagagg aagggtgtcag ttccatgtct ccaggggcca gtggggaaga ggctgaggtt
 600
 ctgagagcaa ggggatcttc atctgggtgc tcggcccccac tgggagctgt ggtttgaggg
 660
 aatgaagcca aggccggcac ctctcgtgc tggccagaca aaccagctgc tctgcagtg
 720
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 780
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 840
 gtgactgaag gcagcagcaa gctgggcccc atgctgctct ccacctcacc aggtgagnna
 900
 gaaaagtacac ggacctgagg ctggtcttct tcttgggac cattcacagc gagcagctcc
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 1020
 gt
 1022

<210> 2796
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2796
 Ala Ser Ala Ala Cys Pro Ser Arg Ser Cys Trp Leu Arg Ser Ser Cys
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 Pro Lys Val Ala Glu Glu Gly Val Ser Ser Met Ser Pro Gly Ala Ser
 20 25 30
 Gly Glu Glu Ala Glu Val Leu Glu Pro Arg Gly Ser Ser Ser Gly Cys
 35 40 45
 Ser Ala Pro Leu Gly Ala Val Val
 50 55

<210> 2797
 <211> 475
 <212> DNA
 <213> Homo sapiens

<400> 2797
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 120

ctgaactcca tcagcgagtc cccgcatgag cgcatgcacc cctacatcga gctggcctgg
 180
 ggcttctcca ccgtgcttgg catcctactc ttcttgcccg aggtgggtgct gctctgctgg
 240
 atcaagtctc tccccgtgga tgccccggcg cagcctggcc cccacctgg ccttggggagt
 300
 cacacggggt ggagggcgcg cctgggtgtec accatcatca tggtgccccg gggcctcatc
 360
 ttcgtgggtct tcacatcca cttctaccgc tccctgggtgc gccacaaaaa ggagcgccac
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<210> 2798

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2798

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 20 25 30
 Glu Ala Val Ser Asn Ile His Asn Leu Asn Ser Ile Ser Glu Ser Pro
 35 40 45
 His Glu Arg Met His Pro Tyr Ile Glu Leu Ala Trp Gly Phe Ser Thr
 50 55 60
 Val Leu Gly Ile Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp
 65 70 75 80
 Ile Lys Phe Leu Pro Val Asp Ala Arg Arg Gln Pro Gly Pro Pro Pro
 85 90 95
 Gly Pro Gly Ser His Thr Gly Trp Gln Ala Ala Leu Val Ser Thr Ile
 100 105 110
 Ile Met Val Pro Val Gly Leu Ile Phe Val Val Phe Thr Ile His Phe
 115 120 125
 Tyr Arg Ser Leu Val Arg His Lys Thr Glu Arg His Asn Arg Glu Ile
 130 135 140
 Glu Glu Leu His Lys Leu Lys Val Gln Leu Asp Gly His Glu
 145 150 155

<210> 2799

<211> 2872

<212> DNA

<213> Homo sapiens

<400> 2799

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 120
 gggcagccct tgagcttgac tcctctgggg ccagtctcta tcagaaaatg cctgaccagc
 180
 tcatgggtca tgtctccttt tttattctgc tgcattgatgg ttggagggtg cgaagacacc
 240

tctatggcca gcccgtaaca gcttgagatc tccagggagc aggccatcgc gctcctcaag
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gaccaggagc cgggggcctt catcatccgc gacagtcaact ccttccgagg cgcgtagggg
360
ctggccatga aggtgtcttc gccacctcca accatcatgc agcagaataa aaaaggagac
420
atgacccatg agctgggtcag gcattttctg atagagactg gccccagagg agtcaagctc
480
aagggctgcc ccaatgagcc aaacttcgga tcgctgtctg ccttgggtcta ccagcactcc
540
atcatcccat tggccctgcc ttgcaagctg gtcattccaa accgagaccc cacagatgaa
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720
tctaaagcca catctgagac gttggctgca gacccacgc cagctgccac catcgttcac
780
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840
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1080
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1320
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1380
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1860

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 1920
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 1980
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 2040
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 2160
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 2280
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 2460
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 ggcagaaggc ttgcacttgg gccaaagggc ctaagggtcca ctggacagtt gggaaaacac
 2580
 ctgaccacca tttaaggact ctaagccaga atggaaaatt caccaggact ccattcttaa
 2640
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 2700
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 2760
 aataggtaaa ttgacaagaa gtatttattg tttttccata ttgctttatt gccttctctg
 2820
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 2872

<210> 2800

<211> 294

<212> PRT

<213> Homo sapiens

<400> 2800

Met	Ser	Pro	Phe	Leu	Phe	Cys	Cys	Met	Met	Val	Gly	Gly	Gly	Glu	Asp
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Thr	Phe	Met	Ala	Ser	Pro	Tyr	Lys	Pro	Glu	Ile	Ser	Arg	Glu	Gln	Ala
			20						25				30		
Ile	Ala	Leu	Leu	Lys	Asp	Gln	Glu	Pro	Gly	Ala	Phe	Ile	Ile	Arg	Asp
			35				40					45			
Ser	His	Ser	Phe	Arg	Gly	Ala	Tyr	Gly	Leu	Ala	Met	Lys	Val	Ser	Ser
			50			55				60					
Pro	Pro	Pro	Thr	Ile	Met	Gln	Gln	Asn	Lys	Lys	Gly	Asp	Met	Thr	His
65				70					75					80	
Glu	Leu	Val	Arg	His	Phe	Leu	Ile	Glu	Thr	Gly	Pro	Arg	Gly	Val	Lys
				85				90						95	
Leu	Lys	Gly	Cys	Pro	Asn	Glu	Pro	Asn	Phe	Gly	Ser	Leu	Ser	Ala	Leu

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          100              105              110
Val Tyr Gln His Ser Ile Ile Pro Leu Ala Leu Pro Cys Lys Leu Val
          115              120              125
Ile Pro Asn Arg Asp Pro Thr Asp Glu Ser Lys Asp Ser Ser Gly Pro
          130              135              140
Ala Asn Ser Thr Ala Asp Leu Leu Lys Gln Gly Ala Ala Cys Asn Val
          145              150              155              160
Leu Phe Ile Asn Ser Val Asp Met Glu Ser Leu Thr Gly Pro Gln Ala
          165              170              175
Ile Ser Lys Ala Thr Ser Glu Thr Leu Ala Ala Asp Pro Thr Pro Ala
          180              185              190
Ala Thr Ile Val His Phe Lys Val Ser Ala Gln Gly Ile Thr Leu Thr
          195              200              205
Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His Tyr Pro Leu Asn Thr
          210              215              220
Val Thr Phe Cys Asp Leu Asp Pro Gln Glu Arg Lys Trp Met Lys Thr
          225              230              235              240
Glu Gly Gly Ala Pro Ala Lys Leu Phe Gly Phe Val Ala Arg Lys Gln
          245              250              255
Gly Ser Thr Thr Asp Asn Ala Cys His Leu Phe Ala Glu Leu Asp Pro
          260              265              270
Asn Gln Pro Ala Ser Ala Ile Val Asn Phe Val Ser Lys Val Met Leu
          275              280              285
Asn Ala Gly Gln Lys Arg
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<210> 2801

<211> 549

<212> DNA

<213> Homo sapiens

<400> 2801

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120
ttcagcacac cagtggggca gtgcctcgaa aaggcaacag atggctccct gcaaagtga
180
gattggacgt tgaatatgga gatctgtgac atcatcaatg agacggagga agggccaaa
240
gatgccattc gagccctgaa gaagcggctc aacgggaacc ggaactacag agagggtgat
300
ctggcattaa cagtgtgtga gacatgtgtg aagaactgtg gccaccgctt ccacatcctt
360
gtggccaacc gagatttcat cgacagtgtt ctggtcaaaa ttatatctcc caagaacaac
420
cctcccacca ttgtacagga caaagtgcct gctctgatcc aggcattggc tgatgccttt
480
cgaagcagtc ctgatctcac cggcgttggt cacatatatg aggagctgaa gaggaagg
540
gttgaattc
549

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<210> 2802

<211> 151

<212> PRT

<213> Homo sapiens

<400> 2802

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Met Glu Phe Leu Leu Gly Asn Pro Phe Ser Thr Pro Val Gly Gln Cys
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Leu Glu Lys Ala Thr Asp Gly Ser Leu Gln Ser Glu Asp Trp Thr Leu
 20              25              30
Asn Met Glu Ile Cys Asp Ile Ile Asn Glu Thr Glu Gly Pro Lys
 35              40              45
Asp Ala Ile Arg Ala Leu Lys Lys Arg Leu Asn Gly Asn Arg Asn Tyr
 50              55              60
Arg Glu Val Met Leu Ala Leu Thr Val Leu Glu Thr Cys Val Lys Asn
 65              70              75              80
Cys Gly His Arg Phe His Ile Leu Val Ala Asn Arg Asp Phe Ile Asp
 85              90              95
Ser Val Leu Val Lys Ile Ile Ser Pro Lys Asn Asn Pro Pro Thr Ile
100              105              110
Val Gln Asp Lys Val Leu Ala Leu Ile Gln Ala Trp Ala Asp Ala Phe
115              120              125
Arg Ser Ser Pro Asp Leu Thr Gly Val Val His Ile Tyr Glu Glu Leu
130              135              140
Lys Arg Lys Gly Val Glu Phe
145              150

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<210> 2803

<211> 459

<212> DNA

<213> Homo sapiens

<400> 2803

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nccatggcca cgctgggct ccagcagcat cagcagcccc caggaccggg gaggcacagg
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tgccccccac caccggagg agcagctcct gccctgttcc gggggatgac tgattctcct
120
ccgccagccg taggggtgtg gctgtccggg ctcacgggga cctgtctcc gagtcgttcg
180
tgcagcgtgt gtaccagccc ttcctcacca cctgcgacgg gcaccggggc tgcagcacct
240
accgcaatat gccagccgcc atgccggaac ggaggagct gtgtccagcc tggccgctgc
300
cgctgccctg caggatggcg ggggtgacct tgccagtcag atgtggacna gtgcaatgaa
360
ggaagaagtg cacaggctgc agtccagggg ggaacctgctg gaggagaagc tgcagctggg
420
actggcccca ctgcacagcc tggcctcgca ggcaactgga
459

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<210> 2804

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2804

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Xaa Met Ala Thr Pro Gly Leu Gln Gln His Gln Gln Pro Pro Gly Pro
 1           5           10           15
Gly Arg His Arg Trp Pro Pro Pro Gly Gly Ala Ala Pro Ala Pro
 20           25           30
Val Arg Gly Met Thr Asp Ser Pro Pro Ala Val Gly Cys Val Leu
 35           40           45
Ser Gly Leu Thr Gly Thr Leu Ser Pro Ser Arg Ser Cys Ser Val Cys
 50           55           60
Thr Ser Pro Ser Ser Pro Pro Ala Thr Gly Thr Gly Pro Ala Ala Pro
 65           70           75           80
Thr Ala Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln
 85           90           95
Pro Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 100          105          110
Ser Asp Val Asp Xaa Cys Asn Glu Gly Arg Ser Ala Glu Ala Ala Val
 115          120          125
Gln Gly Gly Pro Ala Gly Gly Glu Ala Ala Ala Gly Thr Gly Pro Thr
 130          135          140
Ala Gln Pro Gly Leu Ala Gly Thr Gly
 145          150

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<210> 2805

<211> 771

<212> DNA

<213> Homo sapiens

<400> 2805

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 120
gatctctgga atagctacca ggcaaagaaa aaaactatgg atgccaaaga tggccagaca
 180
atgaatgaga agcaactctt ccatggggaca gatgccggct ccgtgccaca cgtcaatcga
 240
aatggcttta accgcagcta tgccggaaaag aatgctgtgg catatggaaa gggaacctat
 300
tttgcgtgca atgccaatat ttctgccaat gatacgtact ccagaccaga tgcaaatggg
 360
agaaagcatg tgtattatgt gcgagtactt actggaatct atacacatgg aaatcattca
 420
ttaattgtgc ctccctcaaa gaacctctaa aatcctactg acctgtatga cactgtcaca
 480
gataatgtgc accatccaag ttattttgtg gcattttatg actaccaagc ataccagag
 540
taccttatta cgtttagaaa ataactctt ggtatccttc ccacaaaatt attctccatt
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tgtacatata tagttgtaaa acaagtttta gctttttttt ttaattcctc ttaacagatt
 660
tttctaatat ccaaggatca ttctttgtcg ctgcagtcag atctttcttc agcttctctt
 720
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 771

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<210> 2806
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 2806
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 20 25 30
 Lys Ile Glu Arg Ile Gln Asn Pro Asp Leu Trp Asn Ser Tyr Gln Ala
 35 40 45
 Lys Lys Lys Thr Met Asp Ala Lys Asn Gly Gln Thr Met Asn Glu Lys
 50 55 60
 Gln Leu Phe His Gly Thr Asp Ala Gly Ser Val Pro His Val Asn Arg
 65 70 75 80
 Asn Gly Phe Asn Arg Ser Tyr Ala Gly Lys Asn Ala Val Ala Tyr Gly
 85 90 95
 Lys Gly Thr Tyr Phe Ala Val Asn Ala Asn Tyr Ser Ala Asn Asp Thr
 100 105 110
 Tyr Ser Arg Pro Asp Ala Asn Gly Arg Lys His Val Tyr Tyr Val Arg
 115 120 125
 Val Leu Thr Gly Ile Tyr Thr His Gly Asn His Ser Leu Ile Val Pro
 130 135 140
 Pro Ser Lys Asn Pro Gln Asn Pro Thr Asp Leu Tyr Asp Thr Val Thr
 145 150 155 160
 Asp Asn Val His His Pro Ser Leu Phe Val Ala Phe Tyr Asp Tyr Gln
 165 170 175
 Ala Tyr Pro Glu Tyr Leu Ile Thr Phe Arg Lys
 180 185

<210> 2807
 <211> 1660
 <212> DNA
 <213> Homo sapiens

<400> 2807
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 120
 cccaggtgct cagggccgcc tgtgaatgca ggtgccttgt cccaacaga ggacatatta
 180
 atagggccat gatttcctgt tgccacaatt ttgccaaggc aggctggcac cagaacacca
 240
 aagaaggaaa attatagtgg agtagcagtt tgtgaatctg gagtccctgg ttcaatcaca
 300
 gaacaagtag ggagaggagc caggacctag gccttcagggt ttccagcaag gaaggactct
 360
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 420
 ctctgactct cggatagaaa ggcaggacaa tcggagcctg ggggttcacgt gagtcaggaa
 480

agggagctct ccacactgga atcgctgtag ccgaggagggt tctaattggga cgaatcttoga
 540
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 600
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 780
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 900
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 960
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 1200
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 1260
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 ccgtgacaaa atctcagcgg agaaagacac caaggaatct gtgaaattgt cactgagcag
 1380
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 1500
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 1560
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<210> 2808

<211> 390

<212> PRT

<213> Homo sapiens

<400> 2808

Met	Leu	Phe	Glu	Lys	Asp	Gly	Ser	Ser	Cys	Ile	Ser	Arg	Arg	Pro	Leu
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Glu	Leu	Ala	Gly	Cys	Ala	Ser	Cys	Leu	Thr	Val	Gln	Asp	Asn	Trp	Thr
			20					25					30		
Leu	Glu	Leu	Glu	Ser	Ser	Gln	Asp	Ile	Gln	Asp	Val	Leu	Asp	Ala	Asn
			35					40				45			
Lys	Ser	Leu	Pro	Glu	Ser	Ser	Leu	Thr	Asp	Leu	Leu	Ser	Asp	Asn	Phe

50	55	60
Thr Asp Ser Leu Val Ser	Phe Ser Ala Glu Ile	Leu Ser Arg Thr Leu
65	70	75
Cys Glu Pro Leu Val Ala	Ser Leu Trp Met Lys	Leu Gly Asn Thr Gly
85	90	95
Ala Met Arg Arg Cys Val	Lys Leu Thr Val Ala	Leu Glu Thr Ala Glu
100	105	110
Cys Glu Phe Pro Pro His	Leu Asp Val Tyr Ile	Glu Asp Pro His Leu
115	120	125
Pro Pro Ser Leu Gly Leu	Leu Pro Gly Ala Arg	Val His Phe Ser Gln
130	135	140
Leu Glu Lys Arg Val Ser	Arg Ser His Asn Val	Tyr Cys Cys Phe Arg
145	150	155
Ser Ser Thr Tyr Val Gln	Val Leu Ser Phe Pro	Glu Thr Thr Ile
165	170	175
Ser Val Pro Leu Pro His	Ile Tyr Leu Ala Glu	Leu Leu Gln Gly Gly
180	185	190
Gln Ser Pro Phe Gln Ala	Thr Ala Ser Cys His	Ile Val Ser Val Phe
195	200	205
Ser Leu Gln Leu Phe Trp	Val Cys Ala Tyr Cys	Thr Ser Ile Cys Arg
210	215	220
Gln Gly Lys Cys Thr Arg	Leu Gly Ser Thr Cys	Pro Thr Gln Thr Ala
225	230	235
Ile Ser Gln Ala Ile Ile	Arg Leu Leu Val Glu	Asp Gly Thr Ala Glu
245	250	255
Ala Val Val Thr Cys Arg	Asn His His Val Ala	Ala Ala Leu Gly Leu
260	265	270
Cys Pro Arg Glu Trp Ala	Ser Leu Leu Asp Phe	Val Gln Val Pro Gly
275	280	285
Arg Val Val Leu Gln Phe	Ala Gly Pro Gly Ala	Gln Leu Glu Ser Ser
290	295	300
Ala Arg Val Asp Glu Pro	Met Thr Met Phe Leu	Trp Thr Leu Cys Thr
305	310	315
Ser Pro Ser Val Leu Arg	Pro Ile Val Leu Ser	Phe Glu Leu Glu Arg
325	330	335
Lys Pro Ser Lys Ile Val	Pro Leu Glu Pro Pro	Arg Leu Gln Arg Phe
340	345	350
Gln Cys Gly Glu Leu Pro	Phe Leu Thr His Val	Asn Pro Arg Leu Arg
355	360	365
Leu Ser Cys Leu Ser Ile	Arg Glu Ser Glu Tyr	Ser Ser Ser Leu Gly
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<210> 2809

<211> 1502

<212> DNA

<213> Homo sapiens

<400> 2809

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<210> 2810

<211> 102

<212> PRT

<213> Homo sapiens

<400> 2810

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 Ala Cys Val Cys Ala Cys Val Arg Leu Cys Val Arg Leu Cys Ala Cys
 35 40 45
 Val Cys Ala Ser Val Cys Met Cys Ala Arg Ala Xaa Val Cys Val Cys
 50 55 60
 Thr Cys Val Xaa Leu Cys Thr Arg Val Cys Val Cys Val His Ala Cys
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<210> 2811

<211> 591

<212> DNA

<213> Homo sapiens

<400> 2811

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<210> 2812

<211> 131

<212> PRT

<213> Homo sapiens

<400> 2812

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 20 25 30
 Pro Ala Pro Ala Val Asp Glu Pro Gln Pro Xaa Ser Gln Ala Pro Pro

	35		40		45	
Gly	Pro	Arg	Val	Pro	Gly	Pro
50				55		60
Arg	Pro	Arg	Pro	Gly	Glu	Gly
65				70		75
Val	Pro	Gly	Ala	Thr	Glu	Met
				85		90
Pro	Pro	Gly	Pro	Thr	Gly	Arg
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Leu	Gly	Ser				
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<210> 2813

<211> 2417

<212> DNA

<213> Homo sapiens

<400> 2813

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1020

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<210> 2814

<211> 471

<212> PRT

<213> Homo sapiens

<400> 2814

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 35          40          45
Asp Glu Leu Val Glu Phe Gln Glu Gly Ser Arg Glu Leu Glu Ala Glu
 50          55          60
Leu Glu Ala Gln Leu Val Gln Ala Glu Gln Arg Asn Arg Asp Leu Gln
 65          70          75          80
Ala Asp Asn Gln Arg Leu Lys Tyr Glu Val Glu Ala Leu Lys Glu Lys
 85          90          95
Leu Glu His Gln Tyr Ala Gln Ser Tyr Lys Gln Val Ser Val Leu Glu
100          105          110
Asp Asp Leu Ser Gln Thr Arg Ala Ile Lys Glu Gln Leu His Lys Tyr
115          120          125
Val Arg Glu Leu Glu Gln Ala Asn Asp Asp Leu Glu Arg Ala Lys Arg
130          135          140
Ala Thr Ile Val Ser Leu Glu Thr Leu Asn Lys Leu Asn Gln Ala Ile
145          150          155          160
Glu Arg Asn Ala Phe Leu Glu Ser Glu Leu Asp Glu Lys Glu Ser Leu
165          170          175
Leu Val Ser Val Gln Arg Leu Lys Asp Glu Ala Arg Asp Leu Arg Gln
180          185          190
Glu Leu Ala Val Arg Glu Arg Gln Gln Glu Val Thr Arg Lys Ser Ala
195          200          205
Pro Ser Ser Pro Thr Leu Asp Cys Glu Lys Met Asp Ser Ala Val Gln
210          215          220
Ala Ser Leu Ser Leu Pro Ala Thr Pro Val Gly Lys Gly Thr Glu Asn
225          230          235          240
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245          250          255
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260          265          270
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275          280          285
Phe Ala Lys Asp Gln Ala Ser Arg Lys Ser Tyr Ile Ser Gly Asn Val
290          295          300
Asn Cys Gly Val Leu Asn Gly Asn Gly Thr Lys Phe Ser Arg Ser Gly
305          310          315          320
His Thr Ser Phe Phe Asp Lys Gly Ala Val Asn Gly Phe Asp Pro Ala
325          330          335
Pro Pro Pro Pro Gly Leu Gly Ser Ser Arg Pro Ser Ser Ala Pro Gly
340          345          350
Met Cys Leu Ser Val Cys Glu Cys Leu Ala Ser Arg Gly Ala Pro Ala
355          360          365
Leu Leu Gln Gln Pro Arg Thr Pro Thr Pro His Pro Ser Val Pro Gly
370          375          380
Pro Ser Pro Val Pro Leu Arg Leu Pro Pro His Gly Trp Gln Arg Ala
385          390          395          400
Gly Cys Met Gln Trp Arg Leu Leu Gly Pro Ala Gln Pro Arg Asn Ser
405          410          415
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Ile	Thr	Trp	Ser	Leu	Asp	Ala	Glu	Val	Pro	Ile	His	His	Thr	Cys	Pro
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<210> 2815

<211> 1421

<212> DNA

<213> Homo sapiens

<400> 2815

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<210> 2816

<211> 307

<212> PRT

<213> Homo sapiens

<400> 2816

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			20					25					30		
Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	Gln	Arg	Val
		35					40				45				
Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	Ala	Cys	Ser	Thr
	50				55					60					
Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser	Pro	Gly	Leu	Ala
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Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln	Pro	Pro	Cys	Arg
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Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly
		115				120					125				
Trp	Arg	Gly	Asp	Thr	Cys	Gln	Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg
	130				135					140					
Arg	Gly	Gly	Cys	Pro	Gln	Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp
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			165					170					175		
Val	Pro	Lys	Gly	Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val
		180						185				190			
Asp	Ser	Ala	Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp
		195				200					205				
Leu	Leu	Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu
	210				215					220					
Ala	Ser	Gln	Ala	Gly	Ala	Trp	Ala	Pro	Gly	Pro	Arg	Gln	Pro	Pro	Gly
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	260						265					270			
Xaa	Asp	Cys	Pro	Ala	Pro	Gln	Ala	Gly	Leu	Ser	Pro	Ser	Arg	Arg	Pro
	275					280						285			
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<210> 2817
 <211> 219
 <212> DNA
 <213> Homo sapiens

<400> 2817
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<210> 2818
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 2818
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 Pro Gly Ala Ser Leu Gly Pro Gly Val Leu Leu Arg Ala Glu Phe His
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 Gln His Thr Phe Ala Pro Phe Thr Arg
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<210> 2819
 <211> 730
 <212> DNA
 <213> Homo sapiens

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<210> 2820

<211> 195

<212> PRT

<213> Homo sapiens

<400> 2820

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		20						25					30		
Ser	Ala	Gly	Ala	Arg	Gly	His	Thr	Gly	Pro	Lys	Gly	Gln	Lys	Gly	Ser
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Met	Gly	Ala	Pro	Gly	Glu	Arg	Cys	Lys	Ser	His	Tyr	Ala	Ala	Phe	Ser
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Val	Gly	Arg	Glu	Ala	His	Ala	Gln	Gln	Pro	Leu	Leu	Pro	Asp	Val	Ile
65					70					75				80	
Phe	Asp	Thr	Glu	Phe	Val	Asn	Leu	Tyr	Asp	His	Phe	Asn	Met	Phe	Thr
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			100					105					110		
Val	His	Thr	Trp	Asn	Gln	Lys	Glu	Thr	Tyr	Leu	His	Ile	Met	Lys	Asn
			115				120					125			
Glu	Glu	Glu	Val	Val	Ile	Leu	Phe	Ala	Gln	Val	Gly	Asp	Arg	Ser	Ile
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Glu	Leu	Asp	Thr	Tyr	Ile	Thr	Phe	Ser	Gly	Tyr	Leu	Val	Lys	His	Ala
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			195												

<210> 2821

<211> 1746

<212> DNA

<213> Homo sapiens

<400> 2821

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360
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420
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480
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<210> 2822

<211> 424

<212> PRT

<213> Homo sapiens

<400> 2822

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			20					25					30		
Leu	Ser	Asn	Ile	Ile	Asn	Lys	Leu	Leu	Glu	Thr	Lys	Asn	Glu	Leu	His
		35					40					45			
Lys	His	Val	Glu	Phe	Asp	Phe	Leu	Ile	Lys	Gly	Gln	Phe	Leu	Arg	Met
	50					55				60					
Pro	Leu	Asp	Lys	His	Met	Glu	Met	Glu	Asp	Ile	Ser	Ser	Glu	Glu	Val
65					70				75					80	
Val	Glu	Ile	Glu	Tyr	Val	Glu	Lys	Tyr	Thr	Ala	Pro	Gln	Pro	Glu	Gln
				85					90					95	
Cys	Met	Phe	His	Asp	Asp	Trp	Ile	Ser	Ser	Ile	Lys	Gly	Ala	Glu	Glu
			100					105					110		
Trp	Ile	Leu	Thr	Gly	Ser	Tyr	Gly	Lys	Thr	Ser	Arg	Ile	Trp	Ser	Leu
		115					120					125			
Glu	Gly	Lys	Ser	Ile	Met	Thr	Ile	Val	Gly	His	Thr	Asp	Val	Val	Lys
	130					135				140					
Asp	Val	Ala	Trp	Val	Lys	Lys	Asp	Ser	Leu	Ser	Cys	Leu	Leu	Xaa	Glu
145					150				155					160	
Cys	Phe	Tyr	Gly	Ser	Asp	Tyr	Ser	Leu	Met	Gly	Val	Glu	Cys	Arg	Glu
				165				170						175	
Lys	Gln	Ser	Glu	Ser	Pro	Thr	Leu	Leu	Xaa	Arg	Gly	His	Ala	Gly	Ser
		180					185						190		
Val	Asp	Ser	Ile	Ala	Val	Asp	Gly	Ser	Gly	Thr	Lys	Phe	Cys	Ser	Gly
		195					200					205			
Ser	Trp	Asp	Lys	Met	Leu	Lys	Ile	Trp	Ser	Thr	Val	Pro	Thr	Asp	Glu
	210				215					220					
Glu	Asp	Glu	Met	Glu	Glu	Ser	Thr	Asn	Arg	Pro	Arg	Lys	Lys	Gln	Lys
225					230				235					240	
Thr	Glu	Gln	Leu	Gly	Leu	Thr	Arg	Thr	Pro	Ile	Val	Thr	Leu	Ser	Gly
			245						250					255	
His	Met	Glu	Ala	Val	Ser	Ser	Val	Leu	Trp	Ser	Asp	Ala	Glu	Glu	Ile
		260						265					270		
Cys	Ser	Ala	Ser	Trp	Asp	His	Thr	Ile	Arg	Val	Trp	Asp	Val	Glu	Ser
	275					280						285			
Gly	Ser	Leu	Lys	Ser	Thr	Leu	Thr	Gly	Asn	Lys	Val	Phe	Asn	Cys	Ile
	290					295				300					
Ser	Tyr	Ser	Pro	Leu	Cys	Lys	Arg	Leu	Ala	Ser	Gly	Ser	Thr	Asp	Arg
305					310				315					320	
His	Ile	Arg	Leu	Trp	Asp	Pro	Arg	Thr	Lys	Asp	Gly	Ser	Leu	Val	Ser
			325					330					335		
Leu	Ser	Leu	Thr	Ser	His	Thr	Gly	Trp	Val	Thr	Ser	Val	Lys	Trp	Ser


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          340          345          350
Pro Thr His Glu Gln Gln Leu Ile Ser Gly Ser Leu Asp Asn Ile Val
      355          360          365
Lys Leu Trp Asp Thr Arg Ser Cys Lys Ala Pro Leu Tyr Asp Leu Ala
      370          375          380
Ala His Glu Asp Lys Val Leu Ser Val Asp Trp Thr Asp Thr Gly Leu
      385          390          395          400
Leu Leu Ser Gly Gly Ala Asp Asn Lys Leu Tyr Ser Tyr Arg Tyr Ser
          405          410          415
Pro Thr Thr Ser His Val Gly Ala
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<210> 2823

<211> 461

<212> DNA

<213> Homo sapiens

<400> 2823

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180
cagccggaga agctggccct gtgtgggcct gggcctgtag ggtttccag tggttttgcg
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300
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360
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<210> 2824

<211> 81

<212> PRT

<213> Homo sapiens

<400> 2824

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Asp Gln Val Pro Ser Ser Ser Leu Ala Pro Gln Ser His Trp Glu Thr
      20          25          30
Leu Gln Ala Gln Ala His Thr Gly Pro Ala Ser Pro Ala Ala Leu Pro
      35          40          45
Lys Gly Asp Ala Cys Asp Cys Val Cys Leu Pro Thr Gly Val Thr Thr
      50          55          60
His Pro Arg Pro Pro Glu Pro Gln His Glu Gly Ser Ala Pro Phe Pro
      65          70          75          80
His

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<210> 2825
 <211> 1520
 <212> DNA
 <213> Homo sapiens

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 120
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 180
 gcagattcat ttgaatctcc attgacgcta gctgctgtg gaggacatgt tgaattggca
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 360
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 420
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 480
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 540
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 720
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 780
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 840
 gaccatactg tactgtccct ggcttgtgca gggggtcac tgccagtggg ggaactactt
 900
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 1020
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 1080
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<210> 2826

<211> 506

<212> PRT

<213> Homo sapiens

<400> 2826

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			20					25					30		
Thr	Ala	Leu	Met	Glu	Ala	Cys	Met	Asp	Gly	His	Val	Glu	Val	Ala	Arg
		35					40					45			
Leu	Leu	Leu	Asp	Ser	Gly	Ala	Gln	Val	Asn	Met	Pro	Ala	Asp	Ser	Phe
	50					55					60				
Glu	Ser	Pro	Leu	Thr	Leu	Ala	Ala	Cys	Gly	Gly	His	Val	Glu	Leu	Ala
65					70					75				80	
Ala	Leu	Leu	Ile	Glu	Arg	Gly	Ala	Asn	Leu	Glu	Glu	Val	Asn	Asp	Glu
				85					90					95	
Gly	Tyr	Thr	Pro	Leu	Met	Glu	Ala	Ala	Arg	Glu	Gly	His	Glu	Glu	Met
			100					105					110		
Val	Ala	Leu	Leu	Leu	Ser	Thr	Arg	Ser	Xaa	Ile	Ser	Met	His	Arg	Gln
		115					120					125			
Lys	Lys	Leu	Lys	Lys	Leu	Leu	Leu	Thr	Leu	Ala	Cys	Cys	Gly	Gly	Phe
	130					135						140			
Leu	Glu	Val	Ala	Asp	Phe	Leu	Ile	Lys	Ala	Gly	Ala	Asp	Ile	Glu	Leu
145				150						155				160	
Gly	Cys	Ser	Thr	Pro	Leu	Met	Glu	Ala	Ala	Gln	Glu	Gly	His	Leu	Glu
				165					170					175	
Leu	Val	Lys	Tyr	Leu	Leu	Ala	Ala	Gly	Ala	Asn	Val	His	Ala	Thr	Thr
		180						185					190		
Ala	Thr	Gly	Asp	Thr	Ala	Leu	Thr	Tyr	Ala	Cys	Glu	Asn	Gly	His	Thr
		195					200					205			
Asp	Val	Ala	Asp	Val	Leu	Leu	Gln	Ala	Gly	Ala	Asp	Leu	Asp	Lys	Gln
	210					215					220				
Glu	Asp	Met	Lys	Thr	Ile	Leu	Glu	Gly	Ile	Asp	Pro	Ala	Lys	His	Leu
225					230					235				240	
Glu	His	Glu	Ser	Glu	Gly	Gly	Arg	Thr	Pro	Leu	Met	Lys	Ala	Ala	Arg
				245					250					255	
Ala	Gly	His	Val	Cys	Thr	Val	Gln	Phe	Leu	Ile	Ser	Lys	Gly	Ala	Asn
		260						265					270		
Val	Asn	Arg	Thr	Thr	Ala	Asn	Asn	Asp	His	Thr	Val	Leu	Ser	Leu	Ala
		275					280						285		
Cys	Ala	Gly	Gly	His	Leu	Ala	Val	Val	Glu	Leu	Leu	Leu	Ala	His	Gly
	290					295					300				
Ala	Asp	Pro	Thr	His	Arg	Leu	Lys	Asp	Gly	Ser	Thr	Met	Leu	Ile	Glu
305					310					315				320	
Ala	Ala	Lys	Gly	Gly	His	Thr	Ser	Val	Val	Cys	Tyr	Leu	Leu	Asp	Tyr
				325					330					335	
Pro	Asn	Asn	Leu	Leu	Ser	Ala	Pro	Pro	Pro	Asp	Val	Thr	Gln	Leu	Thr

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Pro Pro Ser His Asp Leu Asn Arg Ala Pro Arg Val Pro Val Gln Ala
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Leu Pro Met Val Val Pro Pro Gln Glu Pro Asp Lys Pro Pro Ala Asn
   370              375              380
Val Ala Thr Thr Leu Pro Ile Arg Asn Lys Ala Ala Ser Lys Gln Lys
   385              390              395
Ser Ser Ser His Leu Pro Ala Asn Ser Gln Asp Val Gln Gly Tyr Ile
   405              410              415
Thr Asn Gln Ser Pro Glu Ser Ile Val Glu Glu Ala Gln Gly Lys Leu
   420              425              430
Thr Glu Leu Glu Gln Arg Ile Lys Glu Ala Ile Glu Lys Asn Ala Gln
   435              440              445
Leu Gln Ser Leu Glu Leu Ala His Ala Asp Gln Leu Thr Lys Glu Lys
   450              455              460
Ile Glu Glu Leu Asn Lys Thr Arg Glu Glu Gln Ile Gln Lys Lys Gln
   465              470              475
Lys Ile Leu Glu Glu Leu Gln Lys Val Glu Arg Glu Leu Gln Leu Lys
   485              490              495
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<210> 2827

<211> 481

<212> DNA

<213> Homo sapiens

<400> 2827

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180
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300
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481

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<210> 2828

<211> 160

<212> PRT

<213> Homo sapiens

<400> 2828

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Arg Glu Ala Ala Ala Ala Ala Gly Asp Ala Ser Glu Asp Ser Asp Ala

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Leu Tyr Pro Gly Gly Cys Gln Gln Leu Leu His Leu Cys Val Gln Gln	35	40	45
Pro Leu Gln Leu Leu Gln Val Glu Phe Leu Arg Leu Asn Thr His Glu	50	55	60
Asp Pro Gln Leu Leu Glu Ala Thr Leu Ala Gln Leu Pro Gln Asn Leu	65	70	75
Ser Cys Leu Arg Ser Leu Val Leu Lys Arg Gly Gln Arg Arg Asp Thr	85	90	95
Leu Gly Ala Cys Leu Arg Gly Ala Leu Thr Asn Leu Pro Ala Gly Leu	100	105	110
Ser Gly Leu Ala His Leu Ala His Leu Asp Leu Ser Phe Asn Ser Leu	115	120	125
Glu Thr Leu Pro Ala Cys Val Leu Gln Met Arg Gly Leu Gly Ala Leu	130	135	140
Leu Leu Ser His Asn Cys Leu Ser Glu Leu Pro Glu Ala Leu Gly Ala	145	150	155
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<210> 2829

<211> 3648

<212> DNA

<213> Homo sapiens

<400> 2829

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<210> 2830

<211> 668

<212> PRT

<213> Homo sapiens

<400> 2830

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<210> 2831

<211> 3986

<212> DNA

<213> Homo sapiens

<400> 2831

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 <213> Homo sapiens

<400> 2832

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Val Pro Val Ile Ala Lys Ala Asp Thr Leu Thr Leu Glu Glu Arg Val
      465              470              475              480
His Phe Lys Gln Arg Ile Thr Ala Asp Leu Leu Ser Asn Gly Ile Asp
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Val Tyr Pro Gln Lys Glu Phe Asp Glu Asp Ser Glu Asp Arg Leu Val
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Asn Glu Lys Phe Arg Glu Met Ile Pro Phe Ala Val Val Gly Ser Asp
      515              520              525
His Glu Tyr Gln Val Asn Gly Lys Arg Ile Leu Gly Arg Lys Thr Lys
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Trp Gly Thr Ile Glu Val Glu Asn Thr Thr His Cys Glu Phe Ala Tyr
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Leu Arg Asp Leu Leu Ile Arg Thr His Met Gln Asn Ile Lys Asp Ile
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 Gly Arg Gly Ala Ala Thr Gly Gly Arg Gln Gly Gly Arg Phe Asp Thr
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 <212> DNA
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<210> 2837

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<212> DNA

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<210> 2838

<211> 370

<212> PRT

<213> Homo sapiens

<400> 2838

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Ser	Glu	Glu	Glu	Glu	Ala	Asn	Tyr	Trp	Lys	Asp	Leu	Ala	Met	Thr	Tyr
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Lys	Gln	Arg	Ala	Glu	Asn	Thr	Gln	Glu	Glu	Leu	Arg	Glu	Phe	Gln	Glu
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Gly	Ser	Arg	Glu	Tyr	Glu	Ala	Glu	Leu	Glu	Thr	Gln	Leu	Gln	Gln	Ile
					70					75				80	
Glu	Thr	Arg	Asn	Arg	Asp	Leu	Leu	Ser	Glu	Asn	Asn	Arg	Leu	Arg	Met
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Glu	Leu	Glu	Thr	Ile	Lys	Glu	Lys	Phe	Glu	Val	Gln	His	Ser	Glu	Gly
			100						105					110	
Tyr	Arg	Gln	Ile	Ser	Ala	Leu	Glu	Asp	Asp	Leu	Ala	Gln	Thr	Lys	Ala


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      115              120              125
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Phe Glu Gln Arg Leu Asn Gln Ala Ile Glu Arg Asn Ala Phe Leu Glu
      165              170              175
Ser Glu Leu Asp Glu Lys Glu Asn Leu Glu Ser Val Gln Arg Leu
      180              185              190
Lys Asp Glu Ala Arg Asp Leu Arg Gln Glu Leu Ala Val Gln Gln Lys
      195              200              205
Gln Glu Lys Pro Arg Thr Pro Met Pro Ser Ser Val Glu Ala Glu Arg
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Thr Asp Thr Ala Val Gln Ala Thr Gly Ser Val Pro Ser Thr Pro Ile
      225              230              235
Ala His Arg Gly Pro Ser Ser Ser Leu Asn Thr Pro Gly Ser Phe Arg
      245              250              255
Arg Gly Leu Asp Asp Xaa His Arg Gly Thr Pro Leu Thr Pro Ala Ala
      260              265              270
Arg Ile Ser Ala Leu Asn Ile Val Gly Asp Leu Leu Arg Lys Val Gly
      275              280              285
Ala Leu Glu Ser Lys Leu Ala Ser Cys Arg Asn Leu Val Tyr Asp Gln
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Ser Pro Asn Arg Thr Gly Gly Pro Ala Ser Gly Arg Ser Ser Lys Asn
      305              310              315
Arg Asp Gly Gly Glu Arg Arg Pro Ser Ser Thr Ser Val Pro Leu Gly
      325              330              335
Asp Lys Gly Ser Val Pro Ser Asn Lys Pro Leu Ala Gly Gly Glu Asn
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<210> 2839

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<212> DNA

<213> Homo sapiens

<400> 2839

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420

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 35 40 45
 Pro Tyr Gln Pro Asn Glu Tyr Leu Lys Ala Leu Val Ala Val Gly Glu
 50 55 60
 Ile Cys Gln Asp Tyr Asp Ser Asp Lys Met Phe Pro Ala Phe Gly Phe
 65 70 75 80
 Gly Ala Arg Ile Pro Pro Glu Tyr Thr Val Ser His Asp Phe Ala Ile
 85 90 95
 Asn Phe Asn Glu Asp Asn Pro Glu Cys Ala Gly Ile Gln Gly Val Val
 100 105 110
 Glu Ala Tyr Gln Ser Cys Leu Pro Lys Leu Gln Leu Tyr Gly Pro Thr
 115 120 125
 Asn Ile Ala Pro Ile Ile Gln Lys Val Ala Lys Ser Ala Ser Glu Glu
 130 135 140
 Thr Asn Thr Lys Glu Ala Ser Gln Tyr Phe Ile Leu Leu Ile Leu Thr
 145 150 155 160
 Asp Gly Val Ile Thr Asp Met Gly Asp Thr Arg Glu Ala Ile Val His
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 Ala Ser His Leu Pro Met Ser Val Ile Ile Val Gly Val Gly Asn Ala
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 Asp Phe Ser Asp Met Gln Met Leu Asp Gly
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<210> 2841
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 <212> DNA
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<210> 2842

<211> 540

<212> PRT

<213> Homo sapiens

<400> 2842

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 35 40 45
 Cys Lys Ser Glu Pro Pro Leu Leu Arg Thr Ser Lys Arg Thr Ile Tyr
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 Thr Ala Gly Arg Pro Pro Trp Tyr Asn Glu His Gly Thr Gln Ser Lys
 65 70 75 80
 Glu Ala Phe Ala Ile Gly Leu Gly Gly Gly Ser Ala Ser Gly Lys Thr
 85 90 95
 Thr Val Ala Arg Met Ile Ile Glu Ala Leu Asp Val Pro Trp Val Val
 100 105 110
 Leu Leu Ser Met Asp Ser Phe Tyr Lys Val Leu His Ser Leu Pro His
 115 120 125
 Gln Val Leu Thr Glu Gln Gln Gln Glu Gln Ala Ala His Asn Asn Phe
 130 135 140
 Asn Phe Asp His Pro Asp Ala Phe Asp Phe Asp Leu Ile Ile Ser Thr
 145 150 155 160
 Leu Lys Lys Leu Lys Gln Gly Lys Ser Val Lys Val Pro Ile Tyr Asp
 165 170 175
 Phe Thr Thr His Ser Arg Lys Lys Asp Trp Lys Thr Leu Tyr Gly Ala
 180 185 190
 Asn Val Ile Phe Glu Gly Ile Met Ala Phe Ala Asp Lys Thr Leu
 195 200 205
 Leu Glu Leu Leu Asp Met Lys Ile Phe Val Asp Thr Asp Ser Asp Ile
 210 215 220
 Arg Leu Val Arg Arg Leu Arg Arg Asp Ile Ser Glu Arg Gly Arg Asp
 225 230 235 240
 Ile Glu Gly Val Ile Lys Gln Tyr Asn Lys Phe Val Lys Pro Ser Phe
 245 250 255
 Asp Gln Tyr Ile Gln Pro Thr Met Arg Leu Ala Asp Ile Val Val Pro
 260 265 270
 Arg Gly Ser Gly Asn Thr Val Ala Ile Asp Leu Ile Val Gln His Val
 275 280 285
 His Ser Gln Leu Glu Glu Arg Glu Leu Ser Val Arg Ala Ala Leu Ala

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Thr Ser Arg Asp Glu Phe Ile Phe Tyr Ser Lys Arg Leu Met Arg Leu
      340              345              350
Leu Ile Glu His Ala Leu Ser Phe Leu Pro Phe Gln Asp Cys Val Val
      355              360              365
Gln Thr Pro Gln Gly Gln Asp Tyr Ala Gly Lys Cys Tyr Ala Gly Lys
      370              375              380
Gln Ile Thr Gly Val Ser Ile Leu Arg Ala Gly Glu Thr Met Glu Pro
385              390              395              400
Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr Ile Leu Ile
      405              410              415
Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr Leu Arg Leu
      420              425              430
Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp Cys Thr Val
      435              440              445
Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu Leu Asp His
450              455              460
Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu Met Ala Glu
465              470              475              480
Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val Arg Ile Ile
      485              490              495
Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg Ile Ile Pro
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<210> 2843

<211> 497

<212> DNA

<213> Homo sapiens

<400> 2843

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<210> 2844
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<213> Homo sapiens

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35 40 45
Ser Ser Lys Phe Gln Glu Gly Ala Glu Met Leu Leu Asn Pro Glu Glu
50 55 60
Lys Ser Pro Leu Asn Ile Ser Val Gly Val His Pro Leu Asp Ser Phe
65 70 75 80
Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly Asp Leu Pro Ile Gly Pro
85 90 95
Pro Phe Glu Met Pro Thr Gly Ala Leu Leu Ser Thr Pro Gln Phe Glu
100 105 110
Met Leu Gln Asn Pro Leu Gly Leu Thr Gly Ala Leu Arg Gly Pro Gly
115 120 125
Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln Gly Pro Arg Pro Asn Ile
130 135 140
Cys Gly Ile Trp Gly Lys Ser Phe Gly Arg Asp Tyr Pro Asp Pro Ala
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<210> 2845
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<210> 2846

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2846

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			20					25					30		
Cys	His	Lys	Gly	Leu	Ser	Asp	Arg	Cys	Ser	Pro	Ser	Leu	Pro	Cys	Leu
		35					40					45			
Pro	His	Arg	Pro	Ser	Pro	Pro	Glu	Pro	Ala	Phe	Leu	Pro	Gln	His	Leu
		50				55				60					
Pro	Ser	Leu	Ala	Thr	Gly	Tyr	Ile	Cys	Val	Asp	Cys	Leu	Ser	Leu	His
				70						75				80	
Gly	Asn	Val	Arg	Thr	Ile	Phe	Val	Cys	Cys	Gly	Thr	Ala	Ala	Leu	Arg
			85					90						95	
Ala	Ala	Ser	Ser	Thr	Gln	Val	Ala	Leu	Asp	Thr	Asp	Cys	Thr	Gln	Gly
			100					105						110	
Glu	Leu	Gly	Leu	Ile	Thr	Pro	Leu	Thr	Arg	Gly	Glu	Thr	Leu	Gln	Leu
		115				120						125			
Glu	Val	Thr	Phe	Ile	Pro	Leu	Gln	Leu	Arg	Pro	Phe	His	Ser	Pro	Arg
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<210> 2847

<211> 2830

<212> DNA

<213> Homo sapiens

<400> 2847

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<210> 2848

<211> 856

<212> PRT

<213> Homo sapiens

<400> 2848

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<211> 380

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 2850

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		20					25					30			
Glu	Glu	Asp	Lys	Lys	Asp	Gly	Lys	Glu	Pro	Ser	Asp	Lys	Pro	Gln	Lys
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<212> PRT

<213> Homo sapiens

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Val	Asp	Pro	Ala	Ser	Phe	Leu	Ser	Thr	Thr	Leu	Gly	Asn	Val	Leu
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<212> DNA

<213> Homo sapiens

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cagtccttag tctctctttt tcacccacct tcttcagttt gctcacttac cccaggccca
 4620
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 4680
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 4740
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 4800
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 4860
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 4980
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<210> 2854

<211> 1235

<212> PRT

<213> Homo sapiens

<400> 2854

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 Glu Leu Phe Phe Lys Asp Asp Pro Glu Lys Leu Phe Ser Asp Leu Arg
 20 25 30
 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
 35 40 45
 Arg Asn Ser Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
 50 55 60
 Gln Ser Asn Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Arg Phe Leu
 65 70 75 80
 Gln Lys Leu Arg His Pro Asn Thr Ile Gln Tyr Arg Gly Cys Tyr Leu
 85 90 95
 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
 100 105 110
 Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
 115 120 125
 Ala Ala Val Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
 130 135 140
 His Asn Met Ile His Arg Asp Val Lys Ala Gly Asn Ile Leu Leu Ser
 145 150 155 160
 Glu Pro Gly Leu Val Lys Leu Gly Asp Phe Gly Ser Ala Ser Ile Met
 165 170 175
 Ala Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
 180 185 190
 Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val
 195 200 205
 Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro
 210 215 220
 Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn
 225 230 235 240
 Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr Phe Arg Asn

[illegible]

675					680					685					
Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	Arg	Ala	Glu
690					695					700					
Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	Leu	Glu	Tyr
705					710					715					
Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	Ala	Gln	Val
720					725					730					
Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Val	Arg	Ala	Gly	Gln	Arg	Pro	Pro
735					740					745					
Gly	Leu	Pro	Leu	Pro	Ile	Pro	Gly	Ala	Leu	Gly	Pro	Pro	Asn	Thr	Gly
750					755					760					
Thr	Pro	Ile	Glu	Gln	Gln	Pro	Cys	Ser	Pro	Gly	Gln	Glu	Ala	Val	Leu
765					770					775					
Asp	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Glu	Ala	Val	Gly	Glu	Arg	Arg
780					785					790					
Ile	Leu	Gly	Lys	Glu	Gly	Ala	Thr	Leu	Glu	Pro	Lys	Gln	Gln	Arg	Ile
800					805					810					
Leu	Gly	Glu	Glu	Ser	Gly	Ala	Pro	Ser	Pro	Ser	Pro	Gln	Lys	His	Gly
815					820					825					
Ser	Leu	Val	Asp	Glu	Glu	Val	Trp	Gly	Leu	Pro	Glu	Glu	Ile	Glu	Glu
830					835					840					
Leu	Arg	Val	Pro	Ser	Leu	Val	Pro	Gln	Glu	Arg	Ser	Ile	Val	Gly	Gln
845					850					855					
Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp	Glu	Ser	Leu
860					865					870					
Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro	Ala	Leu	Thr
875					880					885					
Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Pro	Ile	Gly	Pro
890					900					905					
Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp	Ile	Pro	Pro
910					915					920					
Glu	Pro	Pro	Pro	Thr	His	Leu	Arg	Pro	Cys	Pro	Ala	Ser	Gln	Leu	Pro
925					930					935					
Gly	Leu	Leu	Ser	His	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Phe	Ala	Val	Gly
940					945					950					
Ser	Ser	Ser	Gly	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Leu
955					960					965					
Leu	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Leu	Gln	Ala	Ala	Leu	Leu	Ala	Leu
970					975					980					
Glu	Val	Gly	Leu	Val	Gly	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	Leu	Cys	Thr
985					990					995					
Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala	Gln	Gly	Thr
1000					1005					1010					
Ala	Leu	Gly	Ala	Val	Leu	Gly	Leu	Ser	Trp	Arg	Arg	Gly	Leu	Met	Gly
1015					1020					1025					
Val	Pro	Leu	Gly	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Ala	Trp	Pro	Gly	Leu
1030					1035					1040					
Ala	Leu	Pro	Leu	Val	Ala	Met	Ala	Ala	Gly	Gly	Arg	Trp	Val	Arg	Gln
1045					1050					1055					
Gln	Gly	Pro	Arg	Val	Arg	Arg	Gly	Ile	Ser	Arg	Leu	Trp	Leu	Arg	Val
1060					1065					1070					
Leu	Leu	Arg	Leu	Ser	Pro	Met	Ala	Phe	Arg	Ala	Leu	Gln	Gly	Cys	Gly
1075					1080					1085					
Ala	Val	Gly	Asp	Arg	Gly	Leu	Phe	Ala	Leu	Tyr	Pro	Lys	Thr	Asn	Lys
1090					1095					1100					

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1105          1110          1115          1120
Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg Arg Arg Asn
          1125          1130          1135
Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg Val Trp Val
          1140          1145          1150
Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser Gln Gly Leu
          1155          1160          1165
Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala Ser Trp Gly
          1170          1175          1180
Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu Leu Pro Arg
1185          1190          1195          1200
Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser His Gln Pro Leu Pro Gly
          1205          1210          1215
Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg Ala Leu Pro
          1220          1225          1230
Pro Trp Arg
          1235

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<210> 2855

<211> 1676

<212> DNA

<213> Homo sapiens

<400> 2855

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120
gaggaagcca tctttgacac cctttgcacc gatgacagct ctgaagaggg aaagacactc
180
acaatggaca tattgacatt ggctcacacc tccacagaag ctaagggcct gtcctcagag
240
agcagcgccct cttccgacgg ccccatccca gtcacacccc cgtcacgggc ctcagagagc
300
agcgccctctt ccgacggccc ccatccagtc atcaccccg tcaaggcgctc agagagcagc
360
gcctcttccg acggccccc tccagtcacc accccgctcat ggtccccggg atctgatgtc
420
actctctctg ctgaagccct ggtgactgtc acaaacatcg aggttattaa ttgcagcatc
480
acagaaaatg aaacaacgac ttccagcate cctggggcct cagacacaga tctcatcccc
540
acggaagggg tgaaggcctc gtccacctcc gateccaccg ctctgcctga ctcennactg
600
aagcaaaacc acacatcact gaggtcanca gcctctgccg agaccctgtc cacagccggc
660
accacagagt cagctgcacc tgatgccacg gttgggaccc cactccccac taacagcacc
720
atagaaaagag aagtgcagc acccagggcc acgaccctca gtggagctct ggtcacagtt
780
agcaggaate ccctggaaga aacctcagcc ctctctgttg agacaccaag ttacgtcaaa
840
gtctcaggag cagctccggt ctccatagag gctgggtcag cagtgggcaa aacaacttc
900

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tttgctggga gctctgcttc ctctacagc ccctcggaag ccgcccctcaa gaacttcacc
 960
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 1020
 cctcttctct ctgtccctcc gactacaacc aacagcagcc gagggacgaa cagcacctta
 1080
 gccaaagatca caacctcagc gaagaccacg atgaagcccc caacagccac gccccagact
 1140
 gctcggacga ggccgaccac agacgtgagt gcaggtgaaa atggagggtc ctctctctgc
 1200
 ggctgagtgt ggcttccccg gaagacctca ctgaccccag agtggcagaa aggctgatgc
 1260
 agcagctcca ccgggaactc cagccccacg cgcctcactt ccagggtctc ttactgcgtg
 1320
 tcaggagagg ctaacggaca tcagctgcag ccaggcatgt ccggtatgcc aaaagagggt
 1380
 gctgccccta gcctggggccc ccaccgacag actgcagctg cggtactgtg ctgagaggta
 1440
 cccagaaggt tccatgaag ggcatgtgt ccaagcccc gacccagatg gtggcaacag
 1500
 gaccctcgct cacatccacc ggagtgtatg tgtggggagg ggcttcacct gttcccagag
 1560
 gtgtccttgg actcaccttg gcacatgttc tgtgtttcag taaagagaga cctgatcacc
 1620
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 1676

<210> 2856

<211> 401

<212> PRT

<213> Homo sapiens

<400> 2856

Leu	Thr	Thr	Ser	Pro	Asn	Phe	Met	Val	Leu	Ile	Ala	Thr	Ser	Val	Glu
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Thr	Ser	Ala	Ala	Ser	Gly	Ser	Pro	Glu	Gly	Ala	Arg	Met	Thr	Thr	Val
			20					25					30		
Gln	Thr	Ile	Thr	Gly	Ser	Asp	Pro	Glu	Glu	Ala	Ile	Phe	Asp	Thr	Leu
		35					40				45				
Cys	Thr	Asp	Asp	Ser	Ser	Glu	Glu	Ala	Lys	Thr	Leu	Thr	Met	Asp	Ile
	50					55					60				
Leu	Thr	Leu	Ala	His	Thr	Ser	Thr	Glu	Ala	Lys	Gly	Leu	Ser	Ser	Glu
65				70				75							80
Ser	Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro	Val	Ile	Thr	Pro	Ser	Arg
				85				90					95		
Ala	Ser	Glu	Ser	Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro	Val	Ile	Thr
			100					105					110		
Pro	Ser	Arg	Ala	Ser	Glu	Ser	Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro
		115						120				125			
Val	Ile	Thr	Pro	Ser	Trp	Ser	Pro	Gly	Ser	Asp	Val	Thr	Leu	Leu	Ala
	130					135					140				
Glu	Ala	Leu	Val	Thr	Val	Thr	Asn	Ile	Glu	Val	Ile	Asn	Cys	Ser	Ile
145				150					155						160
Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	Thr

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165              170              175
Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser Asp Pro
180              185              190
Pro Ala Leu Pro Asp Ser Xaa Leu Lys Gln Asn His Thr Ser Leu Arg
195              200              205
Ser Xaa Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr Thr Glu Ser
210              215              220
Ala Ala Pro Asp Ala Thr Val Gly Thr Pro Leu Pro Thr Asn Ser Thr
225              230              235              240
Ile Glu Arg Glu Val Thr Ala Pro Arg Ala Thr Thr Leu Ser Gly Ala
245              250              255
Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu Ser
260              265              270
Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val Ser
275              280              285
Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly Ser
290              295              300
Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe Thr
305              310              315              320
Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro
325              330              335
Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser
340              345              350
Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys
355              360              365
Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr Arg
370              375              380
Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Ser Ser Ser Cys
385              390              395              400
Gly

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<210> 2857

<211> 1668

<212> DNA

<213> Homo sapiens

<400> 2857

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120
aggctagcca gagggtaatt acacaggtgt aggccggcgg ggcgggcgga gggctcggga
180
ggcgagggg actggaagag ttggctgcgc ccaggcacca ggtggaagaa tttccatacc
240
agccctgcgg aggtgcctct gtttccagag gcgtttttgt acgaagggca ttttgaaggc
300
gaagcagaag ccgtagaatc agcggcgagc ctgttgaaag aaccacagg tgcatctcac
360
agcactctgg gcgaaaattg gatgtgaaaa tgaagccaga ccgagatact ctggatgaat
420
attttgaata tgatgcagag gagttcttgg tctctttggc cttgctgata acagaaggac
480

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gaacacctga atgttctgta aaaggtcgaa cagaaagcct tcattgccct ccagcacagt
 540
 cttgttacc agtaactacc aaacatgaat gtagtgacaa gctggcccag tgccgccaag
 600
 ccagacgaac taggtctgag gtcacattgt tgtggaagaa taaccttcca atcatgggtg
 660
 aaatgatgct actaccagac tgctgctaca gcgatgatgg gccaccaca gaggggaattg
 720
 atctaaatga tcttgcgatt aagcaagatg cattattatt agaaagatgg atcttggagc
 780
 cagttcctcg acagaatggt gaccgattta ttgaagagaa gacgcttctg ttggctgtcc
 840
 gtcattttgt gtttttttct cagttaagtg catggctgag tgtttctcat ggtgctatcc
 900
 cagcaaatat tctctacaga atcagtgctg ctgatgtaga cctacagtggt aatttttcac
 960
 agactccaat tgagcatgtg tttcctgttc ccaatgttcc tcacaatggt gccttgaaag
 1020
 tcagtggtca atccctggcc caaacaatct aattatccag ttttgacgtg cagtattcac
 1080
 actaatattg gcctttatga gaaaagaatt caacaacata aacttaaaac tcatacagac
 1140
 cataacccaa atgaagcaga acaatgtggt acaaacagtt cacagcgtct gtgtagcaaa
 1200
 caaacttgga ccatggcacc tgaaagtgtg ttacatgcaa aaagtggccc aagtcagaa
 1260
 tatactcgag ctgtcaaaaa tatcaaaacta tatccaggca ctggcagtaa atctgacct
 1320
 gggacatctc aagccaatat tctaggcttt agtggatatag gtgatataaa atcacaagaa
 1380
 acatcagtag gaactttaaa atcattttca atggttgatt ccagtatctc taaccgccag
 1440
 agtttctggc agtcagctgg tgagactaac cctttaatag gctctttaat tcaggagcgg
 1500
 caagaaatca ttgcaagaat tgctcaacat ttgattcatt gtgatccaa' cacttcacat
 1560
 gtttctggac gtccatttaa tactcaagag tctagttcac tccattcaaa acttttccgg
 1620
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 1668

<210> 2858

<211> 220

<212> PRT

<213> Homo sapiens

<400> 2858

Met	Lys	Pro	Asp	Arg	Asp	Thr	Leu	Asp	Glu	Tyr	Phe	Glu	Tyr	Asp	Ala
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Glu	Glu	Phe	Leu	Val	Ser	Leu	Ala	Leu	Leu	Ile	Thr	Glu	Gly	Arg	Thr
			20					25					30		
Pro	Glu	Cys	Ser	Val	Lys	Gly	Arg	Thr	Glu	Ser	Phe	His	Cys	Pro	Pro
		35				40					45				
Ala	Gln	Ser	Cys	Tyr	Pro	Val	Thr	Thr	Lys	His	Glu	Cys	Ser	Asp	Lys


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      50              55              60
Leu Ala Gln Cys Arg Gln Ala Arg Arg Thr Arg Ser Glu Val Thr Leu
65              70              75              80
Leu Trp Lys Asn Asn Leu Pro Ile Met Val Glu Met Met Leu Leu Pro
      85              90              95
Asp Cys Cys Tyr Ser Asp Asp Gly Pro Thr Thr Glu Gly Ile Asp Leu
      100              105              110
Asn Asp Pro Ala Ile Lys Gln Asp Ala Leu Leu Leu Glu Arg Trp Ile
      115              120              125
Leu Glu Pro Val Pro Arg Gln Asn Gly Asp Arg Phe Ile Glu Glu Lys
      130              135              140
Thr Leu Leu Leu Ala Val Arg Ser Phe Val Phe Phe Ser Gln Leu Ser
      145              150              155              160
Ala Trp Leu Ser Val Ser His Gly Ala Ile Pro Arg Asn Ile Leu Tyr
      165              170              175
Arg Ile Ser Ala Ala Asp Val Asp Leu Gln Trp Asn Phe Ser Gln Thr
      180              185              190
Pro Ile Glu His Val Phe Pro Val Pro Asn Val Ser His Asn Val Ala
      195              200              205
Leu Lys Val Ser Gly Gln Ser Leu Ala Gln Thr Ile
      210              215              220

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<210> 2859

<211> 1029

<212> DNA

<213> Homo sapiens

<400> 2859

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120
caccgcggcaa tgttccctcg aaggggcagc ggtagtggca ggcctctgc tctcaatgca
180
gcagggtaccg gcgtcggtag taatgccaca tcttccgagg attttccgcc tccgtcgctg
240
cttcagccgc cgccccctgc agcatcttct acgtcgggac cacagcctcc gcctccacaa
300
agcctgaacc tcttttcgca ggctcagctg caggcacagc ctcttgcgcc aggcggaact
360
caaatgaaaa agaaaagtgg cttccagata actagcgtaa ctctcgteta gatctccgct
420
agtatcagct ctaacaacag tatagcagag gacactgaga gctatgatga tctggatgaa
480
tctcacacgg aagatctctc tcttccggag atccttgatg tgtcactttc cagggctact
540
gacttagggg agcccgaaac cagctcctca gaagagacc taaataactt ccaggaagcc
600
gagacacctg gggcagtcct tcccaaccag cccacacctc ctcagcctca tttgcctcac
660
cttccacaac agaattgtgt gatcaatggg aatgctcctc cacaccacct ccatcaccac
720
catcagattc atcatgggca ccacctccaa catggtcacc accatccatc tcatgttgct
780

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gtggccagtg catccattac tgggtgggcca ccctcaagcc cagtatctag aaaactctct
 840
 acaactggaa gctctgacag tatcacacca gttgcaccaa cttctgctgt atcatccagt
 900
 gggtcacctg catctgtaat gactaatatg cgtgctccaa gtactacagg tggaataggt
 960
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 1020
 ttttaattcc
 1029

<210> 2860

<211> 343

<212> PRT

<213> Homo sapiens

<400> 2860

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 Thr Met His Gln Pro Pro Glu Ser Thr Ala Ala Ala Ala Ala Ala
 20 25 30
 Asp Ile Ser Ala Arg Lys Met Ala His Pro Ala Met Phe Pro Arg Arg
 35 40 45
 Gly Ser Gly Ser Gly Ser Ala Ser Ala Leu Asn Ala Ala Gly Thr Gly
 50 55 60
 Val Gly Ser Asn Ala Thr Ser Ser Glu Asp Phe Pro Pro Pro Ser Leu
 65 70 75 80
 Leu Gln Pro Pro Pro Pro Ala Ala Ser Ser Thr Ser Gly Pro Gln Pro
 85 90 95
 Pro Pro Pro Gln Ser Leu Asn Leu Leu Ser Gln Ala Gln Leu Gln Ala
 100 105 110
 Gln Pro Leu Ala Pro Gly Gly Thr Gln Met Lys Lys Lys Ser Gly Phe
 115 120 125
 Gln Ile Thr Ser Val Thr Pro Ala Gln Ile Ser Ala Ser Ile Ser Ser
 130 135 140
 Asn Asn Ser Ile Ala Glu Asp Thr Glu Ser Tyr Asp Asp Leu Asp Glu
 145 150 155 160
 Ser His Thr Glu Asp Leu Ser Ser Ser Glu Ile Leu Asp Val Ser Leu
 165 170 175
 Ser Arg Ala Thr Asp Leu Gly Glu Pro Glu Arg Ser Ser Ser Glu Glu
 180 185 190
 Thr Leu Asn Asn Phe Gln Glu Ala Glu Thr Pro Gly Ala Val Ser Pro
 195 200 205
 Asn Gln Pro His Leu Pro Gln Pro His Leu Pro His Leu Pro Gln Gln
 210 215 220
 Asn Val Val Ile Asn Gly Asn Ala His Pro His His Leu His His His
 225 230 235 240
 His Gln Ile His His Gly His His Leu Gln His Gly His His His Pro
 245 250 255
 Ser His Val Ala Val Ala Ser Ala Ser Ile Thr Gly Gly Pro Pro Ser
 260 265 270
 Ser Pro Val Ser Arg Lys Leu Ser Thr Thr Gly Ser Ser Asp Ser Ile
 275 280 285
 Thr Pro Val Ala Pro Thr Ser Ala Val Ser Ser Ser Gly Ser Pro Ala

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      290              295              300
Ser Val Met Thr Asn Met Arg Ala Pro Ser Thr Thr Gly Gly Ile Gly
305              310              315              320
Ile Asn Ser Val Thr Gly Thr Ser Thr Val Asn Asn Val Asn Ile Thr
      325              330              335
Ala Val Gly Ser Phe Asn Ser
      340

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<210> 2861
 <211> 756
 <212> DNA
 <213> Homo sapiens

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<400> 2861
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120
aatgggaaca agggccctcc agttggctca aggataagca tgccaaccac aaagcctcgt
180
ccaggactga gagaagaaaa attagcaagt atcatgagta agctgccact agctactccc
240
aaaaaaactag attctactca gactacacat tcttcaagtc ttattgtctg tcacacaggg
300
ccagtagcaa agaaacccca ggatttagct catactggca tctcttcagg ccttattgct
360
ggttcttcca ttcagaaccc taaagtctct ttagaacctt tgccagccag gctacttcaa
420
caaggacttc agaggtcaag ccagattcac acttcttctt cttcacagac ccatgtctcc
480
tcttcttccc aagcccaaat tgctgcctct tctcatgctc tgggaacatc cgaggcccaa
540
gatgcttctt cgtaacaca agtaacaaa gtgcaccagc attcagctgt ccagcagaac
600
tatgtgtctc cattacaggc caccatcagt aaatcccaga ccaaccccg cgtgaagtta
660
agtaataatc cccaactctc ctgttcctcc tcacttatta agacttcaga taagccactt
720
atgtaccgcc ttcccttacc taccctcttc acgcgt
756

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<210> 2862
 <211> 252
 <212> PRT
 <213> Homo sapiens

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<400> 2862
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Ser Leu Asp Glu Asp Leu Ser Phe His Ser Pro Ser Leu Asp Leu Val
20          25          30
Ser Glu Ala Leu Ala Val Ile Asn Asn Gly Asn Lys Gly Pro Pro Val
35          40          45
Gly Ser Arg Ile Ser Met Pro Thr Thr Lys Pro Arg Pro Gly Leu Arg

```

50		55		60											
Glu	Glu	Lys	Leu	Ala	Ser	Ile	Met	Ser	Lys	Leu	Pro	Leu	Ala	Thr	Pro
65					70				75						80
Lys	Lys	Leu	Asp	Ser	Thr	Gln	Thr	Thr	His	Ser	Ser	Ser	Leu	Ile	Ala
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Gly	His	Thr	Gly	Pro	Val	Pro	Lys	Lys	Pro	Gln	Asp	Leu	Ala	His	Thr
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Arg	Ser	Ser	Gln	Ile	His	Thr	Ser	Ser	Ser	Ser	Gln	Thr	His	Val	Ser
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Ser	Ser	Ser	Gln	Ala	Gln	Ile	Ala	Ala	Ser	Ser	His	Ala	Leu	Gly	Thr
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Ser	Glu	Ala	Gln	Asp	Ala	Ser	Ser	Leu	Thr	Gln	Val	Thr	Lys	Val	His
			180						185					190	
Gln	His	Ser	Ala	Val	Gln	Gln	Asn	Tyr	Val	Ser	Pro	Leu	Gln	Ala	Thr
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Ile	Ser	Lys	Ser	Gln	Thr	Asn	Pro	Val	Val	Lys	Leu	Ser	Asn	Asn	Pro
			210								220				
Gln	Leu	Ser	Cys	Ser	Ser	Ser	Leu	Ile	Lys	Thr	Ser	Asp	Lys	Pro	Leu
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<210> 2863

<211> 711

<212> DNA

<213> Homo sapiens

<400> 2863

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<210> 2864

<211> 237

<212> PRT

<213> Homo sapiens

<400> 2864

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      50           55           60
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Thr Ala Cys Tyr Cys His His Lys His Leu Cys Cys Ser Ser Ser Tyr
      85           90           95
Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro His Pro Ala Tyr Ala Thr
      100          105          110          115
Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln Tyr Thr Gln Gly Arg Arg
      115          120          125          130
Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu Thr Pro Gln Val Asn
      130          135          140          145
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Gly Lys Asn Val Ser Ser Ile Leu Gly Phe Asp Ser Asn Gln Leu Pro
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Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser Ala Ala Thr Cys Leu Gln
      180          185          190          195
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      195          200          205          210
Cys Ser Gln Ala Val Ser Glu Arg Leu Phe Tyr Tyr Ile Ala Val Ser
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<211> 585

<212> DNA

<213> Homo sapiens

<400> 2865

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<211> 134

<212> PRT

<213> Homo sapiens

<400> 2866

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			20					25				30			
Ser	Asp	His	Gln	Ser	Arg	Cys	Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys
		35				40					45				
Arg	Asp	Ile	Ser	Ser	Tyr	Lys	Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro
		50			55					60					
Ile	Arg	Leu	Lys	Arg	Asp	Arg	Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln
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His	Glu	Thr	His	Ala	Glu	Glu	Thr	Pro	Asn	Gln	Pro	Phe	Asn	Ser	Val
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His	Leu	Phe	Ser	Phe	Met	Val	Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala
			100					105					110		
Thr	Ile	Thr	Val	Arg	His	Phe	Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr
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			130												

<210> 2867

<211> 444

<212> DNA

<213> Homo sapiens

<400> 2867

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<210> 2868

<211> 84

<212> PRT

<213> Homo sapiens

<400> 2868

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Lys	Gly	Glu	Glu	Leu	Ser	Ala	Ala	Ala	Ile	Lys	Arg	Ile	Val	Ala	Thr
		20						25					30		
Ala	Lys	Ala	Ser	Gly	Lys	Lys	Leu	Gln	Lys	Val	Thr	Leu	Lys	Val	Ser
		35					40					45			
Pro	Arg	Gly	Ile	Ile	Leu	His	Pro	Gly	His	His	Pro	Ala	Pro	Arg	Gln
		50				55					60				
His	Cys	Cys	His	Ser	Arg	Leu	Val	Ala	Ala	Ala	Pro	Arg	Pro	Cys	Trp
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<210> 2869

<211> 5811

<212> DNA

<213> Homo sapiens

<400> 2869

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<211> 258

<212> PRT

<213> Homo sapiens

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<210> 2871

<211> 786

<212> DNA

<213> Homo sapiens

<400> 2871

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<210> 2872

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2872

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			20					25					30		
Ile	Ser	Pro	Asp	Ala	Phe	Phe	Gln	Ile	Asn	Thr	Ala	Gly	Ala	Glu	Met
			35				40					45			
Leu	Tyr	Trp	Thr	Val	Gly	Glu	Leu	Thr	Gly	Val	Asn	Ser	Asp	Thr	Ile
			50			55					60				
Leu	Leu	Asp	Ile	Cys	Cys	Gly	Thr	Gly	Val	Ile	Gly	Leu	Pro	Leu	Ala
65					70				75					80	
Gln	His	Thr	Ser	Arg	Val	Leu	Gly	Ile	Glu	Leu	Leu	Glu	Gln	Ala	Val
				85					90				95		
Glu	Asp	Ala	Arg	Trp	Thr	Ala	Ala	Phe	Asn	Gly	Ile	Thr	Asn	Ser	Glu
			100				105						110		
Phe	His	Thr	Gly	Gln	Ala	Glu	Lys	Ile	Leu	Pro	Gly	Leu	Leu	Lys	Ser
			115				120					125			
Lys	Glu	Asp	Gly	Gln	Ser	Ile	Val	Ala	Val	Val	Asn	Pro	Ala	Arg	Ala

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<210> 2873
<211> 1187
<212> DNA
<213> Homo sapiens

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<211> 248
<212> PRT

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<213> Homo sapiens

<400> 2874

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His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu Tyr Leu Ser Arg Ala
 20           25           30
Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala
 35           40           45
Met Val Ala Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro
 50           55           60
Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala
 65           70           75           80
Gly His Leu Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile
 85           90           95
Glu Ala Val Ser Asn Cys Thr Ile Ser Thr Arg Lys Glu Ser Pro His
100           105           110
Glu Arg Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val
115           120           125
Ile Gly Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val
130           135           140
Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser
145           150           155           160
Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile
165           170           175
Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile Met Val Pro
180           185           190
Phe Gly Leu Ile Phe Ile Val Phe Ala Val His Phe Tyr Arg Ser Leu
195           200           205
Val Ser His Lys Thr Asp Arg Gln Phe Gln Glu Leu Asn Glu Leu Ala
210           215           220
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<210> 2875

<211> 593

<212> DNA

<213> Homo sapiens

<400> 2875

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<210> 2876

<211> 193

<212> PRT

<213> Homo sapiens

<400> 2876

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Gly	Asp	Lys	Leu	Lys	Ala	Cys	Glu	Val	Ser	Lys	Asn	Lys	Asp	Gly	Lys
			20				25					30			
Glu	Gln	Ser	Glu	Thr	Val	Ser	Leu	Ser	Glu	Asp	Glu	Thr	Phe	Ser	Trp
			35				40					45			
Pro	Gly	Pro	Lys	Thr	Val	Thr	Leu	Lys	Arg	Thr	Ser	Gln	Gly	Phe	Gly
			50				55				60				
Phe	Thr	Leu	Arg	His	Phe	Ile	Val	Tyr	Pro	Pro	Glu	Ser	Ala	Ile	Gln
			65			70			75					80	
Phe	Ser	Tyr	Lys	Asp	Glu	Glu	Asn	Gly	Asn	Arg	Gly	Gly	Lys	Gln	Arg
			85					90						95	
Asn	Arg	Leu	Glu	Pro	Met	Asp	Thr	Ile	Phe	Val	Lys	Gln	Val	Lys	Glu
			100					105					110		
Gly	Gly	Pro	Ala	Phe	Glu	Ala	Gly	Leu	Cys	Thr	Gly	Asp	Arg	Ile	Ile
			115				120					125			
Lys	Val	Asn	Gly	Glu	Ser	Val	Ile	Gly	Lys	Thr	Tyr	Ser	Gln	Val	Ile
			130				135					140			
Ala	Leu	Ile	Gln	Asn	Ser	Asp	Thr	Thr	Leu	Glu	Leu	Ser	Val	Met	Pro
				145		150				155				160	
Lys	Asp	Glu	Asp	Ile	Leu	Gln	Val	Val	Ser	Phe	Ile	Tyr	Ser	Tyr	Met
				165					170					175	
Ser	Cys	Phe	Thr	Val	Met	Asn	Val	Arg	Lys	Ile	Phe	Leu	Arg	Trp	Lys
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<210> 2877

<211> 1921

<212> DNA

<213> Homo sapiens

<400> 2877

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<210> 2878

<211> 451

<212> PRT

<213> Homo sapiens

<400> 2878

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		20				25						30			
Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val	Arg	Lys	Asp
	35					40					45				
Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Thr	Pro	Ala	Arg	Thr
	50				55						60				
Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	Gly	Gly	Pro	Gly	Gly	Ser
	65				70				75				80		
Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	Ile	Gly	Pro	Leu	Asp	Ser	Asp
		85							90				95		
Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe
		100					105						110		
Val	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly
		115				120						125			
Ala	Tyr	Ala	Lys	Asp	Leu	Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu
		130			135					140					
Leu	Lys	Thr	Phe	Phe	Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe
			145		150					155				160	
Tyr	Ile	Phe	Ser	Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly
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Leu	Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
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Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	Val
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Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	Ala	Glu
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Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	Asn	Ile	Leu
		260					265						270		
Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	Leu	Glu	Phe	Thr
		275					280					285			
Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	Val	Arg	His	Leu	Gln
		290				295					300				
Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly	Pro	Ile	Arg	Lys	Lys	Leu
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Lys	Ile	Ile	Pro	Glu	Asp	Gln	Ser	Trp	Gly	Gly	Gln	Ala	Thr	Asn	Val

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          355              360              365
Leu Asp Leu Ile Val Asp Thr Ile Gly Gln Glu Ala Trp Val Arg Lys
          370              375              380
Leu Lys Trp Pro Glu Leu Ser Arg Phe Asn Gln Leu Lys Trp Lys Ala
          385              390              395
Leu Tyr Ser Asp Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser
          400              405              410
Tyr Lys Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val
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<210> 2879

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 2879

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<211> 376

<212> PRT

<213> Homo sapiens

<400> 2880

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			20					25					30		
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Ala	Arg	Gly	Glu	Arg	Pro	Pro	Arg	Leu	Gly	Leu	Pro	Thr	Pro	Gly	Val
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Pro	Val	Xaa	Asp	Lys	Tyr	Ala	Pro	Lys	Leu	Asp	Ser	Pro	Tyr	Phe	Arg
			85					90						95	
His	Ser	Ser	Val	Ser	Phe	Phe	Pro	Ser	Phe	Pro	Pro	Ala	Ile	Pro	Gly
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Tyr	Arg	Ala	Val	Val	Lys	Lys	Pro	Gly	Arg	Trp	Cys	Ala	Val	His	Val
			165					170						175	
Gln	Ile	Ala	Trp	Gln	Ile	Tyr	Arg	His	Gln	Gln	Lys	Ile	Lys	Glu	Met
		180				185						190			
Gln	Leu	Asp	Pro	His	Lys	Leu	Glu	Val	Gly	Ala	Lys	Leu	Asp	Leu	Phe
	195					200					205				
Gly	Arg	Pro	Pro	Ala	Pro	Gly	Val	Phe	Ala	Gly	Phe	His	Tyr	Pro	Gln
	210				215						220				
Asp	Leu	Ala	Arg	Pro	Leu	Phe	Pro	Ser	Thr	Gly	Ala	Ala	His	Pro	Ala
	225				230					235				240	
Ser	Asn	Pro	Phe	Gly	Pro	Ser	Ala	His	Pro	Gly	Ser	Phe	Leu	Pro	Thr

245										250					255				
Gly	Pro	Leu	Thr	Asp	Pro	Phe	Ser	Arg	Pro	Ser	Thr	Phe	Gly	Gly	Leu				
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Gly	Ser	Leu	Ser	Ser	His	Ala	Phe	Gly	Gly	Leu	Gly	Ser	His	Ala	Leu				
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Ala	Pro	Gly	Gly	Ser	Ile	Phe	Ala	Pro	Lys	Glu	Gly	Ser	Ser	Val	Leu				
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Gly	Leu	Pro	Ser	Pro	His	Glu	Ala	Trp	Ser	Arg	Leu	His	Arg	Ala	Pro				
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Pro	Ser	Phe	Pro	Ala	Pro	Pro	Pro	Trp	Pro	Lys	Ser	Val	Asp	Ala	Glu				
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Arg	Val	Ser	Ala	Leu	Thr	Asn	His	Asp	Arg	Glu	Pro	Val	Asn	Gly	Lys				
335										340					345				
Glu	Glu	Gln	Glu	Arg	Asp	Leu	Leu	Glu	Lys	Thr	Arg	Leu	Leu	Ser	Arg				
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<210> 2881

<211> 3021

<212> DNA

<213> Homo sapiens

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<210> 2882

<211> 96

<212> PRT

<213> Homo sapiens

<400> 2882

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 35 40 45
 Pro Ala Ile Ser Pro Leu Pro Thr Asp Ser Gln Ser Pro Leu Ala Ser
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<210> 2883

<211> 516

<212> DNA

<213> Homo sapiens

<400> 2883

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<210> 2884

<211> 172

<212> PRT

<213> Homo sapiens

<400> 2884

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 35 40 45
 Met Ser Pro Leu Asp Val Leu Glu Pro Glu Gln Thr Phe Phe Ser Ser
 50 55 60
 Pro Cys Gln Glu Glu His Gly His Pro Arg Arg Ile Pro His Leu Pro
 65 70 75 80
 Gly His Pro Tyr Ser Pro Glu Tyr Ala Pro Ser Pro Leu His Cys Ser
 85 90 95
 His Pro Leu Gly Ser Leu Ala Leu Gly Gln Ser Pro Gly Val Ser Met
 100 105 110
 Met Ser Pro Val Pro Gly Cys Pro Pro Ser Pro Ala Tyr Tyr Ser Pro
 115 120 125
 Ala Thr Tyr His Pro Leu His Ser Asn Leu Gln Ala His Leu Gly Gln
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<210> 2885

<211> 807

<212> DNA

<213> Homo sapiens

<400> 2885

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<210> 2886

<211> 269

<212> PRT

<213> Homo sapiens

<400> 2886

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Phe	Leu	Lys	Lys	Leu	Glu	Ala	Leu	Ile	Ala	Ser	Asn	Asp	Asn	Ala	Asn
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Lys	Thr	Cys	Lys	Met	Met	Leu	Ala	Thr	Glu	Glu	Thr	Ser	Pro	Asp	Leu
65					70				75					80	
Val	Gly	Ile	Lys	Arg	Asp	Leu	Glu	Ala	Leu	Ser	Lys	Gln	Cys	Asn	Lys
				85					90					95	
Leu	Leu	Asp	Arg	Ala	Gln	Ala	Arg	Glu	Glu	Gln	Val	Glu	Gly	Thr	Ile
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Lys	Arg	Leu	Glu	Glu	Phe	Tyr	Ser	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Leu
			115				120					125			
Leu	Gln	Lys	Ala	Glu	Glu	His	Glu	Glu	Ser	Gln	Gly	Pro	Val	Gly	Met
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Glu	Thr	Glu	Thr	Ile	Asn	Gln	Gln	Leu	Asn	Met	Phe	Lys	Val	Phe	Gln
145				150					155					160	
Lys	Glu	Glu	Ile	Glu	Pro	Leu	Gln	Gly	Lys	Gln	Gln	Asp	Val	Asn	Trp
				165					170					175	
Leu	Gly	Gln	Gly	Leu	Ile	Gln	Ser	Ala	Ala	Lys	Ser	Thr	Ser	Thr	Gln
			180					185					190		
Gly	Leu	Glu	His	Asp	Leu	Asp	Asp	Val	Asn	Ala	Arg	Trp	Lys	Thr	Leu
			195				200					205			
Asn	Lys	Lys	Val	Ala	Gln	Arg	Ala	Ala	Gln	Leu	Gln	Glu	Ala	Leu	Leu
			210			215					220				
His	Cys	Gly	Arg	Phe	Gln	Asp	Ala	Leu	Glu	Ser	Leu	Leu	Ser	Trp	Met

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<210> 2887

<211> 1945

<212> DNA

<213> Homo sapiens

<400> 2887

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<210> 2888

<211> 315

<212> PRT

<213> Homo sapiens

<400> 2888

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			20					25					30		
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		35					40				45				
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	50					55				60					
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Arg	Gln	Val	Gly	Val	Tyr	Leu	Leu	Pro	Gly	Arg	Val	Gly	Cys	Val	Ser
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Ser	Arg	Val	Ser	Pro	Ser	Phe	Pro	Gly	Asp	Gly	Leu	Asp	Ser	Gly	Leu
		115					120				125				
Ala	Arg	Arg	Gly	Ser	Ala	Val	Ser	Ala	Leu	Ala	Ser	Gly	Leu	Val	Glu
	130					135					140				
Glu	Pro	Met	Leu	Gly	Pro	Pro	Phe	His	Pro	Thr	Pro	Arg	Phe	Lys	Ala
145					150					155					160
Val	Ser	Ala	Lys	Ser	Lys	Glu	Asp	Leu	Val	Ser	Gln	Gly	Phe	Thr	Glu
				165				170						175	
Phe	Thr	Ile	Glu	Asp	Phe	His	Asn	Thr	Phe	Met	Asp	Leu	Ile	Glu	Gln


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      35           40           45
Lys Ala Glu Gln Ala Glu Gly Met Glu Phe Gly Phe Lys Met Pro Lys
      50           55           60
Met Thr Met Pro Lys Leu Gly Arg Ala Glu Ser Pro Ser Arg Gly Lys
      65           70           75           80
Pro Gly Glu Ala Gly Ala Glu Val Ser Gly Lys Leu Val Thr Leu Pro
      85           90           95
Cys Leu Gln Pro Glu Val Asp Gly Glu Ala His Val Gly Val Pro Ser
      100          105          110
Leu Thr Leu Pro Ser Val Glu Leu Asp Leu Pro Gly Ala Leu Gly Leu
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Gln Gly Gln Val Pro Ala Ala Lys Met Gly Lys Gly Glu Arg Ala Glu
      130          135          140
Gly Pro Glu Val Ala Ala Gly Val Arg Glu Val Gly Phe Arg Val Pro
      145          150          155          160
Ser Val Glu Ile Val Thr Pro Gln Leu Pro Ala Val Glu Ile Glu Glu
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<210> 2891

<211> 565

<212> DNA

<213> Homo sapiens

<400> 2891

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<210> 2892

<211> 90

<212> PRT

<213> Homo sapiens

<400> 2892

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Ser Thr Ser Tyr Arg Lys Ala Leu Pro Ile Leu Arg Pro Ser Ser Arg
      35             40             45
Arg Glu Ala Gly Pro Leu His His Ile Asp Leu Arg Arg Cys Phe Ser
 50             55             60
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<210> 2893

<211> 2270

<212> DNA

<213> Homo sapiens

<400> 2893

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<210> 2894

<211> 490

<212> PRT

<213> Homo sapiens

<400> 2894

Met Phe Ile Ser Leu Gly Gly Ala Pro Asp Arg Gln Ser Leu Phe Pro

1	5	10	15
Gln Leu Gly	Gly Gly Ser Gly Gly	Ser Ala Arg Gly Tyr	Cys Arg
	20	25	30
Gln Val Ser	Val Ser Leu His	Pro Gly Thr Gly Leu	Phe Ser Pro Phe
	35	40	45
Cys Ser Val	Pro Leu Trp Cys Ile Tyr	Phe Leu Ser Phe Cys	Ile Val
	50	55	60
Leu Ser Leu	Pro Ser Ala Ser Leu His	Leu Cys Leu Ser Cys	Leu His
	65	70	75
Phe Leu Asn	Leu Asp Cys Pro Cys Leu	Phe Leu Cys His Ser	Leu Ser
	85	90	95
Ser Pro Ser	Val Cys Gly Ser Ala Ser	Leu Ser His Ser Pro	Tyr Asn
	100	105	110
Trp Pro Leu	Pro Ala Gln Thr Phe Leu	Asp Glu Leu His Glu	Thr Gly
	115	120	125
Gln Leu His	Ser Met Ser Thr Trp Met	Glu Leu Tyr Pro Ala	Val Ser
	130	135	140
Thr Asp Val	Arg Phe Ala Asn Met Leu	Gly Gln Pro Gly Ser	Thr Pro
	145	150	155
Leu Asp Leu	Phe Lys Phe Tyr Val Glu	Glu Leu Lys Ala Arg	Phe His
	165	170	175
Asp Glu Lys	Lys Ile Ile Lys Asp Ile	Leu Lys Asp Arg Gly	Phe Cys
	180	185	190
Val Glu Val	Asn Thr Ala Phe Glu Asp	Phe Ala His Val Ile	Ser Phe
	195	200	205
Asp Lys Arg	Ala Ala Ala Leu Asp	Ala Gly Asn Ile Lys	Leu Thr Phe
	210	215	220
Asn Ser Leu	Leu Glu Lys Ala Glu Ala	Arg Glu Arg Glu Arg	Glu Lys
	225	230	235
Glu Glu Ala	Arg Arg Met Arg Arg Arg	Glu Ala Ala Phe Arg	Ser Met
	245	250	255
Leu Arg Gln	Ala Val Pro Ala Leu	Glu Leu Gly Thr Ala	Trp Glu Glu
	260	265	270
Val Arg Glu	Arg Phe Val Cys Asp Ser	Ala Phe Glu Gln Ile	Thr Leu
	275	280	285
Glu Ser Glu	Arg Ile Arg Leu Phe Arg	Glu Phe Leu Gln Val	Leu Glu
	290	295	300
Thr Glu Cys	Gln His Leu His Thr Lys	Gly Arg Lys His Gly	Arg Lys
	305	310	315
Gly Lys Lys	His His His Lys Arg Ser	His Ser Pro Ser Gly	Ser Glu
	325	330	335
Ser Glu Glu	Glu Glu Leu Pro Pro Pro	Ser Leu Arg Pro Pro	Lys Arg
	340	345	350
Arg Arg Arg	Asn Pro Ser Glu Ser Gly	Ser Glu Pro Ser Ser	Ser Leu
	355	360	365
Asp Ser Val	Glu Ser Gly Gly Ala Ala	Leu Gly Gly Arg Gly	Ser Pro
	370	375	380
Ser Ser His	Leu Leu Gly Ala Asp His	Gly Leu Arg Lys Ala	Lys Lys
	385	390	395
Pro Lys Lys	Lys Thr Lys Lys Arg Arg	His Lys Ser Asn Ser	Pro Glu
	405	410	415
Ser Glu Thr	Asp Pro Glu Glu Lys Ala	Gly Lys Glu Ser Asp	Glu Lys
	420	425	430
Glu Gln Glu	Gln Asp Lys Asp Arg Glu	Leu Gln Gln Ala Glu	Leu Pro

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          435              440              445
Asn Arg Ser Pro Gly Phe Gly Ile Lys Lys Glu Lys Thr Gly Trp Asp
   450              455              460
Thr Ser Glu Ser Glu Leu Ser Glu Gly Glu Leu Glu Arg Arg Arg Arg
   465              470              475              480
Thr Leu Leu Gln Gln Leu Asp Asp His Gln
          485              490

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<210> 2895
 <211> 697
 <212> DNA
 <213> Homo sapiens

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<400> 2895
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120
tgcaggcggg agcacgtctc cagcatcaac ctgaagtcg ccacgaactc ggtgatgccc
180
ccgtactggc cgctggcgaa cttctcttcc atctgcagca gacacatgcc ctgtccgggg
240
tgctgcggga aggcgcgacc gcccgcggcc cgcgtgcgcg gcccttctgc cacctcctcc
300
tgccgcgggt gcaacgcccc ccaagggctg cagaaagggg gcggtgaggc cccggtgctt
360
ctcctgcagg aactcgcccc ggatgcggta gcccttctg tagctcgtag gtcagctcct
420
gtcctcttga gcaaccgcct ccgatcccca tcgcctccat ctcttctctc tgatcgtccg
480
cgctctccag cgaggaggca ctcttctcgt gggccggccc tgagggtctgg gcccgcgctg
540
ccactctctc ctctgtctcc tctctctcgg ccgcgcgttg gcggcgctct tcctccccag
600
ccggctccat cgctccgggc gtcccgggca cactcatgcc ccggcaggcc taggctgggc
660
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697

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<210> 2896
 <211> 174
 <212> PRT
 <213> Homo sapiens

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<400> 2896
Met Pro Pro Tyr Trp Pro Leu Ala Asn Phe Ser Ser Ile Cys Ser Arg
   1           5           10           15
His Met Pro Cys Pro Gly Cys Cys Gly Lys Ala Arg Pro Pro Arg Pro
   20           25           30
Pro Leu Arg Gly Pro Ser Ala Thr Ser Ser Cys Arg Gly Gly Asn Ala
   35           40           45
Pro Gln Gly Leu Gln Lys Gly Gly Glu Ala Pro Val Leu Leu Leu
   50           55           60
Gln Glu Leu Ala Gln Asp Ala Val Ala Pro Ala Val Ala Arg Arg Ser

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65		70		75		80									
Ala	Pro	Ala	Pro	Cys	Ser	Asn	Arg	Leu	Arg	Ser	Pro	Ser	Pro	Pro	Ser
				85				90					95		
Leu	Pro	Pro	Asp	Arg	Pro	Arg	Pro	Pro	Ala	Arg	Arg	His	Ser	Phe	Arg
			100					105				110			
Gly	Pro	Ala	Leu	Arg	Ser	Gly	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Arg	Arg
		115				120					125				
Pro	Leu	Leu	Arg	Pro	Pro	Val	Ala	Ala	Ala	Leu	Pro	Pro	Gln	Pro	Ala
		130				135					140				
Pro	Ser	Leu	Pro	Ala	Ser	Arg	Ala	His	Ser	Cys	Pro	Gly	Arg	Pro	Arg
145				150						155				160	
Leu	Gly	Gly	Val	Glu	Gln	Pro	Leu	Glu	Val	Leu	Gly	Asp	Ala		
			165					170							

<210> 2897

<211> 3184

<212> DNA

<213> Homo sapiens

<400> 2897

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120
ctataattgt atgagaagaa taaaaacagt tcctttagaa ttcttattgt ttctctatt
180
ctttttcagg ctaagacaat gcatagcttt tgggtgatac aggtaaccct ggttaccact
240
aaaggggtgat ccccttcaga taataaaccc atttaactcc agtctcactc ccttcaccag
300
gagggcgact cacagtcagc ttggtggtga tgggggtttt gctgccagat gggtttccct
360
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420
tgaaggctgg gttatccacg atgatggaga aggtcaccat gtgatagaag acattcttga
480
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540
gagccattcc aaagaggggg atgatatact ctccacctgc gagcgatgat aggatcagga
600
tgcccttggt ctacccagg tggctgggct cgaataagac ttccacactg gcttcagtgc
660
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720
tcctgcagta gtattctgtc ctctgccgtg tgtaattgat gaacttcaca aggatgattt
780
ggctgctgcc aaggacagtc tgggaagtga caggcttttc cggaagtgct ggctgggctt
840
tcagatagag ctcatattgg tagtaaccca agtcagtgtt gtgcaaagtt agtcttccga
900
aggtttctcc agctttcagg ggctgaaatt caaatgagaa cgtgccctcg gagttggcag
960
gcaccacaaa ctgggagggc agggcgatgt cgggcatccg gcattccgtg gagaaggtca
1020

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1080
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1140
acaagaactc atttgtcacc tcgtttcggga agatcacctt tgcacgctac gttccctcct
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1920
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1980
gataccaccac ggggtccaaag ggaatatgtt cctggtccag tgagatctcc agggcctggc
2040
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2100
cagagaaggg agggacacgc ttcttcgggg caaagatgac ttccagtta cagacttctt
2160
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2640

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 2760
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 3060
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 3180
 agcc
 3184

<210> 2898

<211> 933

<212> PRT

<213> Homo sapiens

<400> 2898

Met	Asn	Val	Glu	Ile	Lys	Cys	Lys	Asp	Arg	Thr	Gly	Ser	Ile	Thr	Leu
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Leu	Thr	Pro	Asn	Gln	Thr	Asn	Ile	Ile	Asn	Phe	Tyr	Glu	Val	Glu	Leu
			20					25					30		
Asn	Glu	Cys	Val	Gln	Cys	Glu	Phe	Asn	Phe	Ile	Asn	Thr	Gly	Lys	Phe
		35					40					45			
Thr	Phe	Ser	Phe	Gln	Ala	Gln	Leu	Cys	Gly	Ser	Lys	Thr	Leu	Leu	Gln
		50				55					60				
Tyr	Leu	Glu	Phe	Ser	Pro	Ile	Asp	Ser	Thr	Val	Asp	Val	Gly	Gln	Ser
65				70						75				80	
Val	His	Ala	Thr	Leu	Ser	Phe	Gln	Pro	Leu	Lys	Lys	Cys	Val	Leu	Thr
			85					90					95		
Asp	Leu	Glu	Leu	Ile	Ile	Lys	Ile	Ser	His	Gly	Pro	Thr	Phe	Met	Cys
			100					105					110		
Asn	Ile	Ser	Gly	Cys	Ala	Val	Ser	Pro	Ala	Ile	His	Phe	Ser	Phe	Thr
		115					120					125			
Ser	Tyr	Asn	Phe	Gly	Thr	Cys	Phe	Ile	Tyr	Gln	Ala	Gly	Met	Pro	Pro
	130					135					140				
Tyr	Lys	Gln	Thr	Leu	Val	Ile	Thr	Asn	Lys	Glu	Glu	Thr	Pro	Met	Ser
145				150						155				160	
Ile	Asp	Cys	Leu	Tyr	Thr	Asn	Thr	Thr	His	Leu	Glu	Val	Asn	Ser	Arg
			165					170					175		
Val	Asp	Val	Val	Lys	Pro	Gly	Asn	Thr	Leu	Glu	Ile	Pro	Ile	Thr	Phe
		180					185					190			
Tyr	Pro	Arg	Glu	Ser	Ile	Asn	Tyr	Gln	Glu	Leu	Ile	Pro	Phe	Glu	Ile
		195					200					205			
Asn	Gly	Leu	Ser	Gln	Gln	Thr	Val	Glu	Ile	Lys	Gly	Lys	Gly	Thr	Glu

210	215	220
Met Lys Ile Leu Val Leu Asp Pro Ala Asn Arg Ile Val Lys Leu Gly		
225	230	235
Ala Val Leu Pro Gly Gln Val Val Lys Arg Thr Val Ser Ile Met Asn		240
	245	250
Asn Ser Leu Ala Gln Leu Thr Phe Asn Gln Ser Ile Leu Phe Thr Ile		255
	260	265
Pro Glu Leu Gln Glu Pro Lys Val Leu Thr Leu Ala Pro Phe His Asn		270
	275	280
Ile Thr Leu Lys Pro Lys Glu Val Cys Lys Leu Glu Val Ile Phe Ala		285
	290	295
Pro Lys Lys Arg Val Pro Pro Phe Ser Glu Glu Val Phe Met Glu Cys		300
305	310	315
Met Gly Leu Leu Arg Pro Leu Phe Leu Leu Ser Gly Cys Cys Gln Ala		320
	325	330
Leu Glu Ile Ser Leu Asp Gln Glu His Ile Pro Phe Gly Pro Val Val		335
	340	345
Tyr Gln Thr Gln Ala Thr Arg Arg Ile Leu Met Leu Asn Thr Gly Asp		350
	355	360
Val Gly Ala Arg Phe Lys Trp Asp Ile Lys Lys Phe Glu Pro His Phe		365
	370	375
Ser Ile Ser Pro Glu Glu Gly Tyr Ile Thr Ser Gly Met Glu Val Ser		380
385	390	395
Phe Glu Val Thr Tyr His Pro Thr Glu Val Gly Lys Glu Ser Leu Cys		400
	405	410
Lys Asn Ile Leu Cys Tyr Ile Gln Gly Gly Ser Pro Leu Ser Leu Thr		415
	420	425
Leu Ser Gly Val Cys Val Gly Pro Pro Ala Val Lys Glu Val Val Asn		430
	435	440
Phe Thr Cys Gln Val Arg Ser Lys His Thr Gln Thr Ile Leu Leu Ser		445
	450	455
Asn Arg Thr Asn Gln Thr Trp Asn Leu His Pro Ile Phe Glu Gly Glu		460
465	470	475
His Trp Glu Gly Pro Glu Phe Ile Thr Leu Glu Ala His Gln Gln Asn		480
	485	490
Lys Pro Tyr Glu Ile Thr Tyr Arg Pro Arg Thr Met Asn Leu Glu Asn		495
	500	505
Arg Lys His Gln Gly Thr Leu Phe Phe Pro Leu Pro Asp Gly Thr Gly		510
	515	520
Trp Leu Tyr Ala Leu His Gly Thr Ser Glu Leu Pro Lys Ala Val Ala		525
	530	535
Asn Ile Tyr Arg Glu Val Pro Cys Lys Thr Pro Tyr Thr Glu Leu Leu		540
545	550	555
Pro Ile Thr Asn Trp Leu Asn Lys Pro Gln Arg Phe Arg Val Ile Val		560
	565	570
Glu Ile Leu Lys Pro Glu Lys Pro Asp Leu Ser Ile Thr Met Lys Gly		575
	580	585
Leu Asp Tyr Ile Asp Val Leu Ser Gly Ser Lys Lys Asp Tyr Lys Leu		590
	595	600
Asn Phe Phe Ser His Lys Glu Gly Thr Tyr Ala Ala Lys Val Ile Phe		605
	610	615
Arg Asn Glu Val Thr Asn Glu Phe Leu Tyr Tyr Asn Val Ser Phe Arg		620
625	630	635
Val Ile Pro Ser Gly Ile Ile Lys Thr Ile Glu Met Val Thr Pro Val		640

645 650 655
 Arg Gln Val Ala Ser Ala Ser Ile Lys Leu Glu Asn Pro Leu Pro Tyr
 660 665 670
 Ser Val Thr Phe Ser Thr Glu Cys Arg Met Pro Asp Ile Ala Leu Pro
 675 680 685
 Ser Gln Phe Val Val Pro Ala Asn Ser Glu Gly Thr Phe Ser Phe Glu
 690 695 700
 Phe Gln Pro Leu Lys Ala Gly Glu Thr Phe Gly Arg Leu Thr Leu His
 705 710 715 720
 Asn Thr Asp Leu Gly Tyr Tyr Gln Tyr Glu Leu Tyr Leu Lys Ala Thr
 725 730 735
 Pro Ala Leu Pro Glu Lys Pro Val His Phe Gln Thr Val Leu Gly Ser
 740 745 750
 Ser Gln Ile Ile Leu Val Lys Phe Ile Asn Tyr Thr Arg Ala Arg Thr
 755 760 765
 Glu Tyr Tyr Cys Arg Thr Asp Cys Thr Asp Phe His Ala Glu Lys Leu
 770 775 780
 Ile Asn Ala Ala Pro Gly Gly Gln Gly Gly Thr Glu Ala Ser Val Glu
 785 790 795 800
 Val Leu Phe Glu Pro Ser His Leu Gly Glu Thr Lys Gly Ile Leu Ile
 805 810 815
 Leu Ser Ser Leu Ala Gly Gly Glu Tyr Ile Ile Pro Leu Phe Gly Met
 820 825 830
 Ala Leu Pro Pro Lys Pro Gln Gly Pro Phe Ser Ile Arg Ala Gly Tyr
 835 840 845
 Ser Ile Ile Ile Pro Phe Lys Asn Val Phe Tyr His Met Val Thr Phe
 850 855 860
 Ser Ile Ile Val Asp Asn Pro Ala Phe Thr Ile Arg Ala Gly Glu Ser
 865 870 875 880
 Val Arg Pro Lys Lys Ile Asn Asn Ile Thr Val Ser Phe Glu Gly Asn
 885 890 895
 Pro Ser Gly Ser Lys Thr Pro Ile Thr Thr Lys Leu Thr Val Ser Cys
 900 905 910
 Pro Pro Gly Glu Gly Ser Glu Thr Gly Val Lys Trp Val Tyr Tyr Leu
 915 920 925
 Lys Gly Ile Thr Leu
 930

<210> 2899

<211> 876

<212> DNA

<213> Homo sapiens

<400> 2899

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 120
 gagctgcact gccgaatgac gtagccacta gccacatagg ctgttgattg cttgaaatgt
 180
 gactagtctg aattgagaaa tactcccaac aggggcacaa aacgtccccg ggatgatgatg
 240
 gaagaagaac tgaagacacg ccgcaagcaa actggtactc gagaacgcgg ccgctatcgg
 300

gaagaagaaa tgactgtggt ggaggaagcg gatgatgaca aaaaaaggct gctgcagatt
 360
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 420
 aagaaaatga tcctcacatt tgaaaagaga tcatataaaa accaagaatt gcggaattaag
 480
 ttccagaca atccagagaa gtccatggaa tccgagctgg acctaaatga catcattcag
 540
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 660
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 720
 gtgctcatcg atgctctggt ggatgggagc gtggtagcac tgctggtaca gaattctggag
 780
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 876

<210> 2900

<211> 189

<212> PRT

<213> Homo sapiens

<400> 2900

Met	Thr	Val	Val	Glu	Ala	Asp	Asp	Asp	Lys	Lys	Arg	Leu	Leu	Gln
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Ile	Ile	Asp	Arg	Asp	Gly	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Pro	Leu
		20					25					30		
Asp	Glu	Ser	Ser	Val	Lys	Lys	Met	Ile	Leu	Thr	Phe	Glu	Lys	Arg
	35						40					45		Ser
Tyr	Lys	Asn	Gln	Glu	Leu	Arg	Ile	Lys	Phe	Pro	Asp	Asn	Pro	Glu
	50					55				60				Lys
Phe	Met	Glu	Ser	Glu	Leu	Asp	Leu	Asn	Asp	Ile	Ile	Gln	Glu	Met
65				70					75					80
Val	Val	Ala	Thr	Met	Pro	Asp	Leu	Tyr	His	Leu	Leu	Val	Glu	Leu
			85					90					95	Asn
Ala	Val	Gln	Ser	Leu	Leu	Gly	Leu	Leu	Gly	His	Asp	Asn	Thr	Asp
		100					105					110		Val
Ser	Ile	Ala	Val	Val	Asp	Leu	Leu	Gln	Glu	Leu	Thr	Asp	Ile	Asp
	115					120					125			Thr
Leu	His	Glu	Ser	Glu	Glu	Gly	Ala	Glu	Val	Leu	Ile	Asp	Ala	Leu
130						135					140			Val
Asp	Gly	Gln	Val	Val	Ala	Leu	Leu	Val	Gln	Asn	Leu	Glu	Arg	Leu
145				150					155					160
Glu	Ser	Val	Lys	Glu	Glu	Ala	Asp	Gly	Val	His	Asn	Thr	Leu	Ala
			165					170					175	Ile
Val	Glu	Asn	Met	Ala	Glu	Phe	Arg	Pro	Glu	Met	Cys	Thr		
		180						185						

<210> 2901

<211> 756

<212> DNA

<213> Homo sapiens

<400> 2901

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 120
 ctggaccctc tgggcattat gcgctccaag aagcccaaga aacatcccaa agtggccgtg
 180
 aaagccaagc cctcgccccg gctcaccatc ttgacgagg aggtggacc tgatgagggg
 240
 ctctttggcc cgggcaggaa gctgtctcca caggaccctt cggaggagct gtcacccatg
 300
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 360
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 420
 gcctccaagg aactgttcag gtaccacctg tccccagcgg cgcttggcca gctctgagag
 480
 tgtctctgac agagccaagg gcccggtcca ttgccagtc tcagccccag cctcctctga
 540
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 600
 gtgaaggggg ctgaggggga ggnaaantcgc ccagggtctg tcagctagtt ccagaaagag
 660
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 720
 agaataatta aattatataa ttgccagggc aaaaaa
 756

<210> 2902

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2902

Thr	Arg	Arg	Arg	Gly	Ala	Phe	Asp	Phe	Phe	Glu	Lys	Gln	Asp	Gln	Val
1				5					10					15	
Ala	Glu	Glu	Gly	Pro	Pro	Val	Gln	Ser	Leu	Lys	Gly	Glu	Asp	Ala	Glu
			20					25					30		
Glu	Ser	Leu	Glu	Glu	Glu	Ala	Leu	Asp	Pro	Leu	Gly	Ile	Met	Arg	
			35				40					45			
Ser	Lys	Lys	Pro	Lys	Lys	His	Pro	Lys	Val	Ala	Val	Lys	Ala	Lys	Pro
			50			55					60				
Ser	Pro	Arg	Leu	Thr	Ile	Phe	Asp	Glu	Glu	Val	Asp	Pro	Asp	Glu	Gly
					70					75				80	
Leu	Phe	Gly	Pro	Gly	Arg	Lys	Leu	Ser	Pro	Gln	Asp	Pro	Ser	Glu	Asp
				85					90					95	
Val	Ser	Ser	Met	Asp	Pro	Leu	Lys	Leu	Phe	Asp	Asp	Pro	Asp	Leu	Gly
			100					105					110		
Gly	Ala	Ile	Pro	Leu	Gly	Asp	Ser	Leu	Leu	Leu	Pro	Ala	Ala	Cys	Glu
			115			120					125				
Ser	Gly	Gly	Pro	Thr	Pro	Ser	Leu	Ser	His	Arg	Asp	Ala	Ser	Lys	Glu

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 <211> 542
 <212> DNA
 <213> Homo sapiens
 <400> 2903
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 120
 gactcacaga acctcagtgc ctacaacacc cggtctttca aagaggtcga tggagaaggg
 180
 aagccctact acgaggtgcg gctggctttt gtgcttggct cagagccttc cctggactct
 240
 gaggtgactt ccaagctgaa gagctatgaa ttcgggggaa gccctttcca ggtgaccggg
 300
 ggggactacg cgcccatcct ccagaagggt gtggagcagc tggagaaaag caaggcctat
 360
 cgagccaaca gccaccaggg gcagatgctg gcccagtata tagagagctt caccacaggg
 420
 tccatcgagg ccacaagag gggctccccg ttctggatcc aggacaaaag cccccatcgt
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 540
 gt
 542
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 <211> 180
 <212> PRT
 <213> Homo sapiens
 <400> 2904
 Lys Leu Met Phe Ser Leu Tyr Pro Arg Leu Arg His Leu Gly Leu Gly
 1 5 10 15
 Lys Glu Gly Ile Thr Thr Tyr Phe Ser Gly Asn Cys Thr Met Glu Asp
 20 25 30
 Ala Lys Leu Ala Gln Asp Phe Leu Asp Ser Gln Asn Leu Ser Ala Tyr
 35 40 45
 Asn Thr Arg Leu Phe Lys Glu Val Asp Gly Glu Gly Lys Pro Tyr Tyr
 50 55 60
 Glu Val Arg Leu Ala Ser Val Leu Gly Ser Glu Pro Ser Leu Asp Ser
 65 70 75 80
 Glu Val Thr Ser Lys Leu Lys Ser Tyr Glu Phe Arg Gly Ser Pro Phe
 85 90 95
 Gln Val Thr Arg Gly Asp Tyr Ala Pro Ile Leu Gln Lys Val Val Glu
 100 105 110
 Gln Leu Glu Lys Ala Lys Ala Tyr Ala Ala Asn Ser His Gln Gly Gln
 115 120 125
 Met Leu Ala Gln Tyr Ile Glu Ser Phe Thr Gln Gly Ser Ile Glu Ala


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      130              135              140
His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys Gly Pro His Arg
145              150              155              160
Gly Glu Val Arg Arg Gln Leu His Pro Thr Cys Pro Leu Leu Pro Ala
      165              170              175
Pro Pro Ser Arg
      180

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<210> 2905

<211> 814

<212> DNA

<213> Homo sapiens

<400> 2905

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120
ggattcctcc tctgcccagg tttctgctgt cccccaaaa gaaagacatg tagctgggca
180
tggtgggtaca catctgtggt cccagttact caggaggctg aggaggagg attgcttgag
240
cccagtggtt caaggttga gtgggctgtg aatgctctac ttcactccag cctgagcaac
300
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360
ctggaaatgg gcttcggggt ggttaaccaa gccagggaa acttgcgtgg ccagcatct
420
tccgtccgct gcaggaggag cacacgccc cgcccgggt cagcaagacg cgagaaagcg
480
gccacgccgg gcgtccggga gctgaggctg gagggcgctt ggcaggcagg gcggggccca
540
ggcggcgagg gtgcttatga ccggcgctgg ggggaacttc tggacgtcaa ggggccacta
600
taaagcggca cagtcttgag ccttcgctct tcacctaat cagtgcgcgc ccttcgaaa
660
gcctctgtgg aggtaacat tgggggttcg cctccaaatc caggaaatga cctcaaaaat
720
gtcctctacac cgtaagaccg gtcccttcaa tgcaaaaggg actgtgcggc gaggcaccga
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<210> 2906

<211> 200

<212> PRT

<213> Homo sapiens

<400> 2906

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Phe Ser Tyr Pro Ser Phe Val Tyr Leu Gly Thr Phe Thr Leu Val Asp
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Asn Arg Ile Pro Val Thr Arg Ser Phe Phe Cys Ile Thr Asn Ser Ala
      20              25              30
Thr Leu Phe Gln Asn Trp Val Ser Gly Phe Leu Leu Cys Pro Gly Phe

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          35              40              45
Cys  Cys  Pro  Pro  Lys  Arg  Lys  Thr  Cys  Ser  Trp  Ala  Trp  Trp  Tyr  Thr
  50              55              60
Ser  Val  Val  Pro  Val  Thr  Gln  Glu  Ala  Glu  Ala  Gly  Gly  Leu  Leu  Glu
  65              70              75              80
Pro  Arg  Cys  Ser  Arg  Leu  Gln  Trp  Ala  Val  Asn  Ala  Leu  Leu  His  Ser
          85              90              95
Ser  Leu  Ser  Asn  Arg  Ala  Arg  Pro  Arg  Pro  Ser  Ser  Arg  Leu  Ser  Ile
          100              105              110
Pro  Pro  Pro  Gln  His  Pro  Phe  Leu  Leu  Glu  Met  Gly  Phe  Gly  Val  Val
          115              120              125
Asn  Gln  Ala  Gln  Gly  Asn  Leu  Arg  Gly  Pro  Ala  Ser  Ser  Val  Arg  Cys
          130              135              140
Arg  Arg  Ser  Thr  Arg  Pro  Arg  Pro  Gly  Ser  Ala  Arg  Arg  Glu  Lys  Ala
          145              150              155              160
Ala  Thr  Pro  Gly  Val  Arg  Glu  Leu  Arg  Leu  Glu  Gly  Ala  Trp  Gln  Ala
          165              170              175
Gly  Arg  Gly  Pro  Gly  Gly  Gly  Ser  Ala  Tyr  Asp  Arg  Arg  Trp  Gly  Glu
          180              185              190
Leu  Leu  Asp  Val  Lys  Gly  Pro  Leu
          195              200

```

<210> 2907

<211> 379

<212> DNA

<213> Homo sapiens

<400> 2907

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  120
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  180
caaaaggcaa ggaattcttc ccttaatggt ggacgggtcct gagactgtc caccctgggc
  240
tcattacact gggaccagct ttaagcttcc ctgttcaacg cggagagctc cacagcccag
  300
gacgacagag cagatgatgg cagcagcccc tcaaaaccca gacaggcctt cttggcttgc
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<210> 2908

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2908

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Met  Thr  Val  Ser  Asp  Arg  Pro  Ser  Ala  Gly  Cys  Asp  Leu  Pro  Lys  Leu
  1              5              10              15
Met  Thr  Ala  Ser  Leu  Asn  Gly  Trp  Val  Leu  Arg  Asn  Ser  Ile  Phe  Thr
          20              25              30
Phe  Pro  Arg  Leu  Leu  Ser  Asn  Phe  Gln  His  Cys  Pro  Gln  Asp  Tyr  Lys

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tgaactgcag gtctcacgct ggctgcatga cttggtgccc cctggctggc tgagccactg
 1140
 cctgccacct tctcatacca ttactgtggg gtctaaagag gacatcatcc ccaaccaaag
 1200
 aatagtgaga gagaaatcc caaacatttg agacagggtt caaaagcacc cagacgcctt
 1260
 ctgtctcttt ccagttccc atctggctag ggactgtgaa tcagaattca gaatctgtgc
 1320
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 1380
 tgaccttctt ccaccactgc tgcgggttat tcctcgatgg gaactgaagg atccaaggga
 1440
 ggaatccggt cgcgcccaa acctccctgc acaacatcga atgcgggagt ctggctgctg
 1500
 cttctgcaca ggacagagcc tccagttctt tgcttgagag catcatttat ggcattggact
 1560
 gggaacgcaa tgtgttcaca caaatgcacg acaattgtac atcagcatct ttacaatatt
 1620
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 1680
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 1800
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 1920
 agctggggat ggctccctga gctggggacc tagaagacgc tgctgacaga tgggcccctt
 1980
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 2100
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 2280
 caggcagctg gtccaccctg cagccatgct gcacgtctga ctgagaactg agcaccagat
 2340
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 2400
 aatatgtaga aaaatagcca
 2420

<210> 2910

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2910

Met Gly Thr Glu Gly Ser Lys Gly Gly Ile Arg Ser Ala Pro Lys Pro

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Pro Cys Thr Thr Ser Asn Ala Gly Val Trp Leu Leu Leu His Arg			
	20	25	30
Thr Glu Pro Pro Val Phe Cys Leu Arg Ala Ser Phe Met Ala Trp Thr			
	35	40	45
Gly Asn Ala Met Cys Ser His Lys Cys Thr Thr Ile Val His Gln His			
	50	55	60
Leu Tyr Asn Ile Lys Gly Val Ile Tyr Lys Ser Thr Ala Ile Val His			
	65	70	75
Arg Met Val Met Ala Gly Glu Pro Arg Pro Pro Val Leu Cys Ser Phe			
	85	90	95
Ser Thr Gly Glu His Leu Gly Ser Cys His Lys Ala Arg Gly Gly Pro			
	100	105	110
Ser Leu Gly Leu Ser Trp Gly Arg Gln Gln Val Cys Lys Asp Ser Ser			
	115	120	125
Gly Pro Val Leu Thr Gly Ile Arg Gly Gln Glu Arg Gln Val Cys Leu			
	130	135	140
Cys Leu Gly Leu Ile Gly Arg Leu Val			
145	150		

<210> 2911

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 2911

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120
gctgcggagc ccgggaagcg gagcgagggc gggaagaccc ccgtggcccg gagcagcgga
180
ggcgggggct gggcagaccc ccgaacgtgc ctgagcctgc tgctgcgtgg gacgtgcctg
240
ggcctggcct ggtttgtatt tcagcagtcg gaaaaatttg caaagggtga aaaccaatac
300
cagttactga aactagaaac caatgaattc caacaacttc aaagtaaaat cagtttaatt
360
tcagaaaagt ggcagaaatc tgaagctatc atggaacaat tgaagctttt tcaataaatt
420
gtcatcttaa agcgtctaca ggaagaaatt aatgaggtaa aaacttggtc caatagcata
480
actgaaaaac aggatatact gaacaacagt ctgacgagcg tttctcaaga cattacaaaa
540
gtagacaaaa gtacaacttc catggcaaaa gatgttggtc tcaagattac aagtgtaaaa
600
acagatatat gacggatttc aggttttagt actgatgtaa tatcattgac agattctgtg
660
caagaactag aaaataaaat agagaaagta gaaaaaata cagtaaaaaa tatagggtat
720
cttctttcaa gcagtattga tcgaacagca acgctccgaa agacagcctc tgaataattca
780
caaagaatta actctgttaa gaagacgcta accgaactaa agagtgaact cgacaaaacat
840

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acagatagat ttctaagctt agaaggtgac agagccaaag ttctgaagac agtgactttt
 900
 gcaaatgac taaaaccaa ggtgtataat ctaagaagg acttttcccg tttagaacca
 960
 ttagtaaatg atttaacact acgcattggg agattgggta cgcacttact acaagagag
 1020
 aaagaaattg ctttcttaag tgaaaaaata tctaatttaa caatagtcca agctgagatt
 1080
 aaggatatta aagatgaaat agcacacatt tcagatatga attagtgtga cattattgag
 1140
 attagactaa ggtaattttt ttaatgggac ctctcatgag aagactggta aatcaaaaa
 1200
 aatgatattt tggagcaaaa gtcattttat atttaatcct atttgtaca gtaaaaaata
 1260
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 1320
 aaaaaaa
 1327

<210> 2912

<211> 350

<212> PRT

<213> Homo sapiens

<400> 2912

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Ala	Ala	Glu	Pro	Gly	Lys	Arg	Ser	Glu	Gly	Gly	Lys	Thr	Pro	Val	Ala
		20						25					30		
Arg	Ser	Ser	Gly	Gly	Gly	Trp	Ala	Asp	Pro	Arg	Thr	Cys	Leu	Ser	
		35				40					45				
Leu	Leu	Ser	Leu	Gly	Thr	Cys	Leu	Gly	Leu	Ala	Trp	Phe	Val	Phe	Gln
	50					55					60				
Gln	Ser	Glu	Lys	Phe	Ala	Lys	Val	Glu	Asn	Gln	Tyr	Gln	Leu	Leu	Lys
65				70						75				80	
Leu	Glu	Thr	Asn	Glu	Phe	Gln	Gln	Leu	Gln	Ser	Lys	Ile	Ser	Leu	Ile
			85						90					95	
Ser	Glu	Lys	Trp	Gln	Lys	Ser	Glu	Ala	Ile	Met	Glu	Gln	Leu	Lys	Ser
			100					105					110		
Phe	Gln	Ile	Ile	Ala	His	Leu	Lys	Arg	Leu	Gln	Glu	Glu	Ile	Asn	Glu
		115					120					125			
Val	Lys	Thr	Trp	Ser	Asn	Arg	Ile	Thr	Glu	Lys	Gln	Asp	Ile	Leu	Asn
		130				135					140				
Asn	Ser	Leu	Thr	Thr	Leu	Ser	Gln	Asp	Ile	Thr	Lys	Val	Asp	Gln	Ser
145				150						155				160	
Thr	Thr	Ser	Met	Ala	Lys	Asp	Val	Gly	Leu	Lys	Ile	Thr	Ser	Val	Lys
			165					170						175	
Thr	Asp	Ile	Arg	Arg	Ile	Ser	Gly	Leu	Val	Thr	Asp	Val	Ile	Ser	Leu
			180					185					190		
Thr	Asp	Ser	Val	Gln	Glu	Leu	Glu	Asn	Lys	Ile	Glu	Lys	Val	Glu	Lys
		195				200						205			
Asn	Thr	Val	Lys	Asn	Ile	Gly	Asp	Leu	Leu	Ser	Ser	Ser	Ile	Asp	Arg
	210					215					220				
Thr	Ala	Thr	Leu	Arg	Lys	Thr	Ala	Ser	Glu	Asn	Ser	Gln	Arg	Ile	Asn

```

225                230                235                240
Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser Asp Phe Asp Lys His
                245                250                255
Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg Ala Lys Val Leu Lys
                260                265                270
Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys Val Tyr Asn Leu Lys
                275                280                285
Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn Asp Leu Thr Leu Arg
                290                295                300
Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg Glu Lys Glu Ile Ala
305                310                315                320
Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile Val Gln Ala Glu Ile
                325                330                335
Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser Asp Met Asn
                340                345                350

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<210> 2913
<211> 361
<212> DNA
<213> Homo sapiens

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<400> 2913
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120
cggcgcgatg acgtcttcac tgaggetgag ttgagggtga agttcttcca ggcccgagat
180
gcttggtccc ggtccatcct gactgccatt cctaattgatg atccctattt ccatattaca
240
aaaaccatcg agggcctccc gtgtccatct ctttgatatc atcaccacgt accgggcat
300
cttctcagac gaggaccac tgctgcccc tgccatgggt gagcacactg ggatgagagt
360
g
361

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<210> 2914
<211> 112
<212> PRT
<213> Homo sapiens

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<400> 2914
Met Ala Gly Gly Ser Ser Gly Ser Ser Ser Glu Lys Met Ala Arg Tyr
1                5                10                15
Trp Val Met Ile Ser Lys Arg Trp Thr Arg Glu Ala Leu Asp Gly Phe
                20                25                30
Cys Asn Met Glu Ile Gly Ile Ile Arg Asn Gly Ser Gln Asp Gly
                35                40                45
Pro Glu Pro Ser Ile Ser Gly Leu Lys Lys Leu His Pro Gln Leu Ser
                50                55                60
Leu Ser Glu Asp Val His Ala Pro Gln Val Ala Asn Asp Thr Glu Ala
65                70                75                80
Gly Arg Lys Leu Asp Val Gly Pro Gln Leu Leu Asp Gln Leu Ala Gln

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	85		90		95
His	Gln	Leu	His	Gly	Leu
		Ala	His	Phe	Val
			His	Asp	Ala
				Leu	Asp
	100		105		110

<210> 2915

<211> 1782

<212> DNA

<213> Homo sapiens

<400> 2915

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120
tcagctgccg atagagaaat atacttactt agaacttccc ttcatcgaga aagagaacaa
180
gcgcaacaac ttcatacaact tcttgcatcg aaagaacagg aacacaggaa ggaacttgaa
240
acaagggagt tttttactga tgctgacttc caggatgcct tagctaaga aatagccaaa
300
gaagagaaaa agcatgagca aatgataaaa gaataccaag agaaaattga cgtgttaagc
360
cagcagtata tggatttaga aaatgaattc cgtattgctt taactgttga agccagaaga
420
tttcaagatg ttaaagatgg ttttgaaaaa gttgcaactg agttagcaaa gagcaaacat
480
gctcttattt gggctcaacg aaaagaaaaa gagtcttcct cttaatttaa agatctgacc
540
tgtatggtaa aggaacaaaa aacaaaactg gcagaagttt ctaaatgaa acaagaaaaa
600
gcagcaaatt tacagaatca aatcaacacc cttgaaattt taattgaaga tgacaagcag
660
aagagtattc aaatagaact tctcaagcac gaaaaagtcc agcttatttc tgagctagca
720
gccaaaggat cactaatatt tgggttaagg acagaaagaa aagtatgggg acatgagctg
780
gcacaacaag gatcttctct agcccaaaat cgtggaaaat tggaggctca aattgagagt
840
ttatctagag agaatgaatg tctgcgaaag acaaatgaaa gtgatagtga tgcattaaga
900
ataaagtgca aaatcataga cgaccaaact gaaactatta gaaaattaaa agattgttta
960
caagaaaaag atgaacacat caaaagatta caagaaaaga tcacagaaat agaaaaatgc
1020
actcaagaac aacttgatga aaaatcttca caactggatg aggtacttga gaagtggaa
1080
aggcacaatg aaagaaaaga aaaactaaaa caacagttga aaggaaaagg agtagaactt
1140
gaagaaatca gaaaagctta cagtacactg aatcggaagt ggcgatgata aggagaactt
1200
ctatgtcatc ttgaaacaca agtaaaagaa gtgaaagaaa aatttgaaaa caaggaaaa
1260
aaacttaag cggaagaga caaaagtatt gaactacaaa agaatgcaat ggaaaaactt
1320

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catagtatgg atgatgcctt taaaagacaa gttgatgcaa ttgttgaagc tcacaaagct
 1380
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 1440
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 1620
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 1680
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 1782

<210> 2916

<211> 519

<212> PRT

<213> Homo sapiens

<400> 2916

Gln	Glu	Asp	His	Leu	Lys	His	Leu	Arg	Thr	Leu	Glu	Lys	Thr	Leu	Glu
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Lys	Met	Glu	Arg	Gln	Lys	Arg	Gln	Gln	Ala	Ala	Gln	Ile	Arg	Leu	
			20					25				30			
Ile	Gln	Glu	Val	Glu	Leu	Lys	Ala	Ser	Ala	Ala	Asp	Arg	Glu	Ile	Tyr
			35				40				45				
Leu	Leu	Arg	Thr	Ser	Leu	His	Arg	Glu	Arg	Glu	Gln	Ala	Gln	Gln	Leu
	50					55					60				
His	Gln	Leu	Leu	Ala	Leu	Lys	Glu	Gln	Glu	His	Arg	Lys	Glu	Leu	Glu
					70				75					80	
Thr	Arg	Glu	Phe	Phe	Thr	Asp	Ala	Asp	Phe	Gln	Asp	Ala	Leu	Ala	Lys
			85						90					95	
Glu	Ile	Ala	Lys	Glu	Glu	Lys	Lys	His	Glu	Gln	Met	Ile	Lys	Glu	Tyr
			100					105					110		
Gln	Glu	Lys	Ile	Asp	Val	Leu	Ser	Gln	Gln	Tyr	Met	Asp	Leu	Glu	Asn
			115				120					125			
Glu	Phe	Arg	Ile	Ala	Leu	Thr	Val	Glu	Ala	Arg	Arg	Phe	Gln	Asp	Val
			130			135					140				
Lys	Asp	Gly	Phe	Glu	Asn	Val	Ala	Thr	Glu	Leu	Ala	Lys	Ser	Lys	His
					150					155				160	
Ala	Leu	Ile	Trp	Ala	Gln	Arg	Lys	Glu	Asn	Glu	Ser	Ser	Ser	Leu	Ile
			165					170						175	
Lys	Asp	Leu	Thr	Cys	Met	Val	Lys	Glu	Gln	Lys	Thr	Lys	Leu	Ala	Glu
			180					185					190		
Val	Ser	Lys	Leu	Lys	Gln	Glu	Thr	Ala	Ala	Asn	Leu	Gln	Asn	Gln	Ile
			195				200					205			
Asn	Thr	Leu	Glu	Ile	Leu	Ile	Glu	Asp	Asp	Lys	Gln	Lys	Ser	Ile	Gln
			210			215						220			
Ile	Glu	Leu	Leu	Lys	His	Glu	Lys	Val	Gln	Leu	Ile	Ser	Glu	Leu	Ala
					230					235				240	
Ala	Lys	Glu	Ser	Leu	Ile	Phe	Gly	Leu	Arg	Thr	Glu	Arg	Lys	Val	Trp
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Lys Leu Glu Ala Gln Ile Glu Ser Leu Ser Arg Glu Asn Glu Cys Leu
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Arg Lys Thr Asn Glu Ser Asp Ser Asp Ala Leu Arg Ile Lys Cys Lys
290                295                300
Ile Ile Asp Asp Gln Thr Glu Thr Ile Arg Lys Leu Lys Asp Cys Leu
305                310                315                320
Gln Glu Lys Asp Glu His Ile Lys Arg Leu Gln Glu Lys Ile Thr Glu
325                330                335
Ile Glu Lys Cys Thr Gln Glu Gln Leu Asp Glu Lys Ser Ser Gln Leu
340                345                350
Asp Glu Val Leu Glu Lys Leu Glu Arg His Asn Glu Arg Lys Glu Lys
355                360                365
Leu Lys Gln Gln Leu Lys Gly Lys Glu Val Glu Leu Glu Glu Ile Arg
370                375                380
Lys Ala Tyr Ser Thr Leu Asn Arg Lys Trp His Asp Lys Gly Glu Leu
385                390                395                400
Leu Cys His Leu Glu Thr Gln Val Lys Glu Val Lys Glu Lys Phe Glu
405                410                415
Asn Lys Glu Lys Lys Leu Lys Ala Glu Arg Asp Lys Ser Ile Glu Leu
420                425                430
Gln Lys Asn Ala Met Glu Lys Leu His Ser Met Asp Asp Ala Phe Lys
435                440                445
Arg Gln Val Asp Ala Ile Val Glu Ala His Gln Ala Glu Ile Ala Gln
450                455                460
Leu Ala Asn Glu Lys Gln Lys Cys Ile Asp Ser Ala Asn Leu Lys Val
465                470                475                480
His Gln Ile Glu Lys Glu Met Arg Glu Leu Leu Glu Glu Thr Cys Lys
485                490                495
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<210> 2917

<211> 2636

<212> DNA

<213> Homo sapiens

<400> 2917

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420

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<210> 2918

<211> 509

<212> PRT

<213> Homo sapiens

<400> 2918

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		20						25					30		
Met	Asp	Glu	Leu	Val	Pro	Leu	Gly	Glu	Leu	Thr	Lys	His	Ser	Thr	Ser
	35						40					45			
Ala	Val	Asp	Leu	Ser	Thr	Xaa	Phe	Ala	Gln	Ile	Ser	His	Thr	Ala	Arg
	50					55					60				
Gln	Leu	Asp	Trp	Pro	Asp	Pro	Glu	Glu	Ala	Phe	Met	Ile	Thr	Val	Lys
65					70				75					80	
Phe	Val	Glu	Asp	Thr	Cys	Arg	Leu	Ala	Leu	Val	Tyr	Cys	Ser	Leu	Ile
				85				90						95	
Lys	Ala	Arg	Ala	Arg	Glu	Leu	Ser	Ser	Gly	Gln	Lys	Asp	Gln	Gly	Gln
			100					105					110		
Ala	Ala	Asn	Met	Leu	Cys	Val	Val	Val	Asn	Asp	Met	Glu	Gln	Leu	Arg
		115					120					125			
Leu	Val	Ile	Gly	Lys	Leu	Pro	Ala	Gln	Leu	Ala	Trp	Glu	Ala	Leu	Glu
	130					135					140				
Gln	Arg	Val	Gly	Ala	Val	Leu	Glu	Gln	Gly	Gln	Leu	Gln	Asn	Thr	Leu
145				150					155					160	
His	Ala	Gln	Leu	Gln	Ser	Ala	Leu	Ala	Gly	Leu	Gly	His	Glu	Ile	Arg
			165					170						175	
Thr	Gly	Val	Arg	Thr	Leu	Ala	Glu	Gln	Leu	Glu	Val	Gly	Ile	Ala	Lys
		180					185						190		
His	Ile	Gln	Lys	Leu	Val	Gly	Val	Arg	Glu	Ser	Val	Leu	Pro	Glu	Asp
	195						200					205			
Ala	Ile	Leu	Pro	Leu	Met	Lys	Phe	Leu	Glu	Val	Glu	Leu	Cys	Tyr	Met

210	215	220
Asn Thr Asn Leu Val Gln Glu Asn Phe Ser Ser Leu Leu Thr Leu Leu		
225	230	235
Trp Thr His Thr Leu Thr Val Leu Val Glu Ala Ala Ala Ser Gln Arg		240
	245	250
Ser Ser Ser Leu Ala Ser Asn Arg Leu Lys Ile Ala Leu Gln Asn Leu		255
	260	265
Glu Ile Cys Phe His Ala Glu Gly Cys Gly Leu Pro Pro Lys Ala Leu		270
	275	280
His Thr Ala Thr Phe Gln Ala Leu Gln Arg Asp Leu Glu Leu Gln Ala		285
	290	295
Ala Ser Ser Arg Glu Leu Ile Arg Lys Tyr Phe Cys Ser Arg Ile Gln		300
	305	310
Gln Gln Ala Glu Thr Thr Ser Glu Glu Leu Gly Ala Val Thr Val Lys		315
	320	325
Ala Ser Tyr Arg Ala Ser Glu Gln Lys Leu Arg Val Glu Leu Leu Ser		330
	335	340
Ala Ser Ser Leu Leu Pro Leu Asp Ser Asn Gly Ser Ser Asp Pro Phe		345
	350	355
Val Gln Leu Thr Leu Glu Pro Arg His Glu Phe Pro Glu Leu Ala Ala		360
	365	370
Arg Glu Thr Gln Lys His Lys Lys Asp Leu His Pro Leu Phe Asp Glu		375
	380	385
Thr Phe Glu Phe Leu Val Pro Ala Glu Pro Cys Arg Lys Ala Gly Ala		390
	395	400
Cys Leu Leu Leu Thr Val Leu Asp Tyr Asp Thr Leu Gly Ala Asp Asp		405
	410	415
Leu Glu Gly Glu Ala Phe Leu Pro Leu Arg Glu Val Pro Gly Leu Ser		420
	425	430
Gly Ser Glu Glu Pro Gly Glu Val Pro Gln Thr Arg Leu Pro Leu Thr		435
	440	445
Tyr Pro Ala Pro Asn Gly Asp Pro Ile Leu Gln Leu Leu Glu Gly Arg		450
	455	460
Lys Gly Asp Arg Glu Ala Gln Val Phe Val Arg Leu Arg Arg His Arg		465
	470	475
Ala Lys Gln Ala Ser Gln His Ala Leu Arg Pro Ala Pro		480
	485	490
	495	
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<210> 2919

<211> 455

<212> DNA

<213> Homo sapiens

<400> 2919

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 120
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 180
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 240
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 300

gcaagatggt tagtgagaag gctggacacc tgccgggcca gacctgagtg cacagcctct
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<210> 2920

<211> 143

<212> PRT

<213> Homo sapiens

<400> 2920

Met	Ala	Trp	Ala	Ala	Phe	Gln	Val	Leu	Ala	Ile	Arg	Cys	Phe	Glu	Trp
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Glu	Lys	Glu	Glu	Gly	Gly	Ser	Thr	Glu	Ala	Val	His	Ser	Gly	Leu	Ala
		20						25					30		
Arg	Gln	Val	Ser	Ser	Leu	Leu	Thr	Asn	His	Leu	Ala	Arg	Ala	Thr	Glu
		35				40						45			
Cys	Cys	Gly	Asn	Gln	Ala	Ala	Gly	Asn	Asp	Ala	Leu	Gln	Asp	Val	Leu
	50				55					60					
Ser	Leu	Leu	Asn	Asp	Leu	Ser	Arg	Ser	His	Ile	Gly	Lys	Ala	Ile	Leu
	65			70					75				80		
Ser	Gln	Pro	Ala	Cys	Val	Ser	Lys	Leu	Leu	Ser	Leu	Leu	Leu	Asp	Gln
			85					90						95	
Arg	Pro	Ser	Pro	Lys	Leu	Val	Leu	Ile	Ile	Leu	Gln	Leu	Cys	Arg	Ala
			100				105						110		
Ala	Leu	Pro	Leu	Met	Ser	Val	Glu	Asp	Cys	Gly	Asn	Val	Glu	Leu	Pro
		115				120						125			
Pro	Trp	Ser	Tyr	Ser	Val	Pro	Ser	Leu	Asn	Ser	Glu	Gln	Glu	Asp	
	130					135					140				

<210> 2921

<211> 1855

<212> DNA

<213> Homo sapiens

<400> 2921

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 120
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 180
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 1680
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 1740
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<210> 2922

<211> 452

<212> PRT

<213> Homo sapiens

<400> 2922

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Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr Asp Glu Gln Gly Ala			
	35	40	45
Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His Val Gly His Cys His			
	50	55	60
Pro Leu Val Val Gln Ala Ala His Glu Gln Asn Gln Val Leu Asn Thr			
	65	70	75
Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp Tyr Ala Gln Arg Leu			
	85	90	95
Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe Tyr Phe Leu Asn Ser			
	100	105	110
Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu Ala Arg His Tyr Thr			
	115	120	125
Gly His Gln Asp Val Val Val Leu Asp His Ala Tyr His Gly His Leu			
	130	135	140
Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe Arg Asn Leu Asp Gly			
	145	150	155
Gln Lys Glu Trp Val His Val Ala Pro Leu Pro Asp Thr Tyr Arg Gly			
	165	170	175
Pro Tyr Arg Xaa Arg Thr Thr Pro Thr Gln Leu Trp Xaa Tyr Ala Asn			
	180	185	190
Glu Val Lys Arg Val Val Ser Ser Ala Gln Glu Lys Gly Arg Lys Ile			
	195	200	205
Ala Ala Phe Phe Ala Glu Ser Leu Pro Ser Val Gly Gly Gln Ile Ile			
	210	215	220
Pro Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu His Ile Arg Lys Ala			
	225	230	235
Gly Gly Val Phe Val Ala Asp Glu Ile Gln Val Gly Phe Gly Arg Val			
	245	250	255
Gly Lys His Phe Trp Ala Phe Gln Leu Gln Gly Lys Asp Phe Val Pro			
	260	265	270
Asp Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly His Pro Val Ala			
	275	280	285
Cys Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe Glu Ala Thr Gly			
	290	295	300
Val Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val Ser Cys Ala Val			
	305	310	315
Gly Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln Leu Gln Asp His			
	325	330	335
Ala Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu Trp Gln Gln Lys			
	340	345	350
Ile Arg His Pro Ile Val Gly Asp Val Arg Gly Val Gly Leu Phe Ile			
	355	360	365
Gly Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr Pro Ala Thr Glu			
	370	375	380
Glu Ala Xaa Val Tyr Leu Val Ser Arg Leu Lys Glu Asn Tyr Val Leu			
	385	390	395
Leu Ser Thr Asp Gly Pro Gly Arg Asn Ile Leu Lys Phe Lys Pro Pro			
	405	410	415
Met Cys Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala Lys Leu Asp			
	420	425	430
Ala Ile Leu Thr Asp Met Glu Glu Lys Val Arg Ser Cys Glu Thr Leu			

435
Arg Leu Gln Pro
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<210> 2923
<211> 572
<212> DNA
<213> Homo sapiens

<400> 2923
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120
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240
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300
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480
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<210> 2924
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2924
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20 25 30
Arg Arg Asn Ser Val Tyr Cys Gly Gly Glu Leu Gly Gly Ala Gln Pro
35 40 45
Arg Arg Thr Gly Ser Thr Ala Ala Pro Ala Ser Ala Pro Pro Ile Ala
50 55 60
Gly Thr Gly Ser Pro Gly Trp Gln Arg Ser Leu Gln Pro Ala Leu Gly
65 70 75 80
Pro Arg Thr Ala Ser Trp Gln Trp Trp Glu Gln
85 90

<210> 2925
<211> 1999
<212> DNA
<213> Homo sapiens

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180
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240
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300
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420
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720
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780
gatttaaaga cgaatacaag agaagatccc aaagaaaata gaaaaacaa aaaagaaaaa
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<212> PRT

<213> Homo sapiens

<400> 2926

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 50 55 60
 Gln Asn Pro Leu Val Ser Glu Arg Leu Glu Leu Ser Val Leu Tyr Lys
 65 70 75 80
 Glu Tyr Ala Glu Asp Asp Asn Ile Tyr Gln Gln Lys Ile Lys Asp Leu
 85 90 95
 His Lys Lys Tyr Ser Tyr Ile Arg Lys Thr Arg Pro Asp Gly Asn Cys
 100 105 110
 Phe Tyr Arg Ala Phe Gly Phe Ser His Leu Glu Ala Leu Leu Asp Asp
 115 120 125
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 <212> PRT
 <213> Homo sapiens

<400> 2930

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Gln Lys Glu Asn Met Ile Asp Lys Asp Val Glu Leu Ser Val Val Leu
          50          55          60
Pro Gly Asp Ile Ile Lys Ser Thr Thr Val His Gly Ser Lys Pro Met
65          70          75          80
Met Asp Leu Leu Ile Phe Leu Cys Ala Gln Tyr His Leu Asn Pro Ser
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Ser Tyr Thr Ile Asp Leu Leu Ser Ala Glu Gln Asn His Ile Lys Phe
          100          105          110
Lys Pro Asn Thr Pro Ile Gly Met Leu Glu Val Glu Lys Val Ile Leu
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Lys Pro Lys Met Leu Asp Lys Lys Lys Pro Thr Pro Ile Ile Pro Glu
          130          135          140
Lys Thr Val Arg Val Val Ile Asn Phe Lys Lys Thr Gln Lys Thr Ile
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Val Arg Val Ser Pro His Ala Ser Leu Gln Glu Leu Ala Pro Ile Ile
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Cys Ser Lys Cys Glu Phe Asp Pro Leu His Thr Leu Leu Leu Lys Asp
          180          185          190
Tyr Gln Ser Gln Glu Pro Leu Asp Leu Thr Lys Ser Leu Asn Asp Leu
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Ile Ser Gln Asn Leu Asp Ile Met Lys Glu Lys Glu Asn Lys Gly Phe
225          230          235          240
Phe Ser Phe Phe Gln Arg Ser Lys Lys Lys Arg Asp Gln Thr Ala Ser
          245          250          255
Ala Pro Ala Thr Pro Leu Val Asn Lys His Arg Pro Thr Phe Thr Arg
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Ser Asn Thr Ile Ser Lys Pro Tyr Ile Ser Asn Thr Leu Pro Ser Asp
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Ala Pro Lys Lys Arg Arg Ala Pro Leu Pro Pro Met Pro Ala Ser Gln
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Ile Val Lys Ser Met Ser Val Asp Glu Thr Asp Lys Ser Pro Cys Glu
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Phe Glu Cys Pro Gly Thr Pro Glu Ala Ala Ile Thr Ser Leu Thr Ser
      435              440              445
Gly Ile Ser Ser Asp Tyr Ser Leu Glu Glu Ile Asp Glu Lys Glu Glu
      450              455              460
Leu Ser Glu Val Pro Lys Val Glu Ala Glu Asn Ile Ser Pro Lys Ser
      465              470              475              480
Gln Asp Ile Pro Phe Val Ser Thr Asp Ile Ile Asn Thr Leu Lys Asn
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Asp Pro Asp Ser Ala Leu Gly Asn Gly Ser Gly Glu Phe Ser Gln Asn
      500              505              510
Ser Met Glu Glu Lys Gln Glu Thr Lys Ser Thr Asp Gly Gln Glu Pro
      515              520              525
His Ser Val Val Tyr Asp Thr Ser Asn Gly Lys Lys Val Val Asp Ser
      530              535              540
Ile Arg Asn Leu Lys Ser Leu Gly Pro Asn Gln Glu Asn Val Gln Asn
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Glu Ile Ile Val Tyr Pro Glu Asn Thr Glu Asp Asn Met Lys Asn Gly
      565              570              575
Val Lys Lys Thr Glu Ile Asn Val Glu Gly Val Ala Lys Asn Asn Asn
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Ile Asp Met Glu Val Glu Arg Pro Ser Asn Ser Glu Ala His Glu Thr
      595              600              605
Asp Thr Ala Ile Ser Tyr Lys Glu Asn His Leu Ala Ala Ser Ser Val
      610              615              620
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      625              630              635              640
Ala Ile Gln Thr Thr Pro Ser Cys Asn Ser Phe Asp Gly Lys His Gln
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Asp His Asn Leu Ser Asp Ser Lys Val Glu Glu Cys Val Gln Thr Ser
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      675              680              685
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      885              890              895
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<212> DNA

<213> Homo sapiens

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240
ctgttatttt ttgtctgagc tgaatgttcc ctacttggtg atctattagg ctccagatgc
300
ggtgggggat ctagaactgg gcttcctctg ggggtgcctc caggagagaa gatatgtgtg
360
agccaggcca aaggagcaaa gtggacattg ggttgcttcc atcaccagga gagacagggt
420
ttccatggag ggcagacaat gtgaaaagta acaagaaaaa aaggctagca ctagattctg
480
aagcagcagt ctctgctgat aaaccagact cagtactgac tcatcatgtc cccaggaacc
540
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cacagtgcac agtcccttca cgcgt
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<210> 2932

<211> 90

<212> PRT

<213> Homo sapiens

<400> 2932

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Met Cys Glu Pro Gly Gln Arg Ser Lys Val Asp Ile Gly Leu Leu Pro
1          5          10          15
Ser Pro Gly Glu Thr Gly Val Pro Trp Arg Ala Asp Asn Val Glu Ser
          20          25          30
Asn Lys Lys Lys Arg Leu Ala Leu Asp Ser Glu Ala Ala Val Ser Ala
          35          40          45
Asp Lys Pro Asp Ser Val Leu Thr His His Val Pro Arg Asn Leu Gln
          50          55          60
Lys Leu Cys Lys Glu Arg Ala Gln Lys Leu Cys Arg Asn Ser Thr Arg
65          70          75          80
Val Pro Ala Gln Cys Thr Val Pro Ser Arg
          85          90

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<210> 2933

<211> 688

<212> DNA

<213> Homo sapiens

<400> 2933

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120
cgagaaagtc aagaaacgac tagagaactt ctgaaagtta aagacagatt aattgaagta
180
gaaagaaata atgctacact gcaagcagag aagcaagcgt tgaaaactca actgaagcaa
240

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cttgagacac agaacaataa ttgacaggct cagattcttg cacttcagag gcagacagt
 300
 tcattacaag aacagaatac cactcttcaa acacagaatg ccaagcttca ggttgaaaa
 360
 tccaccctta attcccaaaag tacctcactc atgaaccaga atgcccaact cctaaccag
 420
 cagtcttctc tagaaaaatga aaatgaatct gtaatcaaag agcgagaaga cctaaatct
 480
 ctctatgatt ctctgatcaa agatcatgaa aagctggaac ttcttcatga acgtcaggct
 540
 tcagagtatg aatctcttat ctctaaacat ggaactctga agtctgcccc caaaaatctt
 600
 gaggtggaac atagagacct tgaagacctg tacaatcagt tattaataca gaaaggacag
 660
 ttggaagatt tggaaaaaat gctcaaaag
 688

<210> 2934

<211> 229

<212> PRT

<213> Homo sapiens

<400> 2934

Gln	Leu	Arg	Gln	Glu	Leu	Lys	Thr	Val	Lys	Lys	Asn	Tyr	Glu	Ala	Leu
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Lys	Gln	Arg	Gln	Asp	Glu	Glu	Arg	Met	Val	Gln	Ser	Ser	Pro	Pro	Ile
			20					25					30		
Ser	Gly	Glu	Asp	Asn	Lys	Trp	Glu	Arg	Glu	Ser	Gln	Glu	Thr	Thr	Arg
	35						40					45			
Glu	Leu	Leu	Lys	Val	Lys	Asp	Arg	Leu	Ile	Glu	Val	Glu	Arg	Asn	Asn
	50					55				60					
Ala	Thr	Leu	Gln	Ala	Glu	Lys	Gln	Ala	Leu	Lys	Thr	Gln	Leu	Lys	Gln
65				70					75					80	
Leu	Glu	Thr	Gln	Asn	Asn	Asn	Leu	Gln	Ala	Gln	Ile	Leu	Ala	Leu	Gln
			85					90						95	
Arg	Gln	Thr	Val	Ser	Leu	Gln	Glu	Gln	Asn	Thr	Thr	Leu	Gln	Thr	Gln
	100							105					110		
Asn	Ala	Lys	Leu	Gln	Val	Glu	Asn	Ser	Thr	Leu	Asn	Ser	Gln	Ser	Thr
	115						120				125				
Ser	Leu	Met	Asn	Gln	Asn	Ala	Gln	Leu	Leu	Ile	Gln	Gln	Ser	Ser	Leu
	130				135						140				
Glu	Asn	Glu	Asn	Glu	Ser	Val	Ile	Lys	Glu	Arg	Glu	Asp	Leu	Lys	Ser
145				150					155					160	
Leu	Tyr	Asp	Ser	Leu	Ile	Lys	Asp	His	Glu	Lys	Leu	Glu	Leu	Leu	His
			165					170						175	
Glu	Arg	Gln	Ala	Ser	Glu	Tyr	Glu	Ser	Leu	Ile	Ser	Lys	His	Gly	Thr
	180						185						190		
Leu	Lys	Ser	Ala	His	Lys	Asn	Leu	Glu	Val	Glu	His	Arg	Asp	Leu	Glu
	195					200						205			
Asp	Arg	Tyr	Asn	Gln	Leu	Leu	Lys	Gln	Lys	Gly	Gln	Leu	Glu	Asp	Leu
	210					215						220			
Glu	Lys	Met	Leu	Lys											
225															

<210> 2935
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 2935
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tttgaaggtta tgggggaacg aaaaaaatac tattatggag tgcagtgcac agtttgcagt
120
aactctaaaa gataaagcaa gaaatgtcaa gtaggttttg cacattgggc tgctttaggc
180
tgtgccctct gattcttctg gtgtactcat gatactctcc cttgggtgcc tccaggtga
240
cgcagctatt tacgttcaga gtgaaatggg ctgtgtggct gggattggga aaggccttgt
300
taaagctggg agaggtttgg tcatgggtgac aggggacctg aaggccacgc tctctctccc
360
tcttgccaat acagggacaa gttaaagaag aagaagaaag taaaggtaaa gatggaaaag
420
aaatccacgc cctctagggg ctcatcatcc aagtcgtcct caaggcagct aagcgagagc
480
ttcaagagca aagagtttgt gtctagtgat gagagctctt cgggagagaa caagagcaaa
540
aagaagagga ggaggagcga ggactctgaa gaagaagaac tagccagtag tccccccagc
600
tcagaggact cagcgtcagg atccgatgag tagaaacgga ggaaggttct ctttgcgctt
660
gccttctcac acccccgcga agtcagcagg gaaacgcaga gaactcctat gaaccaccaa
720
aaggctgtaa atgatgaaac atgcaaagct agccacataa catcaagtgt ctttcttca
780
gcctctctcg gtaaagcatc atctcgaaag ccatttggga tcttcttccc aaatgttctg
840
tgcagtatga gtgggaagag tctctgtagag agcagcttga atgttaaaac caaaaagaat
900
gcaccatctg caacgatcca ccagggcgaa gaagaaggac cacttgatat ctgggctgtt
960
gtgaaacctg gaaataccaa ggaaaaaatt gcattctttg catcccacca gtgtagtaac
1020
aggataggat ctatgaaat aaaaagttcc tgggatattg atgggagagc tactaagaga
1080
aggaaaaaat caggggatct taaaaagcc aaggtacagg tggaaggat gagggagggt
1140
aacagcaggt gctaccaacc tgagcctttt gcatgtggca ttgagcactg ttctgtgcac
1200

<210> 2936
<211> 109
<212> PRT
<213> Homo sapiens

<400> 2936
Ser Trp Glu Arg Phe Gly His Gly Asp Arg Gly Pro Glu Gly Pro Ala

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      1           5           10           15
Pro Leu Pro Ser Cys Gln Tyr Arg Asp Lys Leu Lys Lys Lys Lys
      20
Val Lys Val Lys Met Glu Lys Lys Ser Thr Pro Ser Arg Gly Ser Ser
      35
Ser Lys Ser Ser Ser Arg Gln Leu Ser Glu Ser Phe Lys Ser Lys Glu
      50
Phe Val Ser Ser Asp Glu Ser Ser Ser Gly Glu Asn Lys Ser Lys Lys
      65
Lys Arg Arg Arg Ser Glu Asp Ser Glu Glu Glu Glu Leu Ala Ser Thr
      85
Pro Pro Ser Ser Glu Asp Ser Ala Ser Gly Ser Asp Glu
      100

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<210> 2937
 <211> 749
 <212> DNA
 <213> Homo sapiens

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<400> 2937
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120
ctctcaaat ttgtcttctg tcaatacaca ttctgggacc agtgtgagtc tacgggtggct
180
gccccgggtgg tggaccccgga ggtgccttca ccacagtcga aggatgcccc gtacacagtg
240
accttctccc actgtaagga ctatgtggtg aatgtaacag aagaatttct ggagttcatt
300
tcagatggag cactggccat tgaagtatgg ggccaccggt gtgctggaaa tggcagctcc
360
atctggggagg tcgattctct tcatgctaag acaagaacac tgcattgacag gtggaatgaa
420
gtaacgcgaa gaatagaaat gtggtatctc atattagaat tgaatgagtt agggagagat
480
gtgagcagtg aacttcacga ggcaaaagat gtcaaacacag gaggcattct tcaacttaga
540
caggggtcatt cccgtagagt acaagtcacg gtgaaacctg tgcagcattc aggggacactg
600
ccacttatgg ttgaagccat cctgtcagta tccatcggtg gtgtaactgc caggtccacc
660
aaactccaaa gagggctgga cagttaccag agagatgatg aggatggtag tgatatggat
720
agttatcagg aagaagactt aaactgcag
749

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<210> 2938
 <211> 249
 <212> PRT
 <213> Homo sapiens

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<400> 2938
Xaa Asn Ser Ser Glu Ser Gly Ser Leu Glu Val Val Asp Ser Ser Gly

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Glu Ile Ile His Arg Val Lys Lys Leu Thr Cys Arg Val Lys Ile Lys
20           25           30
Glu Ala Thr Gly Leu Pro Leu Asn Leu Ser Asn Phe Val Phe Cys Gln
35           40           45
Tyr Thr Phe Trp Asp Gln Cys Glu Ser Thr Val Ala Ala Pro Val Val
50           55           60
Asp Pro Glu Val Pro Ser Pro Gln Ser Lys Asp Ala Gln Tyr Thr Val
65           70           75
Thr Phe Ser His Cys Lys Asp Tyr Val Val Asn Val Thr Glu Glu Phe
85           90           95
Leu Glu Phe Ile Ser Asp Gly Ala Leu Ala Ile Glu Val Trp Gly His
100          105          110
Arg Cys Ala Gly Asn Gly Ser Ser Ile Trp Glu Val Asp Ser Leu His
115          120          125
Ala Lys Thr Arg Thr Leu His Asp Arg Trp Asn Glu Val Thr Arg Arg
130          135          140
Ile Glu Met Trp Ile Ser Ile Leu Glu Leu Asn Glu Leu Gly Glu Tyr
145          150          155
Ala Ala Val Glu Leu His Gln Ala Lys Asp Val Asn Thr Gly Gly Ile
165          170          175
Phe Gln Leu Arg Gln Gly His Ser Arg Arg Val Gln Val Thr Val Lys
180          185          190
Pro Val Gln His Ser Gly Thr Leu Pro Leu Met Val Glu Ala Ile Leu
195          200          205
Ser Val Ser Ile Gly Cys Val Thr Ala Arg Ser Thr Lys Leu Gln Arg
210          215          220
Gly Leu Asp Ser Tyr Gln Arg Asp Asp Glu Asp Gly Asp Asp Met Asp
225          230          235          240
Ser Tyr Gln Glu Glu Asp Leu Asn Cys
245

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<210> 2939
<211> 2405
<212> DNA
<213> Homo sapiens

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120
ccactgcac cagccaatag gagcccgacc accatggcgg agctgcagga ggtgcagatc
180
acagaggaga agccactgtt gccaggacag acgcctgagg cgGCCAAGAC tcactctgtg
240
gagacaccat acggtcttgt cactttcact gtctatggca cccccaaacc caaacgccca
300
gcgatcctta cctaccacga tgtgggactc aactataaat cttgcttcca gccactgttt
360
cagttcaggg acatgcagga aatcattcag aactttgtgc ggggttcagt ggatgccctt
420
ggaatggaag agggagcccc tgtgttccct ttgggatatc agtaccatc tctggaccag
480

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cttgacagaca tgatcccttg cgtcctgcag tacctaaatt tctctacaat aattggagtt
540
ggtggtggag ctggagccta catcctggcg agatatgtc ttaaccaccc ggacactgtt
600
gaaggtcttg tctcatcaa cattgatccc aatgccaagg gttggatgga ttgggcagcc
660
cacaagctaa caggcctcac ctctccatt cgggagatga tctctggaca tcttttcagc
720
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780
gcaccaaac tggataacat tgaattgtac tggaacagct acaacaaccg ccgagacctg
840
aactttgagc gtggagggtga tatcacctc aggtgtcctg tgatgtctgtt ggtaggagac
900
caagcacctc atgaagatgc agtgggtgaa tgtaactcaa aactggaccc caccagacc
960
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1080
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1860
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1920
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1980
tagtatgtgt ggagggtgcc ctccgtctc ccacaacttc tgctataaca ataaactgta
2040
gaggaaacaa agatcaaggt catctcccc catgatctgc cctttttccc ttgcttacgg
2100

tgaaccaatg tcccttcagc acctcccagg ttagatatgg gggagggtgag ggctgggtcc
 2160
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 2220
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 2405

<210> 2940

<211> 357

<212> PRT

<213> Homo sapiens

<400> 2940

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 Pro Gly Gln Thr Pro Glu Ala Ala Lys Thr His Ser Val Glu Thr Pro
 20 25 30
 Tyr Gly Ser Val Thr Phe Thr Val Tyr Gly Thr Pro Lys Pro Lys Arg
 35 40 45
 Pro Ala Ile Leu Thr Tyr His Asp Val Gly Leu Asn Tyr Lys Ser Cys
 50 55 60
 Phe Gln Pro Leu Phe Gln Phe Glu Asp Met Gln Glu Ile Ile Gln Asn
 65 70 75 80
 Phe Val Arg Val His Val Asp Ala Pro Gly Met Glu Glu Gly Ala Pro
 85 90 95
 Val Phe Pro Leu Gly Tyr Gln Tyr Pro Ser Leu Asp Gln Leu Ala Asp
 100 105 110
 Met Ile Pro Cys Val Leu Gln Tyr Leu Asn Phe Ser Thr Ile Ile Gly
 115 120 125
 Val Gly Val Gly Ala Gly Ala Tyr Ile Leu Ala Arg Tyr Ala Leu Asn
 130 135 140
 His Pro Asp Thr Val Glu Gly Leu Val Leu Ile Asn Ile Asp Pro Asn
 145 150 155 160
 Ala Lys Gly Trp Met Asp Trp Ala Ala His Lys Leu Thr Gly Leu Thr
 165 170 175
 Ser Ser Ile Pro Glu Met Ile Leu Gly His Leu Phe Ser Gln Glu Glu
 180 185 190
 Leu Ser Gly Asn Ser Glu Leu Ile Gln Lys Tyr Arg Asn Ile Ile Thr
 195 200 205
 His Ala Pro Asn Leu Asp Asn Ile Glu Leu Tyr Trp Asn Ser Tyr Asn
 210 215 220
 Asn Arg Arg Asp Leu Asn Phe Glu Arg Gly Gly Asp Ile Thr Leu Arg
 225 230 235 240
 Cys Pro Val Met Leu Val Val Gly Asp Gln Ala Pro His Glu Asp Ala
 245 250 255
 Val Val Glu Cys Asn Ser Lys Leu Asp Pro Thr Gln Thr Ser Phe Leu
 260 265 270
 Lys Met Ala Asp Ser Gly Gly Gln Pro Gln Leu Thr Gln Pro Gly Lys

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      275              280              285
Leu Thr Glu Ala Phe Lys Tyr Phe Leu Gln Gly Met Gly Tyr Met Ala
  290              295              300
Ser Ser Cys Met Thr Arg Leu Ser Arg Ser Arg Thr Ala Ser Leu Thr
  305              310              315              320
Ser Ala Ala Ser Val Asp Gly Asn Arg Ser Arg Ser Arg Thr Leu Ser
      325              330              335
Gln Ser Ser Glu Ser Gly Thr Leu Ser Ser Gly Pro Pro Gly His Thr
      340              345              350
Met Glu Val Ser Cys
      355

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<210> 2941

<211> 847

<212> DNA

<213> Homo sapiens

<400> 2941

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120
ggtgccaagg ccacagcccc ccagcatctc ttaaagcagg gtcagctctc ggccccgggg
180
ggtgcccagg cctcagtgga ggctccagct gcccctcggc ccacggccac ccagctgacc
240
cgcgacctgc tgcggagccg tggcattgcc ggtctctaca agggactcgg ggccacgctg
300
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360
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420
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540
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600
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660
ctgggggtgc tgcaggaccc ccaggcctga gcccagcacc cgctccaccc cagccagctg
720
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780
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840
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847

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<210> 2942

<211> 229

<212> PRT

<213> Homo sapiens

<400> 2942

Xaa Ala Leu Ser Ser Leu Arg Ala Leu Gly Ser Gln Asp Leu Pro Leu
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 20 25 30
 Gly Arg Gly His Asp His Leu Ala Gly Ala Ser Pro Thr Ala Arg Gln
 35 40 45
 His Leu Phe Lys Gln Gly Gln Leu Ser Ala Gln Gly Gly Ala Gln Pro
 50 55 60
 Ser Val Glu Ala Pro Ala Ala Pro Arg Pro Thr Ala Thr Gln Leu Thr
 65 70 75 80
 Arg Asp Leu Leu Arg Ser Arg Gly Ile Ala Gly Leu Tyr Lys Gly Leu
 85 90 95
 Gly Ala Thr Leu Leu Arg Asp Val Pro Phe Ser Val Val Tyr Phe Pro
 100 105 110
 Leu Phe Ala Asn Leu Asn Gln Leu Gly Arg Pro Ala Ser Glu Glu Lys
 115 120 125
 Ser Pro Phe Tyr Val Ser Phe Leu Ala Gly Cys Val Ala Gly Ser Ala
 130 135 140
 Ala Ala Val Ala Val Asn Pro Cys Asp Val Val Lys Thr Arg Leu Gln
 145 150 155 160
 Ser Leu Gln Arg Gly Val Asn Glu Asp Thr Tyr Ser Gly Ile Leu Asp
 165 170 175
 Cys Ala Arg Lys Ile Leu Arg His Glu Gly Pro Ser Ala Phe Leu Lys
 180 185 190
 Gly Ala Tyr Cys Arg Ala Leu Val Ile Ala Pro Leu Phe Gly Ile Ala
 195 200 205
 Gln Val Val Tyr Phe Leu Gly Ile Ala Glu Ser Leu Leu Gly Leu Leu
 210 215 220
 Gln Asp Pro Gln Ala
 225

<210> 2943

<211> 1501

<212> DNA

<213> Homo sapiens

<400> 2943

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 120
 tctagtgttt ggggtttcttc gcggtctctc aagatgaacc gactcttcgg gaaagcgaaa
 180
 cccaaggctc cgccgcccag cctgactgac tgcattggca cggtggacag tagagcagaa
 240
 tccattgaca agaagatttc tcgattggat gctgagctag tgaagtataa ggatcagatc
 300
 aagaagatga gagagggtcc tgcaaaagaat atggtcaagc agaaagcett gcgagtttta
 360
 aagcaaaaaa ggatgtatga gcagcagcgg gacaatcttg ccaacagtca ttcaacatgg
 420
 aacgccaatt ataccatcca gtctttgaag gacaccaaga ccacggttga tgctatgaaa
 480

ctgggagtaa aggaaatgaa gaaggcatac aagcaagtga agatcgacca gattgaggat
 540
 ttacaagacc agctagagga tatgatggaa gatgcaaattg aaatccaaga agcactgagt
 600
 cgcagttatg gcacccacaga actggatgaa gatgatttag aagcagagtt ggatgcacta
 660
 ggtgatgagc ttctggctga tgaagacagt tcttatttgg atgaggcagc atctgcaccc
 720
 gcaattccag aaggtgttcc cactgataca aaaaaacaagg atggagttct ggtggatgaa
 780
 tttggattgc cacagatccc tgcttcatag atttgcata tccaagcata tcttgtaaaa
 840
 caaacacata ttatgggact aggaaatatt tatctttcca aatttgccat aacagattta
 900
 ggtttctttc ctttctttga aggaaagtgt aattacattg ctcttttatt ttttccatta
 960
 agagactcat tgcttgggaa atgctttctt cgtactaaaa tttgattcct ttttttctta
 1020
 tgaaaaacga actcagttta aaagtatttt tagctcgtat gacttgtttt cattcattaa
 1080
 taataatttg aaataaaaact aaggaaatgg aatcttaaaa gtctatgaca gtgtaactct
 1140
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 1200
 tattatgatt cagaatcatt ttctattgtg gtattatagg ttggttaaag tgatggcctt
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 1320
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 1380
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 1500
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 1501

<210> 2944

<211> 218

<212> PRT

<213> Homo sapiens

<400> 2944

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 20 25 30
 Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
 35 40 45
 Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
 50 55 60
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 Asn Leu Ala Asn Ser His Ser Thr Trp Asn Ala Asn Tyr Thr Ile Gln

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			165						170					175	
Glu	Asp	Ser	Ser	Tyr	Leu	Asp	Glu	Ala	Ala	Ser	Ala	Pro	Ala	Ile	Pro
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<210> 2945

<211> 3331

<212> DNA

<213> Homo sapiens

<400> 2945

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<210> 2946

<211> 463

<212> PRT

<213> Homo sapiens

<400> 2946

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Lys	Arg	Thr	Thr	Pro	Leu	Gln	Thr	His	Ser	Ile	Ile	Ile	Ser	Asp	Gln
		35					40					45			
Val	Pro	Ser	Asp	Gln	Asp	Ala	His	Gln	Tyr	Leu	Arg	Leu	Arg	Asp	Gln
		50				55				60					
Ser	Glu	Ala	Thr	Gln	Val	Met	Ala	Glu	Pro	Gly	Glu	Gly	Gly	Ser	Glu
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Thr	Val	Ala	Leu	Pro	Pro	Pro	Pro	Pro	Ser	Glu	Glu	Gly	Gly	Val	Pro
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Gln	Asp	Ala	Ala	Gly	Arg	Gly	Gly	Thr	Pro	Gln	Ile	Arg	Val	Val	Gly
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Gly	Arg	Gly	His	Val	Ala	Ile	Lys	Ala	Gly	Gln	Glu	Glu	Gly	Gln	Pro
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Pro	Ala	Glu	Gly	Leu	Ala	Ala	Ser	Val	Val	Met	Ala	Ala	Asp	Arg	
		130				135					140				
Ser	Leu	Lys	Lys	Gly	Val	Gln	Gly	Gly	Glu	Lys	Ala	Leu	Glu	Ile	Cys


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Ala Glu Glu Val Lys Thr Gly Lys Cys Ala Thr Val Ser Ala Ala Val
180              185              190
Ala Glu Arg Glu Ser Ala Glu Val Val Val Lys Glu Gly Leu Ala Glu
195              200              205
Lys Glu Val Met Glu Glu Gln Met Glu Val Glu Glu Gln Pro Pro Glu
210              215              220
Gly Glu Glu Ile Glu Val Ala Glu Glu Asp Arg Leu Glu Glu Glu Ala
225              230              235
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245              250              255
Pro Leu Glu Ala Ile Gln Leu Glu Leu Asp Thr Val Asn Ala Gln Ala
260              265              270
Asp Arg Ala Phe Gln Gln Leu Glu His Lys Phe Gly Arg Met Arg Arg
275              280              285
His Tyr Leu Glu Arg Arg Asn Tyr Ile Ile Gln Asn Ile Pro Gly Phe
290              295              300
Trp Met Thr Ala Phe Arg Asn His Pro Gln Leu Ser Ala Met Ile Arg
305              310              315
Gly Gln Asp Ala Glu Met Leu Arg Tyr Ile Thr Asn Leu Glu Val Lys
325              330              335
Glu Leu Arg His Pro Arg Thr Gly Cys Lys Phe Lys Phe Phe Arg
340              345              350
Arg Asn Pro Tyr Phe Arg Asn Lys Leu Ile Val Lys Glu Tyr Glu Val
355              360              365
Arg Ser Ser Gly Arg Val Val Ser Leu Ser Thr Pro Ile Ile Trp Arg
370              375              380
Arg Gly His Glu Pro Gln Ser Phe Ile Arg Arg Asn Gln Asp Leu Ile
385              390              395
Cys Ser Phe Phe Thr Trp Phe Ser Asp His Ser Leu Pro Glu Ser Asp
405              410              415
Lys Ile Ala Glu Ile Ile Lys Glu Asp Leu Trp Pro Asn Pro Leu Gln
420              425              430
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<210> 2947

<211> 997

<212> DNA

<213> Homo sapiens

<400> 2947

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240

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<210> 2948

<211> 332

<212> PRT

<213> Homo sapiens

<400> 2948

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 35 40 45
 Ser Ser Cys Ser Leu Ile Ala Phe Asn Ser Asp Arg Pro Gly Val Leu
 50 55 60
 Gly Ile Val Pro Leu Gln Gly Gln Gly Glu Asp Lys Arg Arg Val Ala
 65 70 75 80
 His Leu Gly Cys His Ser Asp Leu Val Thr Asp Leu Asp Phe Ser Pro
 85 90 95
 Phe Asp Asp Phe Leu Leu Ala Thr Gly Ser Ala Asp Arg Thr Val Lys
 100 105 110
 Leu Trp Arg Leu Pro Gly Pro Gly Gln Ala Leu Pro Ser Ala Pro Gly
 115 120 125
 Val Val Leu Gly Pro Glu Asp Leu Pro Val Glu Val Leu Gln Phe His
 130 135 140
 Pro Thr Ser Asp Gly Ile Leu Val Ser Ala Ala Gly Thr Thr Val Lys
 145 150 155 160
 Val Trp Asp Ala Ala Lys Gln Gln Pro Leu Thr Glu Leu Ala Ala His

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180              185              190
Gly Thr Ala Cys Lys Asp Lys Gln Leu Gln Ile Phe Asp Pro Arg Thr
195              200              205
Lys Pro Arg Ala Ser Gln Ser Thr Gln Ala His Glu Asn Ser Arg Asp
210              215              220
Ser Arg Leu Ala Trp Met Gly Thr Trp Glu His Leu Val Ser Thr Gly
225              230              235              240
Phe Asn Gln Met Arg Glu Arg Glu Val Lys Leu Trp Asp Thr Arg Phe
245              250              255
Phe Ser Ser Ala Leu Ala Ser Leu Thr Leu Asp Thr Ser Leu Gly Cys
260              265              270
Leu Val Pro Leu Leu Asp Pro Asp Ser Gly Leu Leu Val Leu Ala Gly
275              280              285
Lys Gly Glu Arg Gln Leu Tyr Cys Tyr Glu Val Val Pro Gln Gln Pro
290              295              300
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<210> 2949

<211> 880

<212> DNA

<213> Homo sapiens

<400> 2949

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<210> 2950

<211> 279

<212> PRT

<213> Homo sapiens

<400> 2950

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			20					25				30			
Lys	Gly	Lys	Arg	Pro	Asn	Leu	Lys	Val	His	Ile	Asn	Thr	Thr	Ser	Asp
		35				40					45				
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	50					55				60					
Gly	Leu	Leu	Leu	Gly	Tyr	Gly	Ser	Asn	Val	Ser	Pro	Asn	Gln	Tyr	Phe
65				70				75					80		
Pro	Leu	Pro	Ala	Glu	Gly	Lys	Phe	Thr	Glu	Ala	Ile	Val	Asp	Ala	Glu
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Pro	Lys	Tyr	Leu	Ile	Val	Val	Arg	Pro	Ala	Pro	Pro	Pro	Ser	Gln	Lys
			100					105					110		
Lys	Ser	Cys	Ser	Gly	Lys	Thr	Arg	Ser	Arg	Lys	Pro	Leu	Gln	Leu	Val
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Arg	Phe	Tyr	Thr	Ile	Arg	Tyr	Arg	Glu	Lys	Asp	Lys	Glu	Lys	Lys	Trp
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Ile	Phe	Gln	Ile	Cys	Pro	Ala	Pro	Glu	Thr	Ile	Val	Glu	Asn	Leu	Lys
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Ile	Gln	Asn	Val	Thr	His	Lys	Asp	Ser	Ala	Lys	Ser	Pro	Glu	Lys	Ala
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<210> 2951

<211> 3478

<212> DNA

<213> Homo sapiens

<400> 2951

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<212> PRT

<213> Homo sapiens

<400> 2952

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<210> 2953

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<212> DNA

<213> Homo sapiens

<400> 2953

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<212> PRT

<213> Homo sapiens

<400> 2954

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<212> PRT

<213> Homo sapiens

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<210> 2959

<211> 3323

<212> DNA

<213> Homo sapiens

<400> 2959

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<211> 868

<212> PRT

<213> Homo sapiens

<400> 2960

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 Lys Phe Pro Phe Ser Glu Asn Gln Ile Cys Leu Thr Phe Thr Trp Lys
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 Asp Ala Phe Asp Lys Gly Ser Leu Phe Gly Gly Ser Val Lys Leu Ala
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 145 150 155 160
 Leu His Ile Lys Glu Thr Val Leu Ser Ala Leu Ser Arg Glu Pro Thr

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Val	Asp	Ile	Ser	Pro	Asp	Thr	Val	Gly	Thr	Leu	Ser	Leu	Ile	Met	Leu	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995	1000
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Lys	Asp	Ala	Ile	Ile	Ala	Lys	Leu	Ala	Asn	Gln	Ala	Ala	Asp	Tyr	Phe	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905																									

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Ala Thr Ala Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu
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Asn Lys Cys Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu
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Pro Thr Pro Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro
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Ala Pro Ser Gln Thr Pro Gly Ser Ala Pro Pro Gln Ala Gln Gly
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Met Pro Met Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro
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Tyr Pro Pro Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly
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<211> 434

<212> DNA

<213> Homo sapiens

<400> 2961

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<211> 3739

<212> DNA

<213> Homo sapiens

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<211> 386

<212> PRT

<213> Homo sapiens

<400> 2966

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Glu Val Leu Glu Trp Tyr Thr Ala Lys Asp Phe Ile Val Gly Lys Ser
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Leu Thr Ile Leu Gly Arg Thr Phe Phe Ile Tyr Asp Cys Asp Pro Phe
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Thr Arg Arg Tyr Tyr Lys Glu Lys Phe Gly Ile Thr Asp Leu Pro Arg
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Asp Met Ile Ser Ile Phe Glu Pro Pro Val Arg Asn Ser Gly Ile Ile
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<211> 126

<212> PRT

<213> Homo sapiens

<400> 2968

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Trp	Glu	Asp	Lys	Asp	Glu	Phe	Leu	Asp	Val	Ile	Tyr	Trp	Phe	Arg
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Ile	Ile	Ala	Val	Val	Leu	Gly	Val	Ile	Trp	Gly	Val	Leu	Pro	Leu
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<213> Homo sapiens

<400> 2969

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Ser Gln Thr Ile Met Ile Ala Trp Gly Ser Pro Ser Asn Arg Asp Phe
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Met Glu Thr Leu Asn Thr Leu Lys Tyr Ala Asn Arg Ala Arg Asn Ile
      50              55              60
Lys Asn Lys Val Val Val Asn Gln Asp Lys Thr Ala Ser Lys Ser Met

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      100          105          110
Leu Ala Phe Ile His Lys His Gly Phe Phe His Arg Asp Leu Lys Pro
      115          120          125
Glu Asn Leu Leu Cys Met Gly Pro Glu Leu Val Lys Ile Ala Asp Phe
      130          135          140
Gly Leu Ala Arg Glu Ile Arg Ser Lys Pro Pro Tyr Thr Asp Tyr Val
      145          150          155          160
Ser Thr Arg Trp Tyr Arg Ala Pro Glu Val Leu Leu Arg Ser Thr Asn
      165          170          175
Tyr Ser Ser Pro Ile Asp Val Trp Ala Val Gly Cys Ile Met Ala Glu
      180          185          190
Val Tyr Thr Leu Arg Pro Leu Phe Pro Gly Ala Ser Glu Ile Asp Thr
      195          200          205
Ile Phe Lys Ile Cys Gln Val Leu Gly Thr Pro Lys Lys Thr Asp Trp
      210          215          220
Pro Glu Gly Tyr Gln Leu Ser Ser Ala Met Asn Phe Arg Trp Pro Gln
      225          230          235          240
Cys Val Pro Asn Asn Leu Lys Thr Leu Ile Pro Asn Ala Ser Ser Glu
      245          250          255
Ala Val Gln Leu Leu Arg Asp Met Leu Gln Trp Asp Pro Lys Lys Arg
      260          265          270
Pro Thr Ala Ser Gln Ala Leu Arg Tyr Pro Tyr Phe Gln Val Gly His
      275          280          285
Pro Leu Gly Ser Thr Thr Gln Asn Leu Gln Asp Ser Glu Lys Pro Gln
      290          295          300
Lys Gly Ile Leu Glu Lys Ala Gly Pro Pro Pro Tyr Ile Lys Pro Val
      305          310          315          320
Pro Pro Ala Gln Pro Pro Ala Lys Pro His Thr Arg Ile Ser Ser Arg
      325          330          335
Gln His Gln Ala Ser Gln Pro Pro Leu His Leu Thr Tyr Pro Tyr Lys
      340          345          350
Ala Glu Val Ser Arg Thr Asp His Pro Ser His Leu Gln Glu Asp Lys
      355          360          365
Pro Ser Pro Leu Leu Phe Pro Ser Leu His Asn Lys His Pro Gln Ser
      370          375          380
Lys Ile Thr Ala Gly Leu Glu His Lys Asn Gly Glu Ile Lys Pro Lys
      385          390          395          400
Ser Arg Arg Arg Trp Gly Leu Ile Ser Arg Ser Thr Lys Asp Ser Asp

```



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          405                      410                      415
Asp Trp Ala Asp Leu Asp Asp Leu Asp Phe Ser Pro Ser Leu Ser Arg
          420                      425                      430
Ile Asp Leu Lys Asn Lys Lys Arg Gln Ser Asp Asp Thr Leu Cys Arg
          435                      440                      445
Phe Glu Ser Val Leu Asp Leu Lys Pro Ser Glu Pro Val Gly Thr Gly
          450                      455                      460
Asn Ser Ala Pro Thr Gln Thr Ser Tyr Gln Arg Arg Asp Thr Pro Thr
          465                      470                      475                      480
Leu Arg Ser Ala Ala Lys Gln His Tyr Leu Lys His Ser Arg Tyr Leu
          485                      490                      495
Pro Gly Ile Ser Ile Arg Asn Gly Ile Leu Ser Asn Pro Gly Lys Glu
          500                      505                      510
Phe Ile Pro Pro Asn Pro Trp Ser Ser Ser Gly Leu Ser Gly Lys Ser
          515                      520                      525
Ser Gly Thr Met Ser Val Ile Ser Lys Val Asn Ser Val Gly Ser Ser
          530                      535                      540
Ser Thr Ser Ser Ser Gly Leu Thr Gly Asn Tyr Val Pro Ser Phe Leu
          545                      550                      555                      560
Lys Lys Glu Ile Gly Ser Ala Met Gln Arg Val His Leu Ala Pro Ile
          565                      570                      575
Pro Asp Pro Ser Pro Gly Tyr Ser Ser Leu Lys Ala Met Arg Pro His
          580                      585                      590
Pro Gly Arg Pro Phe Phe His Thr Gln Pro Arg Ser Thr Pro Gly Leu
          595                      600                      605
Ile Pro Arg Pro Pro Ala Ala Gln Pro Val His Gly Arg Thr Asp Trp
          610                      615                      620
Ala Ser Lys Tyr Ala Ser Arg Arg
625                      630

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<210> 2973

<211> 858

<212> DNA

<213> Homo sapiens

<400> 2973

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120
gtcagcagcc cagaccccat caggggagag gtggtaaagg catttatagt ccttactcca
180
gcctactcct ctcatgaccc agaggcacta acgcgggaac tccaggagca tgtgaaaagg
240
gtgactgctc catacaaaac cccaggaag gtggcctttg ttccagaact gccaaagacg
300
gtttctggaa agatccaaag gagtaaatg cgaagtcagg agtgggggaa atgaggtgca
360
ccccaggaag gccctgtaga cctccgaaga ctccacaaga aactaatgga tcaactggta
420
gtccccatgg ggagcatcat ctcttcgacc ctaaagatgt caaaggtgtg cagcttccaa
480
acggcatccc caggatcact gggcaatgct ggaaagagca aaagaatatc attggccctg
540

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atcacataga tgctgcgccg cctagcaaat gcttggtggg tcgacttctc cctctgtctg
 600
 ggggcaggct cagcatctgc ccaactggct cactaagagc tttcagattt cctccatag
 660
 gacaggttac catagacttg gggcacttgt gggtaactcat tttctgccag tgggaatgta
 720
 aaggcttcat cctttgtatg taaccatttg gcaaaagtat gcaggaacat aaaataaaa
 780
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 840
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 858

<210> 2974

<211> 117

<212> PRT

<213> Homo sapiens

<400> 2974

Gly Tyr Phe Trp Phe Met Gly Arg Thr Asp Asp Val Ile Asn Ser Ser
 1 5 10 15
 Ser Tyr Arg Ile Gly Pro Val Glu Val Glu Ser Ala Leu Ala Glu His
 20 25 30
 Pro Ala Val Leu Glu Ser Ala Val Val Ser Ser Pro Asp Pro Ile Arg
 35 40 45
 Gly Glu Val Val Lys Ala Phe Ile Val Leu Thr Pro Ala Tyr Ser Ser
 50 55 60
 His Asp Pro Glu Ala Leu Thr Arg Glu Leu Gln Glu His Val Lys Arg
 65 70 75 80
 Val Thr Ala Pro Tyr Lys Thr Pro Arg Lys Val Ala Phe Val Ser Glu
 85 90 95
 Leu Pro Lys Thr Val Ser Gly Lys Ile Gln Arg Ser Lys Leu Arg Ser
 100 105 110
 Gln Glu Trp Gly Lys
 115

<210> 2975

<211> 1425

<212> DNA

<213> Homo sapiens

<400> 2975

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 gacacaatgt atacgggtcaa tggcggtccac ccaactgaccc tgcgctggga agagaccgcc
 120
 acaccagaat cccagccaga tactccgcct ggcacccttc tgggtgtccca agatgagaag
 180
 agagatgctg agctgccgaa gaagcgtatg gggaaagtaa accccggctg ggagaacttg
 240
 gagaagtgtc tagtgttcac cgcagctggg gtgaaaccgg ggnncaagggt ggcgtggcttt
 300
 gatctggagc ggacgctcat caccacacgc tctgggaagg tctttccccc tggccccagt
 360

gactggagga tcttgtaccc agagattccc cgtaagctcc gagagctgga agccgagggc
 420
 tacaagctgg tgatcttcac caaccagatg agcatcgggc gcgggaagct gccagccgag
 480
 gagttcaagg ccaagggtga ggctgtggtg gagaagctgg ggggtcccctt ccagggtgctg
 540
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 600
 gagcaggcca acgacggcac gcccatatcc atcggggaca gcatctttgt gggagacgca
 660
 gccggacgcc cggccaactg ggccccgggg cggaagaaga aagacttctc ctgcgccgat
 720
 cgccctgttg cctcaacct tggcctgccc ttcgccacgc ctgaggaggt ctttctcaag
 780
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 840
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 900
 gtgggatttc ctggggcccg gaagtccacc tttctcaaga agcacctcgt gtcggccgga
 960
 tatgtccacg tgacagggac acgctaggct cctggcagcg ctgtgtgacc acgtgtgaga
 1020
 cagccctgaa gcaagggaaa cgggtcgcca tcgacaacac aaaccagac gccgcgagcc
 1080
 gcgccaggta cgtccagtgt ccccagagcc cgggggtccc ctgcgcgtgc tttctcttca
 1140
 ccgccactct ggagcaggcg cgccacaaca accggtttcg agagatgacg gactcctctc
 1200
 atatccccgt gtcagacatg gtcattgtat gctacaggaa gcagttcgag gcccacacgc
 1260
 tggctgaagg cttctctgcc atcctggaga tcccgttccg gctatgggtg gagccgaggc
 1320
 tggggcggtg gtactgccag ttctccgagg gctgagcccg ccagctccc ctcacaata
 1380
 aacgctgttt ctccttga aa aaaaaaaaaa aaaaaaaaaa aaaaa
 1425

<210> 2976

<211> 328

<212> PRT

<213> Homo sapiens

<400> 2976

Pro Ser Thr Thr Gly Thr Gln Glu Leu Lys Pro Gly Leu Glu Gly Ser
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 Leu Gly Val Gly Asp Thr Met Tyr Thr Val Asn Gly Val His Pro Leu
 20 25 30
 Thr Leu Arg Trp Glu Glu Thr Arg Thr Pro Glu Ser Gln Pro Asp Thr
 35 40 45
 Pro Pro Gly Thr Pro Leu Val Ser Gln Asp Glu Lys Arg Asp Ala Glu
 50 55 60
 Leu Pro Lys Lys Arg Met Gly Lys Ser Asn Pro Gly Trp Glu Asn Leu
 65 70 75 80
 Glu Lys Leu Leu Val Phe Thr Ala Ala Gly Val Lys Pro Gly Xaa Lys

				85					90					95		
Val	Ala	Gly	Phe	Asp	Leu	Asp	Gly	Thr	Leu	Ile	Thr	Thr	Arg	Ser	Gly	
Lys	Val	Phe	Pro	Thr	Gly	Pro	Ser	Asp	Trp	Arg	Ile	Leu	Tyr	Pro	Glu	
Ile	Pro	Arg	Lys	Leu	Arg	Glu	Leu	Glu	Ala	Glu	Gly	Tyr	Lys	Leu	Val	
Ile	Phe	Thr	Asn	Gln	Met	Ser	Ile	Gly	Arg	Gly	Lys	Leu	Pro	Ala	Glu	
Glu	Phe	Lys	Ala	Lys	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly	Val	Pro	
Phe	Gln	Val	Leu	Val	Ala	Thr	His	Ala	Gly	Leu	Tyr	Arg	Lys	Pro	Val	
Thr	Gly	Met	Trp	Asp	His	Leu	Gln	Glu	Gln	Ala	Asn	Asp	Gly	Thr	Pro	
Ile	Ser	Ile	Gly	Asp	Ser	Ile	Phe	Val	Gly	Asp	Ala	Ala	Gly	Arg	Pro	
Ala	Asn	Trp	Ala	Pro	Gly	Arg	Lys	Lys	Asp	Phe	Ser	Cys	Ala	Asp		
Arg	Leu	Phe	Ala	Leu	Asn	Leu	Gly	Leu	Pro	Phe	Ala	Thr	Pro	Glu	Glu	
Phe	Phe	Leu	Lys	Trp	Pro	Ala	Ala	Gly	Phe	Glu	Leu	Pro	Ala	Phe	Asp	
Pro	Arg	Thr	Val	Ser	Arg	Ser	Gly	Pro	Leu	Cys	Leu	Pro	Glu	Ser	Arg	
Ala	Leu	Leu	Ser	Ala	Ser	Pro	Glu	Val	Val	Val	Ala	Val	Gly	Phe	Pro	
Gly	Ala	Gly	Lys	Ser	Thr	Phe	Leu	Lys	Lys	His	Leu	Val	Ser	Ala	Gly	
Tyr	Val	His	Val	Thr	Gly	Thr	Arg									

<210> 2977

<211> 1420

<212> DNA

<213> Homo sapiens

<400> 2977

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 120
 attgcagaga aaagggccgt cctggcccac gtggatgtgc agacgctgtc cagccagctg
 180
 gcagtgcacg tggggcctgg tgaacgtcgg atcggccca gggagccctt ggaactgctg
 240
 tgcaatgtgt cagggggcact tccccacaga ggccgtcatg ctgcatactc tgtaggttgg
 300
 gagatggcac ctgcgggggc acctggggcc ggccgcctgg tagccagctg ggacacagag
 360
 ggtgtgggca gacctgnnngc cctggctatg agggccgacn acattgccat ggagaaggtg
 420
 gcatccagaa cataccggct acggctagag gctgccaggc ctggtgatgc gggcacctac
 480

cgctgcctcg ccaaagccta tgttcgaggg tctgggaccc ggcttcctga agcagccagt
 540
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 660
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 720
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 780
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 840
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 900
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 960
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 1020
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 1080
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 1140
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 1200
 gcctggacac cctctccctc tgtccactct tcctttaatt tatttgacct cccactaccc
 1260
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 1320
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 1380
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 1420

<210> 2978

<211> 369

<212> PRT

<213> Homo sapiens

<400> 2978

Xaa	Ser	Asn	Ile	His	Ala	Glu	Tyr	Arg	Met	Val	Val	Gly	Gly	Ala	Gln
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Ala	Gly	Asp	Ala	Gly	Thr	Tyr	His	Cys	Thr	Ala	Ala	Glu	Trp	Ile	Gln
			20					25					30		
Asp	Pro	Asp	Gly	Ser	Trp	Ala	Gln	Ile	Ala	Glu	Lys	Arg	Ala	Val	Leu
		35					40					45			
Ala	His	Val	Asp	Val	Gln	Thr	Leu	Ser	Ser	Gln	Leu	Ala	Val	Thr	Val
		50				55				60					
Gly	Pro	Gly	Glu	Arg	Arg	Ile	Gly	Pro	Gly	Glu	Pro	Leu	Glu	Leu	Leu
65				70					75				80		
Cys	Asn	Val	Ser	Gly	Ala	Leu	Pro	Pro	Ala	Gly	Arg	His	Ala	Ala	Tyr
				85				90					95		
Ser	Val	Gly	Trp	Glu	Met	Ala	Pro	Ala	Gly	Ala	Pro	Gly	Pro	Gly	Arg
				100			105					110			
Leu	Val	Ala	Gln	Leu	Asp	Thr	Glu	Gly	Val	Gly	Ser	Leu	Xaa	Ala	Leu

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      115              120              125
Ala Met Arg Ala Asp Xaa Ile Ala Met Glu Lys Val Ala Ser Arg Thr
  130              135              140
Tyr Arg Leu Arg Leu Glu Ala Ala Arg Pro Gly Asp Ala Gly Thr Tyr
  145              150              155              160
Arg Cys Leu Ala Lys Ala Tyr Val Arg Gly Ser Gly Thr Arg Leu Arg
      165              170              175
Glu Ala Ala Ser Ala Arg Ser Arg Pro Leu Pro Val His Val Arg Glu
      180              185              190
Glu Gly Val Val Leu Glu Ala Val Ala Trp Leu Ala Gly Gly Thr Val
      195              200              205
Tyr Arg Gly Glu Thr Ala Ser Leu Leu Cys Asn Ile Ser Val Arg Gly
      210              215              220
Gly Pro Pro Gly Leu Arg Leu Ala Ala Ser Trp Trp Val Glu Arg Pro
  225              230              235              240
Glu Asp Gly Glu Leu Ser Ser Val Pro Ala Gln Leu Val Gly Gly Val
      245              250              255
Gly Gln Asp Gly Val Ala Glu Leu Gly Val Arg Pro Gly Gly Gly Pro
      260              265              270
Val Ser Val Glu Leu Val Gly Pro Arg Ser His Arg Leu Arg Leu His
      275              280              285
Ser Leu Gly Pro Glu Asp Glu Gly Val Tyr His Cys Ala Pro Ser Ala
      290              295              300
Trp Val Gln His Ala Asp Tyr Ser Trp Tyr Gln Ala Gly Ser Ala Arg
  305              310              315              320
Ser Gly Pro Val Thr Val Tyr Pro Tyr Met His Ala Leu Asp Thr Leu
      325              330              335
Phe Val Pro Leu Leu Val Gly Thr Gly Val Ala Leu Val Thr Gly Ala
      340              345              350
Thr Val Leu Gly Thr Ile Thr Cys Cys Phe Met Lys Arg Leu Arg Lys
      355              360              365
Arg

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<210> 2979

<211> 2191

<212> DNA

<213> Homo sapiens

<400> 2979

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120
catcatcaac tcattttttt gtatgaataa ccaaaaaatt tcttcaacac ttttttttaa
180
gaagaagcta taaataaata aagcttttaa caatcctggg ttcaagttaa acagtccagg
240
ttcccgaata gttcacagcc ttgttttgtg ggcagttctg ctgttctctg cttccccttc
300
caggaggggg cgtttgcagg tctgggggtc ctggtgacta agctgttagc tccactccct
360
gcctgtttcc gtcctcacag ccttggggag gccccggtgg acagagtcc tacaatttag
420

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480
ggctggacac ttgggggctg agggcaactgc cagctgccgc cgcctctgga cacctcagcc
540
cggcgctggc ccgagaggag actgctttcc aaatgcagcg aagagactga gacaagaccc
600
gtgcttccgt gtgagttggg atgcggggca taagttaaca catattccaa tatgtacaaa
660
acaacctcgc ctccagggccg cgcacccagg aagcccatgg tgaaggtagg gtcaccttga
720
gccaggcctc tggctgggtg tccacctcct gccgggaagc caagggtgcc cacgtggctt
780
gtgcaagacc tcacaatccc ctgaacgtgt tctctctcct ccaaggagtg caccaccccc
840
catgttgagt gtccgagcag attcccatg accctgacct cctcttgaaa gaaccacacc
900
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960
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1020
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1080
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1140
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1200
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1380
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1440
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1620
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1680
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1740
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1800
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1920
ggcagcatcc ctggccaaaag cctccccact cctgggctgc cagttggccc gaggaaggcc
1980
ggcaatgcag ctccggccta ctacccaaac cctgggcaaa aggtctggcca tgctctgttc
2040

ccagcagccg cgcaggtttc cccactggct gcaatggccc taccaaaagc catgttgcac
 2100
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 2160
 ctggtgtctc taggagggcc cacacaggca c
 2191

<210> 2980
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 2980
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 1 5 10 15
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 20 25 30
 Gly Thr Glu His Gly Gln Pro Phe Ala Arg Gly Trp Gly Ala Trp Gly
 35 40 45
 Asn Ala Arg Arg Ala Arg Val Gly Arg Ala Glu Cys Leu Leu Ser Gly
 50 55 60
 Arg Pro Pro Thr Ala Val Leu Pro Arg Leu Val Glu Asn Leu Lys Ala
 65 70 75 80
 Arg Val Pro Val Pro Gly His Thr Glu Pro Leu Trp Ser Glu Gly Thr
 85 90 95
 Ala Pro Gly Gln Gly Leu Trp Ser His Ala Pro Ala Asp Gly Ser Leu
 100 105 110
 Met Asn Leu Ile Arg Thr Leu Val Gly Ala Val Val Phe Glu Leu Leu
 115 120 125
 Ser Met Cys Phe Gly Asp Gly Ala Gly Ala Ala Cys
 130 135 140

<210> 2981
 <211> 617
 <212> DNA
 <213> Homo sapiens

<400> 2981
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 120
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 180
 ccattcttcag ctgcattctc atccttctcc tcttctctc agtcttcac atctacagat
 240
 gcangccagc acagttctac atctgaggaa tccaccaaga gaaccagcca ttccaaactt
 300
 ccggagcagg aggtctccga ggcagattta tccaatatgg aaaggggtatc tctctcgag
 360
 gcagaccccc aaggagtgc ctatgctgag ctaagcacca gcgccctgtc tgaggcagct
 420
 tcagacacca cccaggagcc cccaggatct catgaatatg cggcactgaa agtgtagcaa
 480

gaagacagcc ctggccacta aaagaggggg gatcgtgctg gccagggtta tcggaatct
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 600
 tcttaaaaaa aaaaaa
 617

<210> 2982

<211> 107

<212> PRT

<213> Homo sapiens

<400> 2982

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Ser	Phe	Ser	Ser	Ser	Ser	Gln	Ser	Ser	Ser	Ser	Thr	Asp	Ala	Xaa	Gln
			20					25					30		
His	Ser	Ser	Ser	Ser	Glu	Glu	Ser	Thr	Lys	Arg	Thr	Ser	His	Ser	Lys
			35				40					45			
Leu	Pro	Glu	Gln	Glu	Ala	Ala	Glu	Ala	Asp	Leu	Ser	Asn	Met	Glu	Arg
			50			55					60				
Val	Ser	Leu	Ser	Thr	Ala	Asp	Pro	Gln	Gly	Val	Thr	Tyr	Ala	Glu	Leu
65					70				75					80	
Ser	Thr	Ser	Ala	Leu	Ser	Glu	Ala	Ala	Ser	Asp	Thr	Thr	Gln	Glu	Pro
			85						90					95	
Pro	Gly	Ser	His	Glu	Tyr	Ala	Ala	Leu	Lys	Val					
			100					105							

<210> 2983

<211> 614

<212> DNA

<213> Homo sapiens

<400> 2983

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 120
 gcaatgatgc tgcgttcctt gaccaagaga ttcattggag actatgaacc gaatacaggc
 180
 aagctgtatt cacggctggt ctatgtcgag ggggaccagc tctccttgca gatccaggat
 240
 actcccgagg gcgtccgat ccaagacagc ctccccagg tcgtcgatcc cctgcaaatg
 300
 cgtgcagtag ccgaggggtt tctgctgggt tattccatca cagactatga cagctacttg
 360
 tccatccgac ccctttatca gcacatccgg aaggtccacc ctgactctaa agccccctgc
 420
 atcatcgtgg gcaacaaggg ggaccttttg catgccgggc aggtgcagac acaggacggg
 480
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<210> 2984
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<212> PRT
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<400> 2984
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<211> 988

<212> PRT

<213> Homo sapiens

<400> 2986

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Lys	Ala	Glu	Glu	Leu	Leu	Trp	Arg	Lys	Val	Tyr	Tyr	Glu	Val	Ile	Gln
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Cys	Ala	Tyr	Arg	Thr	His	Leu	Val	Ala	Gly	Ile	Gly	Phe	Tyr	Gln	His
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Leu	Leu	Leu	Tyr	Ile	Gln	Ser	His	Tyr	Gln	Leu	Glu	Leu	Gln	Cys	Cys
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Ala Gly Val Asp Thr Glu Leu Leu Ala Glu Arg Phe Tyr Tyr Gln Ala
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Leu Ala Gly Ser Lys Tyr Tyr Asn Val Glu Ala Met Tyr Cys Tyr Leu
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Arg Cys Ile Gln Ser Glu Val Ser Phe Glu Gly Ala Tyr Gly Asn Leu
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Lys Arg Leu Tyr Asp Lys Ala Ala Lys Met Tyr His Gln Leu Lys Lys
 225              230              235
Cys Glu Thr Arg Lys Leu Ser Pro Gly Lys Lys Arg Cys Lys Asp Ile
      245              250              255
Lys Arg Leu Leu Val Asn Phe Met Tyr Leu Gln Ser Leu Leu Gln Pro
 260              265              270
Lys Ser Ser Ser Val Asp Ser Glu Leu Thr Ser Leu Cys Gln Ser Val
 275              280              285
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Asp Ala Glu Thr Asp Ser Glu Met Asn Ser Gln Glu Ser Arg Ser Asp
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Leu Glu Asp Met Glu Glu Glu Glu Gly Thr Arg Ser Pro Thr Leu Glu
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Pro Pro Arg Gly Arg Ser Glu Ala Pro Asp Ser Leu Asn Gly Pro Leu
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Glu	Glu	Gly	Ser	Glu	Ser	Glu	Gly	Ser	Glu	Ser	Ser	Gly	Arg	Ser	Cys								
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Cys	Glu	Leu	Pro	Asp	Leu	Pro	Ser	Ser	Leu	Leu	Leu	Pro	Glu	Asp	Met								
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Arg	Ile	Cys	Cys	Ile	Arg	Ser	Phe	Gly	His	Phe	Ile	Ala	Arg	Leu	Gln								
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Gly	Ser	Ile	Leu	Gln	Phe	Asn	Pro	Glu	Val	Gly	Ile	Phe	Val	Ser	Ile								
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Ala	Gln	Ser	Glu	Gln	Glu	Ser	Leu	Leu	Gln	Gln	Ala	Gln	Ala	Gln	Phe								
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Arg	Met	Ala	Gln	Glu	Glu	Ala	Arg	Arg	Asn	Arg	Leu	Met	Arg	Asp	Met								
785					790					795					800								
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985

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 <212> DNA
 <213> Homo sapiens

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<212> DNA
<213> Homo sapiens
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<400> 2990

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<210> 2991
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 <212> DNA
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<400> 2991

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<210> 2992

<211> 64

<212> PRT

<213> Homo sapiens

<400> 2992

Val	Val	Ala	Val	Cys	Ser	Pro	Gln	Ser	Ala	Ala	Ala	Asp	Val	Thr	Arg
1			5					10					15		
His	Thr	Gly	Pro	Phe	Thr	Glu	Val	Ser	Pro	Gly	Ala	Leu	Gly	Trp	Pro
		20					25					30			
Val	Leu	Cys	Ser	Gly	Leu	Leu	Leu	Gly	Gly	Leu	Gly	Ala	Ala	His	Phe
		35				40				45					
Ala	Ser	Ala	Val	Ser	Gly	His	Ser	Ser	Ala	Ser	Leu	Gln	Ala	Ala	Ser
	50					55					60				

<210> 2993

<211> 687

<212> DNA

<213> Homo sapiens

<400> 2993

nnatgccccg ggtccaggga gccgctgatg gtcactgaag ctgtggccct agagcggcgg
 60
 cgggagcagg aagaaaagga ggacatggag acccaggctg tggcaacgtc ccccgatggc
 120
 cgatacctca agtttgacat cgagattgga cgtggctcct tcaagacggt gtatcgaggg
 180
 ctagacaccg acaccacagt ggaggtggcc tgggtgtgagc tgcagactcg gaaactgtct
 240
 agagctgagc ggcagcgctt ctcagaggag gtggagatgc tcaaggggct gcagcaccoc
 300
 aacatcgctc gctcttatga ttctgtggaag tcgggtgctga gggggccagg ttgcatcgtg
 360
 ctggtcaccg aactcatgac ctcgggcacg ctcaagacgt acctgaggcg gttccgggag
 420
 atgaagccgc gggctcttca gcgctggagc cgccaaatcc tgcggggact tcatttctca
 480
 cactcccggt ttcctcccat cctgcaccgg gatctcaagt gcgacaatgt ctttatcacg
 540
 ggacctactg gctctgtcaa aatcggggac ctgggacctg ccacgctcaa gcgcgctcc
 600
 tttgccaaga gtgtcatcgg gaccccgaa ttcattggccc ccgagatgta cgaggaaaaa
 660

tacgatgagg ccgtggacgt gtacgcg
687

<210> 2994

<211> 229

<212> PRT

<213> Homo sapiens

<400> 2994

Xaa Cys Pro Arg Ser Arg Glu Pro Leu Met Val Thr Glu Ala Val Ala
1 5 10 15
Leu Glu Arg Arg Arg Glu Gln Glu Glu Lys Glu Asp Met Glu Thr Gln
20 25 30
Ala Val Ala Thr Ser Pro Asp Gly Arg Tyr Leu Lys Phe Asp Ile Glu
35 40 45
Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Arg Gly Leu Asp Thr Asp
50 55 60
Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Thr Arg Lys Leu Ser
65 70 75 80
Arg Ala Glu Arg Gln Arg Phe Ser Glu Glu Val Glu Met Leu Lys Gly
85 90 95
Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Lys Ser Val
100 105 110
Leu Arg Gly Gln Val Cys Ile Val Leu Val Thr Glu Leu Met Thr Ser
115 120 125
Gly Thr Leu Lys Thr Tyr Leu Arg Arg Phe Arg Glu Met Lys Pro Arg
130 135 140
Val Leu Gln Arg Trp Ser Arg Gln Ile Leu Arg Gly Leu His Phe Leu
145 150 155 160
His Ser Arg Val Pro Pro Ile Leu His Arg Asp Leu Lys Cys Asp Asn
165 170 175
Val Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp Leu Gly
180 185 190
Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile Gly Thr
195 200 205
Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp Glu Ala
210 215 220
Val Asp Val Tyr Ala
225

<210> 2995

<211> 1879

<212> DNA

<213> Homo sapiens

<400> 2995

nttttagtagt agtattacat tgtgaatttt attttcaaat ttgatcaata aagatgaaaa
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taataaaatt aagcagtc aaagaagtagc aaaaacaaga tagtcattca tatatacaga
120
acatatagat tcatttctag ttgattcaat cctattttatg tattttaaata acaaaataat
180
ggccatctgg ctagtgtccaa cggtagagca tgagactctt aaaatacaaa atacatctta
240

atgtgtcaag aagaccacag ttagcaccag gaaaggaact ttacttttagc ttctgattac
300
ttttttat ttattttttac tttattatta ttattattat ttttgagatg gagtctcact
360
ctgntcacc aggctggaat acagtgggtg gatctcagct cactgcaacc tccacctccc
420
aggttcaagc gattctctcg cctcagcctc ctgagtagct gggactctga tagatgcctg
480
ccaccacacc cgggtgattt ttgtattttt agtagagacg ggggttcgcc atgttgctca
540
ggctgggtct gaactccga cctcaagtga cttgctcacc ttggcctccc aaagtgcctg
600
gattacaggt gtgagccact gcaccacgac tggcagtgaa ttttaagcct cctatttccc
660
aggtttttagc ttaataatcc tcattagttt ttcagatttt tgtcagtcct gttttggggc
720
tattttgcct tagtgggcct aaacagaata ttaaaataca ttaataatcc atactgagag
780
tagagtata atgggtttct cactccttag ggacacagat ggaacaata catcccatga
840
acacagtgta atgtccctgg ttatccctga gctgggcagt ttcacacaat cattttttct
900
ctgaggccaa agtctgtggt ttgatcatct tagcagcttc cagaacagaa agtaggttta
960
ctttgtctcc aaattctttt tctcggtgct caagaagaat gccctgcttt cctgatccca
1020
ccacgaaaaac tcccccaagg atgaagcctt ctcctccag gtttcagag aagcctccgt
1080
tccaggtctg gaagaagttg taccacactc ccagacgat aaatcccata aacatcatct
1140
tccgcttttg tggaccatag aactttttct tttcatccag gaagattttc ctttgaaat
1200
aaggctggaa atccttactc tcagtctga tgtgctcctt taccactgca tagaggggga
1260
cgcccagctg gtccaacatg cttttcaggg aggacagatc cgcagcttcc tctcgacaga
1320
ggaaaacagc tggcctccgc acggccataa tcacagctcc atttttttcc catagctcct
1380
ttgctttgaa agtccttggc tcctttccca gtgttttcag gtctatatcc tccagtgact
1440
ccaggggcgc tttctggggc ttggacagaa acacgtctgt gttggcaagc agcaatgcca
1500
aggcagcagc cccagggtc cctgcaccaa tggaccacat ccccatggtg aagaaacttg
1560
ggtcctggag gaaagacatt tctcaagtgc ctcccttctg ccggcctttt accgccccga
1620
cgcccgggcg ctaagggggc aaaccgcccg gcccgagggg tcccaggggc gggccccgga
1680
gtacctggag gatatagacc tgaaaaacact ggagaaggaa ccaaggactt tcaagcaaa
1740
ggagctatgg gaaaaaaatg gagctgtgat tatggccgtg cggaggccag gctgtttcct
1800
ctgtcgagag gaagctgcgg atctgtcctc cctgaaaagc atgttggacc agctgggcgt
1860

ccccctctat gcagtggtta
1879

<210> 2996
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2996
His Gln Glu Arg Asn Phe Thr Leu Ala Ser Asp Tyr Phe Phe Ile Phe
1 5 10 15
Ile Phe Thr Leu Leu Leu Leu Leu Phe Leu Arg Trp Ser Leu Thr
20 25 30
Leu Xaa Thr Gln Ala Gly Ile Gln Trp Cys Asp Leu Ser Ser Leu Gln
35 40 45
Pro Pro Pro Pro Arg Phe Lys Arg Phe Ser Cys Leu Ser Leu Ser
50 55 60
Ser Trp Asp Ser Asp Arg Cys Leu Pro Pro His Pro Gly Asp Phe Cys
65 70 75 80
Ile Phe Ser Arg Asp Gly Val Ser Pro Cys Cys Ser Gly Trp Ser Arg
85 90 95
Thr Pro Asp Leu Lys
100

<210> 2997
<211> 800
<212> DNA
<213> Homo sapiens

<400> 2997
actcagatgg gcaccatcag tgctagacaa gaattctatt cctcttatcc aggcctccca
60
gagccatcca aagtgcacatc tccagtggtc acctcttcca ccataaaaga cattgtttct
120
acaaccatac ctgcttcttc tgagataaca agaattgaga tggagtgcaac atccaccctg
180
acccccacac caaggagac cagcacctcc caggagatcc actcagccac aaagccaagc
240
actgttctctt acaaggcact cactagtgcc acgattgagg actccatgac acaagtcagt
300
tcctctagca gaggacctag ccctgatcag tcacaatgt cacaagacat atccactgaa
360
gtgatcacca ggctctctac ctccccatc aagacagaat ctacagaaat gaccattacc
420
acccaaacag ggtctcctgg ggctacatca aggggtaccc ttaccttgga cacttcaaca
480
actttttatgt cagggaacca ctcaactgca tctcaaagat ttccacatc acagatgacc
540
gtctttatga gtagaactcc tggagatgtg ccattggctaa cccatccctc tggggaagag
600
ccgcctctg cctctttctc actggttca cctgtcttga cctcattttt ttctgttttt
660
gccattccc aaaaacctcc accttttttg gttctctggc aaactttttc ctagggctg
720

gggaaaccca aaatgtgggg ccaaccaga actgaaacat tcccccaat ggacaacctt
780

tttgaagaagg gccctttgc

800

<210> 2998

<211> 266

<212> PRT

<213> Homo sapiens

<400> 2998

Thr	Gln	Met	Gly	Thr	Ile	Ser	Ala	Arg	Gln	Glu	Phe	Tyr	Ser	Ser	Tyr
1			5					10						15	
Pro	Gly	Leu	Pro	Glu	Pro	Ser	Lys	Val	Thr	Ser	Pro	Val	Val	Thr	Ser
		20					25					30			
Ser	Thr	Ile	Lys	Asp	Ile	Val	Ser	Thr	Thr	Ile	Pro	Ala	Ser	Ser	Glu
	35				40						45				
Ile	Thr	Arg	Ile	Glu	Met	Glu	Ser	Thr	Ser	Thr	Leu	Thr	Pro	Thr	Pro
	50				55					60					
Arg	Glu	Thr	Ser	Thr	Ser	Gln	Glu	Ile	His	Ser	Ala	Thr	Lys	Pro	Ser
65				70					75					80	
Thr	Val	Pro	Tyr	Lys	Ala	Leu	Thr	Ser	Ala	Thr	Ile	Glu	Asp	Ser	Met
			85					90						95	
Thr	Gln	Val	Met	Ser	Ser	Ser	Arg	Gly	Pro	Ser	Pro	Asp	Gln	Ser	Thr
		100						105					110		
Met	Ser	Gln	Asp	Ile	Ser	Thr	Glu	Val	Ile	Thr	Arg	Leu	Ser	Thr	Ser
		115				120						125			
Pro	Ile	Lys	Thr	Glu	Ser	Thr	Glu	Met	Thr	Ile	Thr	Thr	Gln	Thr	Gly
	130					135					140				
Ser	Pro	Gly	Ala	Thr	Ser	Arg	Gly	Thr	Leu	Thr	Leu	Asp	Thr	Ser	Thr
145				150					155					160	
Thr	Phe	Met	Ser	Gly	Thr	His	Ser	Thr	Ala	Ser	Gln	Arg	Phe	Ser	His
			165					170						175	
Ser	Gln	Met	Thr	Ala	Leu	Met	Ser	Arg	Thr	Pro	Gly	Asp	Val	Pro	Trp
		180						185					190		
Leu	Thr	His	Pro	Ser	Gly	Glu	Glu	Pro	Ala	Ser	Ala	Ser	Phe	Ser	Leu
	195					200						205			
Ala	Ser	Pro	Val	Leu	Thr	Ser	Phe	Phe	Ser	Phe	Phe	Ala	His	Ser	Gln
	210					215					220				
Lys	Pro	Pro	Pro	Phe	Leu	Val	Pro	Gly	Gln	Thr	Phe	Ser	Leu	Gly	Leu
225				230						235				240	
Gly	Lys	Pro	Lys	Met	Trp	Gly	Gln	Pro	Arg	Thr	Glu	Thr	Phe	Pro	Pro
			245					250						255	
Met	Asp	Asn	Leu	Phe	Glu	Lys	Gly	Pro	Phe						
			260					265							

<210> 2999

<211> 550

<212> DNA

<213> Homo sapiens

<400> 2999

ccgggagct gtcacagccc agctgagtgt gcacatgctc ggggtagtgc tgacatgcca
60

acccccttgc cactttggcc cccctccaggc tttgggcact gacaagcatg ggaaggaggc
 120
 tgaggggtgc actgaggaca gccctagtgt ggctgcagg cacccttaa catgaacagc
 180
 ctggtcacca tgaacagcag caggaggcag acaggctcct gggtggaag aagctggtcc
 240
 acagtgaaga cccacctcca agccaggga agcctgaagc ctgggggatg ggctgccagt
 300
 cccagaaacc gcaagggcaa cttgtggtgc tttcccttg gccccacctat ggccgccccat
 360
 ggacgaattg gcatgcactt tctcccctct gagggccata aaagcccctg ggctcagcca
 420
 gagctgagcg gatatcagga cgacaagctg cacagaggta ctaccatac caaggcctcc
 480
 tctctgtga gagctgcaca tacaatggaa tgacctgcct gtagagagag cttccactc
 540
 cagggtctcc
 550

<210> 3000

<211> 167

<212> PRT

<213> Homo sapiens

<400> 3000

Met Cys Ser Ser Gln Arg Gly Gly Leu Gly Met Gly Ser Thr Ser
 1 5 10 15
 Val Gln Leu Val Val Leu Ile Ser Ala Gln Leu Trp Leu Ser Pro Gly
 20 25 30
 Ala Phe Met Gly Leu Arg Gly Glu Lys Val His Ala Asn Ser Ser Met
 35 40 45
 Gly Gly His Gly Trp Ala Gln Gly Lys Ala Pro Gln Val Ala Leu Ala
 50 55 60
 Val Ser Gly Thr Gly Asp Pro Ser Pro Arg Leu Gln Ala Phe Pro Gly
 65 70 75 80
 Leu Glu Val Gly Leu His Cys Gly Pro Ala Ser Phe His Pro Gly Ala
 85 90 95
 Cys Leu Pro Pro Ala Ala Val His Gly Asp Gln Ala Val His Val Lys
 100 105 110
 Gly Cys Leu Gln Ala Ser Thr Gly Leu Ser Ser Val His Pro Ser Ala
 115 120 125
 Ser Phe Pro Cys Leu Ser Val Pro Lys Ala Trp Arg Gly Pro Lys Trp
 130 135 140
 Gln Gly Gly Trp His Val Ser Thr Thr Pro Ser Met Cys Thr Leu Ser
 145 150 155 160
 Trp Ala Val Thr Ala Pro Gly
 165

<210> 3001

<211> 1092

<212> DNA

<213> Homo sapiens

<400> 3001

agatctttgt gaggcctgaa tgaaatggcc ccattcagaa tttcccagga tgtcatccat
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 aatagctctg cctggctgag ttgaaaggc cactgttctg tttcagcgtt gagatgcctt
 120
 gaagtacaga ggttgagccc ctatgtatgc ctgggggagt cccagaaagt ggaatcccaa
 180
 ccttgctcag ctccaccagt tttcttctat aaccagaca ttgcaaagac agcagtaccc
 240
 actgaggcat ccagcccagc tcaggccctg ccaccnca gtaccaaac atcattgtca
 300
 ggcaagggat acagaacaca gtgctctcac cagactgcag ctggggggac acccagcacg
 360
 gagagaagct gaggcggaac tgcactatct accggccctg gttctcccc tacagctact
 420
 tcgtgtgtgc agacaagag agccagctgg aggcctatga cttcccagag gtgcagcagg
 480
 atgagggcaa gtgggacaac tgcctttctg aggacatggc tgagaacatc tgttcgtcct
 540
 cttcctcccc agagaacact tgcctctgag aagccaccaa gaaatccagg catggcctgg
 600
 actccatcac atcccaggac atcctaattg cttccagggt gaccccagca cagcagaatg
 660
 gctacaagtg cgtggcctgc tgcgcgatgt accccacctt ggacttcctc aagagccaca
 720
 tcaagagggg cttcaggagg ggcttcagct gcaagggtga ctaccgcaag ctcaaaggcc
 780
 tctggagcaa ggagcagaag gcccggtctg gagacaggct ctctccggc agctgccagg
 840
 ccttcaatag tcctgctgaa caccttaggc aaattggcgg tgaagcctac ttatgtctct
 900
 agagagatgc caataaagt agtcacagcc ttctgtccag tctgaggta ccccgcacg
 960
 cctgtgtctc tcccagaaac ccggtctca tcacctttgg ctaattggtg ctagcaaca
 1020
 ccaggcacac accctcccc ttctctcttt taaaaataaa gacaatactt gaagtttggg
 1080
 aaaatcaaaa aa
 1092

<210> 3002

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3002

Met	Ala	Pro	Phe	Arg	Ile	Pro	Gln	Asp	Val	Ile	His	Asn	Ser	Ser	Ala
1				5					10					15	
Trp	Leu	Ser	Leu	Lys	Gly	His	Cys	Ser	Val	Ser	Ala	Leu	Arg	Cys	Leu
			20					25					30		
Glu	Val	Gln	Arg	Leu	Ser	Pro	Tyr	Val	Cys	Leu	Gly	Glu	Ser	Gln	Lys
		35					40					45			
Val	Glu	Ser	Gln	Pro	Cys	Ser	Ala	His	Gln	Cys	Phe	Phe	Tyr	Asn	Pro
		50				55				60					
Asp	Ile	Ala	Lys	Thr	Ala	Val	Pro	Thr	Glu	Ala	Ser	Ser	Pro	Ala	Gln

```

65              70              75              80
Ala Leu Pro Pro Xaa Ser Thr Lys Ala Ser Leu Ser Gly Lys Gly Tyr
              85              90              95
Arg Thr Gln Cys Ser His Gln Thr Ala Ala Trp Gly Thr Pro Ser Thr
              100              105              110
Glu Arg Ser
              115

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<210> 3003
<211> 474
<212> DNA
<213> Homo sapiens

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<400> 3003
gcgcgccatg gagccccggg cgggttcaga agccgtggag acgggtgagg aggatgtgat
60
tatggaagct ctgcggtcat acaaccagga gcactcccag agcttcacgt ttgatgatgc
120
ccaacaggag gaccggaaga gactggcgga gctgctggct tccgtcctgg aacagggctt
180
gccaccctcc caccgtgtca tctggctgca gactgtccga atcctgtccc gggaccgcaa
240
ctgcctggac ccgttcacca gccgccagag cctgcaggca ctacgtctgt atgctgacat
300
ctctgtctct gaggggtccg tcccagagtc cgcagacatg gatgtgttac tggagtccct
360
caagtgcctg tgcaacctcg tgctcagcag ccctgtggca cagatgctgg cagcagagggc
420
ccgcctagtg gtgaagctca cagagcgtgt ggggctgtac cgtgagagga gctc
474

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```

<210> 3004
<211> 155
<212> PRT
<213> Homo sapiens

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<400> 3004
Met Glu Pro Arg Ala Val Ala Glu Ala Val Glu Thr Gly Glu Glu Asp
1              5              10              15
Val Ile Met Glu Ala Leu Arg Ser Tyr Asn Gln Glu His Ser Gln Ser
20              25              30
Phe Thr Phe Asp Asp Ala Gln Gln Glu Asp Arg Lys Arg Leu Ala Glu
35              40              45
Leu Leu Val Ser Val Leu Glu Gln Gly Leu Pro Pro Ser His Arg Val
50              55              60
Ile Trp Leu Gln Ser Val Arg Ile Leu Ser Arg Asp Arg Asn Cys Leu
65              70              75              80
Asp Pro Phe Thr Ser Arg Gln Ser Leu Gln Ala Leu Ala Cys Tyr Ala
85              90              95
Asp Ile Ser Val Ser Glu Gly Ser Val Pro Glu Ser Ala Asp Met Asp
100              105              110
Val Val Leu Glu Ser Leu Lys Cys Leu Cys Asn Leu Val Leu Ser Ser
115              120              125
Pro Val Ala Gln Met Leu Ala Ala Glu Ala Arg Leu Val Val Lys Leu

```

130 135 140
 Thr Glu Arg Val Gly Leu Tyr Arg Glu Arg Ser
 145 150 155

<210> 3005
 <211> 799
 <212> DNA
 <213> Homo sapiens

<400> 3005
 gtgcacagcg tggtaacca cagccctcc cagctcctca aggaggtcat cctgggtggac
 60
 gacaacagtg acaacgtgga actcaagttc aatctggacc agtacgtcaa caagcggtag
 120
 ccaggcctcg tgaagattgt ccgcaacagc cggcgggaag gactgatccg cgcgcggtg
 180
 cagggtcgga aggcggccac cgccccagtc gtcggcttct ttgatgccca cgtcgagttc
 240
 aacacgggct gggccgagcc cgcactgtcg cggatccgag aggaccggcg tcgcatcgtg
 300
 ctgccagcca tcgacaacat caagtacagc acgtttgagg tgcagcagta tgcgaacgcc
 360
 gccatggct acaactgggg cctctggtgc atgtacatca tcccccgca ggactggctg
 420
 gaccgcgcg acgagtcagc acccatcagg accccagcca tgatcggtg ctccttcgta
 480
 gtggaccgag agtacttcgg agacattggg ctgctggacc ccgcatgga ggtgtatggc
 540
 ggcgagaacg tagaactggg catgagggtg tggcagtggt gcgcgagcat ggaggtgctg
 600
 ccctgctccc gcgtggccca catcgagcgc accaggaagc cctacaacaa cgacattgac
 660
 tactacgcca agcgcaacgc cctgcgcacc gccgaggtgt ggatggatga cttcaagtcc
 720
 cagctgtaca tggcctggaa catccccatg tcgaaccagc ggggtggactt cggggacgtg
 780
 tctgagaggg tggccctgc
 799

<210> 3006
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 3006
 Val His Ser Val Val Asn His Thr Pro Ser Gln Leu Leu Lys Glu Val
 1 5 10 15
 Ile Leu Val Asp Asp Asn Ser Asp Asn Val Glu Leu Lys Phe Asn Leu
 20 25 30
 Asp Gln Tyr Val Asn Lys Arg Tyr Pro Gly Leu Val Lys Ile Val Arg
 35 40 45
 Asn Ser Arg Arg Glu Gly Leu Ile Arg Ala Arg Leu Gln Gly Trp Lys
 50 55 60
 Ala Ala Thr Ala Pro Val Val Gly Phe Phe Asp Ala His Val Glu Phe

```

65          70          75          80
Asn Thr Gly Trp Ala Glu Pro Ala Leu Ser Arg Ile Arg Glu Asp Arg
      85          90          95
Arg Arg Ile Val Leu Pro Ala Ile Asp Asn Ile Lys Tyr Ser Thr Phe
      100          105          110
Glu Val Gln Gln Tyr Ala Asn Ala Ala His Gly Tyr Asn Trp Gly Leu
      115          120          125
Trp Cys Met Tyr Ile Ile Pro Pro Gln Asp Trp Leu Asp Arg Gly Asp
      130          135          140
Glu Ser Ala Pro Ile Arg Thr Pro Ala Met Ile Gly Cys Ser Phe Val
145          150          155          160
Val Asp Arg Glu Tyr Phe Gly Asp Ile Gly Leu Leu Asp Pro Gly Met
      165          170          175
Glu Val Tyr Gly Gly Glu Asn Val Glu Leu Gly Met Arg Val Trp Gln
      180          185          190
Cys Gly Gly Ser Met Glu Val Leu Pro Cys Ser Arg Val Ala His Ile
      195          200          205
Glu Arg Thr Arg Lys Pro Tyr Asn Asn Asp Ile Asp Tyr Tyr Ala Lys
      210          215          220
Arg Asn Ala Leu Arg Thr Ala Glu Val Trp Met Asp Asp Phe Lys Ser
225          230          235          240
His Val Tyr Met Ala Trp Asn Ile Pro Met Ser Asn Pro Gly Val Asp
      245          250          255
Phe Gly Asp Val Ser Glu Arg Leu Ala Leu
      260          265

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<210> 3007
<211> 536
<212> DNA
<213> Homo sapiens

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<400> 3007
cttaagagag gttgcaatgt gaatgataga gatggattga cagatatgac tcttttacat
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tatacctgca aatctggagc tcatggtatt ggtgatgtgg aaacagctgt aaaatttgca
120
actcagctta ttgacctggg agcagacatt agtttgcgga gtcgctggac aaacatgaat
180
gctttgcatt atgctgctta ttttgatgtc cctgaactta taagagtgat ttgaaaaca
240
tcgaaaccaa aagatgtgga tgccccttgc agtgatttta attttggaac agctttgcatt
300
attgcagcat acaacttgtg tgcaggtgct gtgaagtgcc tcttgaggca gggagcaaat
360
cctgcattta ggaatgacaa aggacagatc cctgctgatg ttgttcaga cccagtagat
420
atgccgttag agatggctga cgccgcagcc actgctaagg aaatcaagca gatgcttcta
480
gatgcggtgc ctctgtcatg taacatctca aaggccatgc tcccccttc acgcgt
536

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<210> 3008
<211> 163
<212> PRT

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<213> Homo sapiens

<400> 3008

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Met Thr Leu Leu His Tyr Thr Cys Lys Ser Gly Ala His Gly Ile Gly
 1           5           10           15
Asp Val Glu Thr Ala Val Lys Phe Ala Thr Gln Leu Ile Asp Leu Gly
      20           25           30
Ala Asp Ile Ser Leu Arg Ser Arg Trp Thr Asn Met Asn Ala Leu His
      35           40           45
Tyr Ala Ala Tyr Phe Asp Val Pro Glu Leu Ile Arg Val Ile Leu Lys
      50           55           60
Thr Ser Lys Pro Lys Asp Val Asp Ala Pro Cys Ser Asp Phe Asn Phe
      65           70           75           80
Gly Thr Ala Leu His Ile Ala Ala Tyr Asn Leu Cys Ala Gly Ala Val
      85           90           95
Lys Cys Leu Leu Glu Gln Gly Ala Asn Pro Ala Phe Arg Asn Asp Lys
      100          105          110
Gly Gln Ile Pro Ala Asp Val Val Pro Asp Pro Val Asp Met Pro Leu
      115          120          125
Glu Met Ala Asp Ala Ala Ala Thr Ala Lys Glu Ile Lys Gln Met Leu
      130          135          140
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<210> 3009

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<212> DNA

<213> Homo sapiens

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<211> 310

<212> PRT

<213> Homo sapiens

<400> 3010

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<212> DNA

<213> Homo sapiens

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			20					25					30		
Leu	Glu	Gln	Asp	Thr	Gln	Gly	Leu	Asp	Gly	Trp	Trp	Leu	Cys	Ser	Leu
			35				40					45			
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	50					55					60				
Gly	Met	Tyr	Asp	Lys	Pro	Ala	Gly	Pro	Gly	Ser	Gly	Pro	Pro	Ala	
65				70					75					80	
Thr	Pro	Ala	Gln	Pro	Gln	Pro	Gly	Leu	His	Ala	Pro	Ala	Pro	Pro	Ala
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Ser	Gln	Tyr	Thr	Pro	Met	Leu	Pro	Asn	Thr	Tyr	Gln	Pro	Gln	Pro	Asp
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			115					120					125		
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 Val Pro Gly Gly Met Val His Pro Ile Phe Leu Glu Pro Val Thr Val

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 4560
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 4680
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<210> 3018

<211> 104

<212> PRT

<213> Homo sapiens

<400> 3018

Cys	His	Leu	Glu	Gln	Val	His	Leu	Lys	Pro	Ile	Pro	Lys	Asp	Thr	Pro
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Thr	Thr	Pro	Thr	Pro	Thr	Leu	Ala	Cys	Pro	Ser	Pro	Gln	Cys	Ala	Phe
			20					25					30		
Gln	Arg	Trp	Ile	Thr	Ile	Gln	His	Arg	Trp	Ser	Ser	Ala	Leu	His	Cys
		35				40						45			
Gln	Gly	Leu	Thr	Pro	Thr	Pro	Gly	Ala	Leu	Pro	Asn	Tyr	Leu	Lys	Val
		50				55				60					
Lys	Ala	Asn	Arg	Ala	Ile	Pro	Gln	Ala	Val	Thr	Ser	Thr	Arg	Leu	Gly
65					70				75					80	
Thr	Thr	Lys	Pro	Pro	Cys	Thr	Ile	Thr	Pro	Pro	Cys	Arg	Ala	Val	Arg
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Ser	Thr	Ser	Pro	Arg	Leu	Pro	Thr								
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<210> 3019

<211> 882

<212> DNA

<213> Homo sapiens

<400> 3019

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 120
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 180
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 240
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 300
 ccggaacccc aaggcatcct tgcgtgtgcg gctctgtgac ctcctgagcc acctgcagcg
 360
 gagctgtgag cgggactgcc aggagttcta ccgagccctg tatatccatg cccagccctt
 420

gcacagcgcg ctgccagcc gccacgctct gcagaactca gattgcacag agctagactc
 480
 gggcagccag agcggcgagc tgagtaacag gggacccatg agcttctctg ctggcctggg
 540
 ccttgctgtg ggactggccc tgctcctgta ctgctatccg ccagacccca agggcctggc
 600
 agggacccgg cgcgtcctcg gtttctcgcc tgtcatcatc gacagacatg tcagccgcta
 660
 cctgctggcc ttcctggcag atgacctagg ggggctctga cagacctgg acccaggggc
 720
 tcacctgcca ctcaacaaa gagtcctcga gccggcccg cagggggact gctgcttctt
 780
 tttctaaatg catatttttc attatttata atttggttaa aaaacacacc ttcacctta
 840
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 882

<210> 3020

<211> 58

<212> PRT

<213> Homo sapiens

<400> 3020

Gln	Gly	Thr	His	Glu	Leu	Pro	Gly	Trp	Pro	Gly	Pro	Cys	Cys	Gly	Thr
1				5				10				15			
Gly	Pro	Ala	Pro	Val	Leu	Leu	Ser	Ala	Arg	Pro	Gln	Gly	Pro	Ala	Arg
			20				25					30			
Asp	Pro	Ala	Arg	Pro	Arg	Phe	Leu	Ala	Cys	His	His	Arg	Gln	Thr	Cys
			35				40					45			
Gln	Pro	Leu	Pro	Ala	Gly	Leu	Pro	Gly	Arg						
	50					55									

<210> 3021

<211> 1008

<212> DNA

<213> Homo sapiens

<400> 3021

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 120
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 180
 aagtgtatac actcacaaa actatactta gaactcaaaa ctgcccaat atatacttaa
 240
 aatggatgca gttggttatg tataaattat acctcaataa agttgattaa aaacatcaat
 300
 tcctcagaaa attcttttct gaccactccc ctctcagacg aggtcgggcc tcctgggtatg
 360
 catacccata cccactacaa cctgtattta ttttttttga aacatggctc ctttctgtcg
 420
 tccaggctgg agtgagtg cgcaatcatg gatcactgca gcccttgacct tcctggctca
 480

agtgcctc cggctcacc cccagtagct ggaaccacag gcgcgttcc acaccggaaa
 540
 gcccattttc tagaggcgga aaccgaagcg cccagtggga aaggcgacc gccggggtg
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 660
 tccgcggact acggttctgg ctgcctagct ctggaaggga gcaccgggag ggaatggtg
 720
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 780
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 ggactcgcgc agacgggaag caggcgcgtg ctggcggtga cctggggccg gagaggaacg
 900
 ctgggtcccc tccttgggag ttgccaccat tccctcccg tgctcccttc cagagctagc
 960
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 1008

<210> 3022

<211> 94

<212> PRT

<213> Homo sapiens

<400> 3022

Met	His	Thr	His	Thr	His	Tyr	Asn	Leu	Tyr	Leu	Phe	Phe	Leu	Lys	His
1					5				10					15	
Gly	Leu	Phe	Leu	Ser	Ser	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Asp
			20					25					30		
His	Cys	Ser	Leu	Asp	Leu	Pro	Gly	Ser	Ser	Asp	Pro	Pro	Gly	Ser	Pro
			35					40				45			
Pro	Val	Ala	Gly	Thr	Thr	Gly	Ala	Leu	Pro	His	Arg	Lys	Ala	His	Phe
	50					55					60				
Leu	Glu	Ala	Glu	Thr	Glu	Ala	Pro	Ser	Gly	Lys	Gly	Asp	Pro	Pro	Gly
65					70					75				80	
Met	Arg	Gly	Ala	Gln	Arg	Ala	Ala	Thr	Trp	Gly	Pro	Thr	Arg		
				85					90						

<210> 3023

<211> 1834

<212> DNA

<213> Homo sapiens

<400> 3023

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 120
 tcagattttt ccctccagtt ggtttaattt ctatttcccta aaacattaaa ataataatgg
 180
 aatgatgtgaa ataataaaca tttttcttat tcaagatttc gtcattggcta ttgtaaagga
 240
 aaccctagga aaatggtgaa aacttgggca gaaaaagaaa tgagggaactt aatcaggcta
 300

aacacagcag agataccatg tccagaacca ataatgctaa gaagtcatgt tcttgtcatg
360
agtttcatcg gtaaagatga catgcctgca cactcttga aaaatgtcca gttatcagaa
420
tccaaggctc gggagttgta cctgcaggtc attcagtaca tgagaagaat gtatcaggat
480
gccagacttg tccatgcaga tctcagttaa ttaacatgc tgtaaccacg tgaggcgctg
540
tatatcattg acgtgtctca gtccgtggag cagcaccacc cacatgcctt ggagttcttg
600
agaaaggatt gcgccaacgt caatgatttc tttatgaggc acagtgttgc tgcctatgact
660
gtgcgggagc tctttgaatt tgtcacagat ccatccatta cacatgagaa catggatgct
720
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780
gatcatgttg atgaagaggt gtttaagcga gcataatatt ctagaacctt gaatgaagtg
840
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960
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1440
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1680
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1740
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1834

<210> 3024

<211> 347

<212> PRT

<213> Homo sapiens

<400> 3024

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Gly Asn Pro Arg Lys Met Val Lys Thr Trp Ala Glu Lys Glu Met Arg
 20          25          30
Asn Leu Ile Arg Leu Asn Thr Ala Glu Ile Pro Cys Pro Glu Pro Ile
 35          40          45
Met Leu Arg Ser His Val Leu Val Met Ser Phe Ile Gly Lys Asp Asp
 50          55          60
Met Pro Ala Pro Leu Leu Lys Asn Val Gln Leu Ser Glu Ser Lys Ala
 65          70          75          80
Arg Glu Leu Tyr Leu Gln Val Ile Gln Tyr Met Arg Arg Met Tyr Gln
 85          90          95
Asp Ala Arg Leu Val His Ala Asp Leu Ser Glu Phe Asn Met Leu Tyr
100          105          110
His Gly Gly Gly Val Tyr Ile Ile Asp Val Ser Gln Ser Val Glu His
115          120          125
Asp His Pro His Ala Leu Glu Phe Leu Arg Lys Asp Cys Ala Asn Val
130          135          140
Asn Asp Phe Phe Met Arg His Ser Val Ala Val Met Thr Val Arg Glu
145          150          155          160
Leu Phe Glu Phe Val Thr Asp Pro Ser Ile Thr His Glu Asn Met Asp
165          170          175
Ala Tyr Leu Ser Lys Ala Met Glu Ile Ala Ser Gln Arg Thr Lys Glu
180          185          190
Glu Arg Ser Ser Gln Asp His Val Asp Glu Glu Val Phe Lys Arg Ala
195          200          205
Tyr Ile Pro Arg Thr Leu Asn Glu Val Lys Asn Tyr Glu Arg Asp Met
210          215          220
Asp Ile Ile Met Lys Leu Lys Glu Glu Asp Met Ala Met Asn Ala Gln
225          230          235          240
Gln Asp Asn Ile Leu Pro Asp Cys Tyr Arg Ile Glu Glu Arg Phe Val
245          250          255
Arg Ser Ser Glu Gly Pro Cys Thr Leu Glu Asn Gln Val Glu Glu Arg
260          265          270
Thr Cys Ser Asp Ser Glu Asp Ile Gly Ser Ser Glu Cys Ser Asp Thr
275          280          285
Asp Ser Glu Glu Gln Gly Asp His Ala Arg Pro Lys Lys His Thr Thr
290          295          300
Asp Pro Asp Ile Asp Lys Lys Glu Arg Lys Lys Met Val Lys Glu Ala
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Gln Arg Glu Lys Arg Lys Asn Lys Ile Pro Lys His Val Lys Lys Arg
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Lys Glu Lys Thr Ala Lys Thr Lys Lys Gly Lys
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<210> 3025

<211> 1370

<212> DNA

<213> Homo sapiens

<400> 3025
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120
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180
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240
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300
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360
aacactatta catgggaaga atatatatct gctgaaaatg gaaaagctcc tcactctgggt
420
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480
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540
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600
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720
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780
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840
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1260
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1370

<210> 3026

<211> 152

<212> PRT

<213> Homo sapiens

<400> 3026

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      20           25           30
Trp Glu Glu Tyr Ile Ser Ala Glu Asn Gly Lys Ala Pro His Leu Gly
      35           40           45
Arg Glu Leu Val Cys Lys Glu Ser Lys Lys Thr Phe Lys Ala Thr Ile
 50           55           60
Ala Met Ser Gln Glu Phe Pro Leu Gly Ile Glu Leu Leu Leu Asn Val
65           70           75           80
Leu Glu Val Val Ala Pro Phe Lys His Phe Asn Lys Leu Arg Glu Phe
      85           90           95
Val Gln Met Lys Leu Pro Pro Gly Phe Pro Val Lys Leu Asp Ile Pro
      100           105           110
Val Phe Pro Thr Ile Thr Ala Thr Val Thr Phe Gln Glu Phe Arg Tyr
      115           120           125
Asp Glu Phe Asp Gly Ser Ile Phe Thr Ile Pro Asp Asp Tyr Lys Glu
      130           135           140
Asp Pro Ser Arg Phe Pro Asp Leu
145           150

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<210> 3027

<211> 1154

<212> DNA

<213> Homo sapiens

<400> 3027

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120
cgcagacggc ggcctccgcg gcgctctcca gtcattggact accggcggct tctcatgagc
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240
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360
tgggactggg atgaaggagt tggaaaactc gccaaagggt atgtctggaa tggaggaagc
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660
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720
aaagaagcta atgtatacca tgctagcaca gcaaatggag agagcagagc aatcaaaatt
780

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 900
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 960
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 1020
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<210> 3028

<211> 331

<212> PRT

<213> Homo sapiens

<400> 3028

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Asp	Asp	Ala	Asp	Ser	Ser	Asp	Ser	Glu	Asn	Arg	Asp	Leu	Lys	Thr	Val
			20					25					30		
Lys	Glu	Lys	Asp	Asp	Ile	Leu	Phe	Glu	Asp	Leu	Gln	Asp	Asn	Val	Asn
		35					40					45			
Glu	Asn	Gly	Glu	Gly	Glu	Ile	Glu	Asp	Glu	Glu	Glu	Gly	Tyr	Asp	
	50					55				60					
Asp	Asp	Asp	Asp	Asp	Trp	Asp	Trp	Asp	Glu	Gly	Val	Gly	Lys	Leu	Ala
				70					75					80	
Lys	Gly	Tyr	Val	Trp	Asn	Gly	Gly	Ser	Asn	Pro	Gln	Ala	Asn	Arg	Gln
			85						90					95	
Thr	Ser	Asp	Ser	Ser	Ala	Lys	Met	Ser	Thr	Pro	Ala	Asp	Lys	Val	
			100				105						110		
Leu	Arg	Lys	Phe	Glu	Asn	Lys	Ile	Asn	Leu	Asp	Lys	Leu	Asn	Val	Thr
		115					120					125			
Asp	Ser	Val	Ile	Asn	Lys	Val	Thr	Glu	Lys	Ser	Arg	Gln	Lys	Glu	Ala
		130				135					140				
Asp	Met	Tyr	Arg	Ile	Lys	Asp	Lys	Ala	Asp	Arg	Ala	Thr	Val	Glu	Gln
					150					155				160	
Val	Leu	Asp	Pro	Arg	Thr	Arg	Met	Ile	Leu	Phe	Lys	Met	Leu	Thr	Arg
				165					170					175	
Gly	Ile	Ile	Thr	Glu	Ile	Asn	Gly	Cys	Ile	Ser	Thr	Gly	Lys	Glu	Ala
			180					185					190		
Asn	Val	Tyr	His	Ala	Ser	Thr	Ala	Asn	Gly	Glu	Ser	Arg	Ala	Ile	Lys
		195					200					205			
Ile	Tyr	Lys	Thr	Ser	Ile	Leu	Val	Phe	Lys	Asp	Arg	Asp	Lys	Tyr	Val
		210				215					220				
Ser	Gly	Glu	Phe	Arg	Phe	Arg	His	Gly	Tyr	Cys	Lys	Gly	Asn	Pro	Arg
				230						235				240	
Lys	Met	Val	Lys	Thr	Trp	Ala	Glu	Lys	Glu	Met	Arg	Asn	Leu	Ile	Arg
				245						250				255	
Leu	Asn	Thr	Ala	Glu	Ile	Pro	Cys	Pro	Glu	Pro	Ile	Met	Leu	Arg	Ser

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                260                265                270
His Val Leu Val Met Ser Phe Ile Gly Lys Asp Asp Ile Ser Phe His
      275                280                285
Ser Arg Pro Ala Pro Leu Leu Lys Asn Val Gln Leu Ser Glu Ser Lys
      290                295                300
Ala Arg Glu Leu Tyr Leu Gln Val Ile Gln Tyr Met Arg Arg Met Tyr
      305                310                315                320
Gln Asp Ala Arg Leu Val His Ala Asp Arg Arg
      325                330

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<210> 3029

<211> 344

<212> DNA

<213> Homo sapiens

<400> 3029

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120
acatttcccg aggaactaga tatgagtact tttattgatg ttgaagatga aaaatctcct
180
cagactgaaa gttgcactga caggggagca gaaaatgaag gtagtgtgca cagtgatcag
240
atgagcaacg atttctccaa tgatgatggt gttgatgaag gaatctgttt tgaaccaaat
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344

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<210> 3030

<211> 114

<212> PRT

<213> Homo sapiens

<400> 3030

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Thr Arg Asp Ala Arg Lys Gly Leu Arg Phe Leu His Phe Pro Tyr Leu
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Leu Thr Leu Gln Leu Lys Arg Phe Asp Phe Asp Tyr Thr Thr Met His
      20      25      30
Arg Ile Lys Leu Asn Asp Arg Met Thr Phe Pro Glu Glu Leu Asp Met
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Ser Thr Phe Ile Asp Val Glu Asp Glu Lys Ser Pro Gln Thr Glu Ser
      50      55      60
Cys Thr Asp Arg Gly Ala Glu Asn Glu Gly Ser Cys His Ser Asp Gln
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Met Ser Asn Asp Phe Ser Asn Asp Asp Gly Val Asp Glu Gly Ile Cys
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<210> 3031

<211> 567

<212> DNA

<213> Homo sapiens

<400> 3031

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<210> 3032

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3032

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Thr	Pro	Arg	Met	Asn	Arg	Arg	Leu	Val	Gly	Pro	Asp	Val	Ile	Pro	Leu
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		100					105						110		
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Ala	Pro	Val	Leu	Ser	Cys	Glu	Ala	Ala	Thr	Gln	Thr	Glu	Arg	Arg	Leu
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 <213> Homo sapiens

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 50 55 60
 Arg Trp Arg Val Glu Lys Glu Val Ile Ser Gly Lys Gly Gln Phe Phe
 65 70 75 80
 Cys Gly Asn Lys Tyr Cys Asp Lys Lys Glu Gly Leu Lys Ser Trp Glu

Val	Asn	Phe	Gly	100	Tyr	Ile	Glu	His	Gly	105	Glu	Lys	Arg	Asn	110	Ala	Leu	Val
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<212> PRT

<213> Homo sapiens

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Leu	Phe	Ile	Val	Pro	Arg	Gln	Arg	Leu	Asp	Leu	Leu	Pro	Phe	Tyr	Ala
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Glu	Leu	Thr	Lys	Phe	Lys	Met	Phe	Thr	Lys	Asn	Asp	Thr	Leu	His	Cys

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<212> DNA

<213> Homo sapiens

<400> 3039

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 1680
 aatcagctgg aattaattct tcgacaactc cagaccgacc ttcggaagga aaaacaagac
 1740
 aaggccggtc tccaagcaga agtgacgac ctgagacagg acaacatgag gctgcaggaa
 1800
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 1836

<210> 3040

<211> 142

<212> PRT

<213> Homo sapiens

<400> 3040

Thr	Leu	Cys	His	Cys	Leu	Asp	Leu	His	Ile	Arg	Ala	Ala	Leu	Met	Pro
1				5					10					15	
Leu	Pro	Asp	Thr	Ala	Thr	Gly	Leu	Asp	Trp	Thr	His	Leu	Val	Asp	Ala
				20					25					30	
Ala	Arg	Ala	Phe	Glu	Asp	Gln	Arg	Val	Ala	Ser	Phe	Cys	Thr	Leu	Thr
				35				40				45			
Asp	Met	Gln	His	Gly	Gln	Asp	Leu	Glu	Gly	Ala	Gln	Glu	Leu	Pro	Leu
				50			55				60				
Cys	Val	Asp	Pro	Gly	Ser	Gly	Lys	Glu	Phe	Met	Asp	Thr	Thr	Gly	Glu
				65			70			75				80	
Arg	Ser	Pro	Ser	Pro	Leu	Thr	Gly	Lys	Val	Asn	Gln	Leu	Glu	Leu	Ile

	85		90		95
Leu Arg Gln Leu Gln Thr Asp Leu Arg Lys Glu Lys Gln Asp Lys Ala					
	100		105		110
Gly Leu Gln Ala Glu Val Gln His Leu Arg Gln Asp Asn Met Arg Leu					
	115		120		125
Gln Glu Glu Ser Gln Thr Ala Thr Ala Gln Leu Arg Lys Leu					
	130		135		140

<210> 3041

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 3041

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120
ccctcaacgt ccgaggcgcc gatgaaggca ctgatcttag tggggggcta tgggacgcgg
180
ctacggccgc tgacgctgag cccccgaag cactgggtgg acttctgcaa taagcccatc
240
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300
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360
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420
cgtgacctac tctctgagac tgcagaccct ttcttcgtcc tcaacagtga cgtgatctgc
480
gatttccctt tccaagccat ggtgcagttc caccggcacc atggccaggga gggctccatc
540
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600
ggccgcattc accgggttcgt ggagaaggca cagggtgttg tgtccaataa gatcaacgca
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ggcatgtata tcttgagccc tgcagtgtct cgccgcattc agctgcagcc tacgtccatt
720
gagaaggagg tcttccccat tatggccaag gaggggcagc tatatgccat ggagttacag
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900
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1020
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1080
gtgggtcagt gggtagcat ggagaacgtg acagtgtctg gtgaggacgt catagttaat
1140
gatgagctct acctcaacgg agccagcgtg ctgccccaca agtctattgg cagtcagtg
1200

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ccagagcctc gtatcatcat gtgaggggat gcagtggggc tggccgagcc cgggttttcc
 1260
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 1320
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 1380
 ctggcaggat ccttctgtggg cacacccac aaaccccat ccctcaagaa gggccagggc
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 1500
 aaaaaaaaaa aa
 1512

<210> 3042

<211> 360

<212> PRT

<213> Homo sapiens

<400> 3042

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Leu	Thr	Leu	Ser	Thr	Pro	Lys	Pro	Leu	Val	Asp	Phe	Cys	Asn	Lys	Pro
		20					25					30			
Ile	Leu	Leu	His	Gln	Val	Glu	Ala	Leu	Ala	Ala	Gly	Val	Asp	His	
	35					40				45					
Val	Ile	Leu	Ala	Val	Ser	Tyr	Met	Ser	Gln	Val	Leu	Glu	Lys	Glu	Met
	50				55					60					
Lys	Ala	Gln	Glu	Gln	Arg	Leu	Gly	Ile	Arg	Ile	Ser	Met	Ser	His	Glu
65				70				75						80	
Glu	Glu	Pro	Leu	Gly	Thr	Ala	Gly	Pro	Leu	Ala	Leu	Ala	Arg	Asp	Leu
		85						90					95		
Leu	Ser	Glu	Thr	Ala	Asp	Pro	Phe	Phe	Val	Leu	Asn	Ser	Asp	Val	Ile
		100					105						110		
Cys	Asp	Phe	Pro	Phe	Gln	Ala	Met	Val	Gln	Phe	His	Arg	His	His	Gly
	115						120				125				
Gln	Glu	Gly	Ser	Ile	Leu	Val	Thr	Lys	Val	Glu	Glu	Pro	Ser	Lys	Tyr
	130				135					140					
Gly	Val	Val	Val	Cys	Glu	Ala	Asp	Thr	Gly	Arg	Ile	His	Arg	Phe	Val
145				150					155					160	
Glu	Lys	Pro	Gln	Val	Phe	Val	Ser	Asn	Lys	Ile	Asn	Ala	Gly	Met	Tyr
		165						170					175		
Ile	Leu	Ser	Pro	Ala	Val	Leu	Arg	Arg	Ile	Gln	Leu	Gln	Pro	Thr	Ser
	180						185						190		
Ile	Glu	Lys	Glu	Val	Phe	Pro	Ile	Met	Ala	Lys	Glu	Gly	Gln	Leu	Tyr
	195						200				205				
Ala	Met	Glu	Leu	Gln	Gly	Phe	Trp	Met	Asp	Ile	Gly	Gln	Pro	Lys	Asp
	210				215					220					
Phe	Leu	Thr	Gly	Met	Cys	Leu	Phe	Leu	Gln	Ser	Leu	Arg	Gln	Lys	Gln
225				230					235					240	
Pro	Glu	Arg	Leu	Cys	Ser	Gly	Pro	Gly	Ile	Val	Gly	Asn	Val	Leu	Val
		245						250					255		
Asp	Pro	Ser	Ala	Arg	Ile	Gly	Gln	Asn	Cys	Ser	Ile	Gly	Pro	Asn	Val
	260					265					270				
Ser	Leu	Gly	Pro	Gly	Val	Val	Val	Glu	Asp	Gly	Val	Cys	Ile	Arg	Arg

```

      275              280              285
Cys Thr Val Leu Arg Asp Ala Arg Ile Arg Ser His Ser Trp Leu Glu
  290              295              300
Ser Cys Ile Val Gly Trp Arg Cys Arg Val Gly Gln Trp Val Arg Met
  305              310              315
Glu Asn Val Thr Val Leu Gly Glu Asp Val Ile Val Asn Asp Glu Leu
      325              330              335
Tyr Leu Asn Gly Ala Ser Val Leu Pro His Lys Ser Ile Gly Glu Ser
      340              345              350
Val Pro Glu Pro Arg Ile Ile Met
      355              360

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<210> 3043

<211> 394

<212> DNA

<213> Homo sapiens

<400> 3043

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tctcatgatg ccagcgcttc ctcttcactg gcgtctgacc caggagcagt ccagaatcac
120
cttctctgac ctcaactcaa ctcacgtgtc tttgacactt taaggggactt cctgttttag
180
ggtcttcttg ctgggtgtca ttgaatgggc agtgattctc taactttaga ctgatgttcc
240
ccagcctttg tttggggact cggaggcaga gtagacagtt acccttacc cttgggttggg
300
gagggtcata ttcctggtat cccagcagg tcaacagggg cttcattttt ctgaggggact
360
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394

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<210> 3044

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3044

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Met Lys Pro Leu Leu Thr Ser Trp Gly Tyr Gln Glu Tyr Asp Pro Pro
  1              5              10              15
Gln Pro Arg Gly Lys Gly Asn Cys Leu Leu Cys Leu Arg Val Pro Lys
      20              25              30
Gln Arg Leu Gly Asn Ile Ser Leu Lys Leu Glu Asn His Cys Pro Phe
      35              40              45
Asn Asp Thr Gln Pro Glu Asp Pro Lys Thr Gly Ser Pro Leu Lys Cys
      50              55              60
Gln Arg His Val Ser Trp Ser Glu Val Arg Glu Ala Asp Ser Gly Leu
      65              70              75              80
Leu Leu Gly Gln Thr Pro Val Lys Arg Lys Arg Trp His His Glu Thr
      85              90              95
Ser Ser Phe Ser Pro Cys Leu Trp Leu Lys Ala Arg Ala Ser Arg Ser
      100              105              110
Lys Glu Ile

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115

<210> 3045

<211> 605

<212> DNA

<213> Homo sapiens

<400> 3045

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gaagaaattc tttgttcaa gctgctatcc atgtccaggg ccaaactatga atcctattgc
120
tcttgggagc cgctggcttg cttatgcaga aaacaagttg attcgaatgc atcagtcacc
180
tggtggagcc tgtggagaca acattcagtc ttatactgcc acagtcatta gtgctgctaa
240
aacattgaaa agtggcctga caatggtagg gaaagtggcg actcagctga caggcacact
300
gccttcagggt gtgacagaag atgatgttg catccacagt aattcacggc ggagtccttt
360
gggtcccaggc atcatcacag ttattgacac cgaaaccgtg gagagggcca ggtgtttgtg
420
agtgaggatc ttgacagtga tggcattgtg gcccaattcc ctgcccata gaagccagtg
480
tgctgcattg cttttaatac aagtgggaat cttctagtca caacagacac ccttggccat
540
gactttcatg tcttccaat tctgactcat ccttggctct catctacgga gagacgacaa
600
cgcggt
605

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<210> 3046

<211> 72

<212> PRT

<213> Homo sapiens

<400> 3046

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His Arg Asn Arg Gly Glu Gly Gln Val Phe Val Ser Glu Asp Leu Asp
1      5      10      15
Ser Asp Gly Ile Val Ala His Phe Pro Ala His Glu Lys Pro Val Cys
20     25     30
Cys Met Ala Phe Asn Thr Ser Gly Met Leu Leu Val Thr Thr Asp Thr
35     40     45
Leu Gly His Asp Phe His Val Phe Gln Ile Leu Thr His Pro Trp Ser
50     55     60
Ser Ser Thr Glu Arg Arg Gln Arg
65      70

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<210> 3047

<211> 391

<212> DNA

<213> Homo sapiens

<400> 3047

attttggagg agaggaagaa tgaaatgacc caagtcatta cccgaaccca agaggagaaa
 60
 ctggaacatg tccgtgctct gatcaaaaag tattctgatac atttgagaa cgtctcaaa
 120
 ttggttgagt caggaattca gtttatggat gagccagaaa tggcagtggt tctgcagaat
 180
 gccaaaaccc tgctaaaaaa aatctcggaa gcatcaaaagg catttcagat ggagaaaata
 240
 gaacatggct atgagaacat gaaccacttc acagtcaacc tcaatagaga agaaaagata
 300
 atacgtgaaa ttgactttta cagagaagat gaagatgaag aagaagaaga aggcggagaa
 360
 ggagaaaaag aagagaagga gaagtgggag a
 391

<210> 3048

<211> 122

<212> PRT

<213> Homo sapiens

<400> 3048

Met	Thr	Gln	Val	Ile	Thr	Arg	Thr	Gln	Glu	Glu	Lys	Leu	Glu	His	Val
1				5				10						15	
Arg	Ala	Leu	Ile	Lys	Lys	Tyr	Ser	Asp	His	Leu	Glu	Asn	Val	Ser	Lys
			20				25						30		
Leu	Val	Glu	Ser	Gly	Ile	Gln	Phe	Met	Asp	Glu	Pro	Glu	Met	Ala	Val
			35				40					45			
Phe	Leu	Gln	Asn	Ala	Lys	Thr	Leu	Leu	Lys	Lys	Ile	Ser	Glu	Ala	Ser
	50					55					60				
Lys	Ala	Phe	Gln	Met	Glu	Lys	Ile	Glu	His	Gly	Tyr	Glu	Asn	Met	Asn
	65				70					75				80	
His	Phe	Thr	Val	Asn	Leu	Asn	Arg	Glu	Glu	Lys	Ile	Ile	Arg	Glu	Ile
			85						90					95	
Asp	Phe	Tyr	Arg	Glu	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Gly	Gly	Glu	
			100				105						110		
Gly	Glu	Lys	Glu	Glu	Lys	Glu	Lys	Trp	Glu						
			115				120								

<210> 3049

<211> 599

<212> DNA

<213> Homo sapiens

<400> 3049

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 120
 tttcctcttc tgaacgaaag ctcggccgag gtgctcgaat acaccattaa ggaagaaaaag
 180
 tcgatattgt acctggaagg ctcggctctt gtgtttgagg acatcttcag attgattgag
 240
 ttctactgtg tcagtagaga cttactgccc ttcacactgc ggctacccca ggccatcctt
 300

gagggcagca gcttcacgga ccttgagacc atcgccaacc tgggtctggg ttctctgggac
 360
 tcctcgtcta atcctccaca agaaagaggg aagccagcag agcccccaag agaccggggc
 420
 cccggattcc ccctagtctc cagcctcagg cccacagccc atgacgcaaa ctgtgctctg
 480
 gaaatcgagc tgtcggtagg aaatgaccgc ctgtgggttg tgaatccat ttctatcgag
 540
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 599

<210> 3050

<211> 177

<212> PRT

<213> Homo sapiens

<400> 3050

Met	Phe	Leu	Val	Arg	Arg	Asp	Ser	Ser	Ser	Lys	Gln	Leu	Val	Leu	Cys
1				5					10					15	
Val	His	Phe	Pro	Ser	Leu	Asn	Glu	Ser	Ser	Ala	Glu	Val	Leu	Glu	Tyr
			20					25					30		
Thr	Ile	Lys	Glu	Glu	Lys	Ser	Ile	Leu	Tyr	Leu	Glu	Gly	Ser	Ala	Leu
		35				40						45			
Val	Phe	Glu	Asp	Ile	Phe	Arg	Leu	Ile	Ala	Phe	Tyr	Cys	Val	Ser	Arg
	50					55				60					
Asp	Leu	Leu	Pro	Phe	Thr	Leu	Arg	Leu	Pro	Gln	Ala	Ile	Leu	Glu	Ala
65					70				75					80	
Ser	Ser	Phe	Thr	Asp	Leu	Glu	Thr	Ile	Ala	Asn	Leu	Gly	Leu	Gly	Phe
				85					90					95	
Trp	Asp	Ser	Ser	Leu	Asn	Pro	Pro	Gln	Glu	Arg	Gly	Lys	Pro	Ala	Glu
			100					105					110		
Pro	Pro	Arg	Asp	Arg	Ala	Pro	Gly	Phe	Pro	Leu	Val	Ser	Ser	Leu	Arg
		115				120						125			
Pro	Thr	Ala	His	Asp	Ala	Asn	Cys	Ala	Cys	Glu	Ile	Glu	Leu	Ser	Val
					135							140			
Gly	Asn	Asp	Arg	Leu	Trp	Phe	Val	Asn	Pro	Ile	Phe	Ile	Glu	Asp	Cys
145					150					155				160	
Ser	Ser	Ala	Leu	Pro	Thr	Asp	Gln	Pro	Pro	Leu	Gly	Asn	Cys	Pro	Ser
				165					170					175	

Arg

<210> 3051

<211> 820

<212> DNA

<213> Homo sapiens

<400> 3051

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 120
 tgaagactct caggttacca gcacaatatc cccctacat tctcctcaca agggactccc
 180

tcctcggcca ccgtcgaca acaggcctcc tcctccccag tccttgagg gactccgaca
 240
 gatgcactat caccgncaac gactatgaca agtcacccat caagcccaaa atgtggagt
 300
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 360
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 420
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 660
 cgcggaactg tagcagcaac ggctcagacc ccatggacga ctgctcgtcg tgcaccagcc
 720
 actcgagctc ggagcactac taccggcgcc agatgaacgc caactactcc acgctggccc
 780
 aggactcgcc gtccaaggcg cggtcgcagt gatattcgac
 820

<210> 3052

<211> 62

<212> PRT

<213> Homo sapiens

<400> 3052

Arg	Leu	Ser	Gly	Tyr	Gln	His	Asn	Ile	Pro	Pro	Thr	Phe	Ser	Ser	Gln
1				5					10					15	
Gly	Thr	Pro	Ser	Ser	Ala	Thr	Val	Ala	Gln	Gln	Ala	Ser	Ser	Ser	Pro
			20					25					30		
Val	Pro	Gly	Gly	Thr	Pro	Thr	Asp	Ala	Leu	Ser	Pro	Xaa	Thr	Thr	Met
		35					40					45			
Thr	Ser	His	Pro	Ser	Ser	Pro	Lys	Cys	Gly	Val	Ser	Pro	Leu		
	50					55					60				

<210> 3053

<211> 2625

<212> DNA

<213> Homo sapiens

<400> 3053

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 gagcctcoga catctaata gaatcttagaa gatataaccg taaaagatgg actttctctc
 120
 cagtttaaaa gatttagaga aactgtacca acttgggata caataagaga tgaagaagat
 180
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 240
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 300

gatgttatta atgctatcct taagcaacat acagaagaaa aagaatttgt tgagaagcac
360
tttaatgact taaacatgaa agctgtggaa caagatgaac caatacctca aaaacctcag
420
tcagcatttt attattgcag attgcttctt agtatattgg gaatgaattc ctgggacaaa
480
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600
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660
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720
aaaaacaaaa gcaactggatt gaccactcca tattttgcta cctctacagt agaggtaata
780
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840
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900
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960
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1080
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1320
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1380
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1620
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1740
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1860
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1920

aaacactcaa aataaatggt ctttagcatc tcaaattcca actgaaatca ttttagtatt
 1980
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 2220
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 2280
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 2340
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 2400
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 2460
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 2520
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 2625

<210> 3054

<211> 417

<212> PRT

<213> Homo sapiens

<400> 3054

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Glu	Lys	Pro	Glu	Glu	Pro	Pro	Thr	Ser	Asn	Glu	Cys	Leu	Glu	Asp	Ile
			20					25					30		
Thr	Val	Lys	Asp	Gly	Leu	Ser	Leu	Gln	Phe	Lys	Arg	Phe	Arg	Glu	Thr
			35				40					45			
Val	Pro	Thr	Trp	Asp	Thr	Ile	Arg	Asp	Glu	Glu	Asp	Val	Leu	Asp	Glu
			50			55					60				
Leu	Leu	Gln	Tyr	Leu	Gly	Val	Thr	Ser	Pro	Glu	Cys	Leu	Gln	Arg	Thr
			65			70				75				80	
Gly	Ile	Ser	Leu	Asn	Ile	Pro	Ala	Pro	Gln	Pro	Val	Cys	Ile	Ser	Glu
				85				90						95	
Lys	Gln	Glu	Asn	Asp	Val	Ile	Asn	Ala	Ile	Leu	Lys	Gln	His	Thr	Glu
			100					105					110		
Glu	Lys	Glu	Phe	Val	Glu	Lys	His	Phe	Asn	Asp	Leu	Asn	Met	Lys	Ala
			115				120					125			
Val	Glu	Gln	Asp	Glu	Pro	Ile	Pro	Gln	Lys	Pro	Gln	Ser	Ala	Phe	Tyr
			130			135					140				
Tyr	Cys	Arg	Leu	Leu	Leu	Ser	Ile	Leu	Gly	Met	Asn	Ser	Trp	Asp	Lys
			145		150					155				160	
Arg	Arg	Ser	Phe	His	Leu	Leu	Lys	Lys	Asn	Glu	Lys	Leu	Leu	Arg	Glu
				165					170					175	
Leu	Arg	Asn	Leu	Asp	Ser	Arg	Gln	Cys	Arg	Glu	Thr	His	Lys	Ile	Ala

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                180                185                190
Val Phe Tyr Val Ala Glu Gly Gln Glu Asp Lys His Ser Ile Leu Thr
      195                200                205
Asn Thr Gly Gly Ser Gln Ala Tyr Glu Asp Phe Val Ala Gly Leu Gly
      210                215                220
Trp Glu Val Asn Leu Thr Asn His Cys Gly Phe Met Gly Gly Leu Gln
      225                230                235                240
Lys Asn Lys Ser Thr Gly Leu Thr Thr Pro Tyr Phe Ala Thr Ser Thr
      245                250                255
Val Glu Val Ile Phe His Val Ser Thr Arg Met Pro Ser Asp Ser Asp
      260                265                270
Asp Ser Leu Thr Lys Lys Leu Arg His Leu Gly Asn Asp Glu Val His
      275                280                285
Ile Val Trp Ser Glu His Thr Arg Asp Tyr Arg Arg Gly Ile Ile Pro
      290                295                300
Thr Glu Phe Gly Asp Val Leu Ile Val Ile Tyr Pro Met Lys Asn His
      305                310                315                320
Met Phe Ser Ile Gln Ile Met Lys Lys Pro Glu Val Pro Phe Phe Gly
      325                330                335
Pro Leu Phe Asp Gly Ala Ile Val Asn Gly Lys Val Leu Pro Ile Met
      340                345                350
Val Arg Ala Thr Ala Ile Asn Ala Ser Arg Ala Leu Lys Ser Leu Ile
      355                360                365
Pro Leu Tyr Gln Asn Phe Tyr Glu Glu Arg Ala Arg Tyr Leu Gln Thr
      370                375                380
Ile Val Gln His His Leu Glu Pro Thr Thr Phe Glu Asp Phe Ala Ala
      385                390                395                400
Gln Val Phe Ser Pro Ala Pro Tyr His His Leu Pro Ser Asp Ala Asp
      405                410                415
His

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<210> 3055

<211> 905

<212> DNA

<213> Homo sapiens

<400> 3055

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180
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300
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360
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420
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480

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<210> 3056

<211> 195

<212> PRT

<213> Homo sapiens

<400> 3056

Met	Ser	Tyr	Arg	Thr	Leu	Tyr	Ile	Gly	Thr	Gly	Ala	Asp	Met	Asp	Val
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Cys	Leu	Thr	Asn	Tyr	Gly	His	Cys	Asn	Tyr	Val	Ser	Gly	Lys	His	Ala
			20					25					30		
Cys	Ile	Phe	Tyr	Asp	Glu	Asn	Thr	Lys	His	Tyr	Glu	Leu	Leu	Asn	Tyr
		35					40					45			
Ser	Glu	His	Gly	Thr	Thr	Val	Asp	Asn	Val	Leu	Tyr	Ser	Cys	Asp	Phe
		50				55					60				
Ser	Glu	Lys	Thr	Pro	Pro	Thr	Pro	Pro	Ser	Ser	Ile	Val	Ala	Lys	Val
65					70					75				80	
Gln	Ser	Val	Ile	Arg	Arg	Arg	Arg	His	Gln	Lys	Gln	Asp	Glu	Glu	Pro
			85					90						95	
Ser	Glu	Glu	Ala	Ala	Met	Met	Ser	Ser	Gln	Ala	Gln	Gly	Pro	Gln	Arg
			100					105					110		
Arg	Pro	Cys	Asn	Cys	Lys	Ala	Ser	Ser	Ser	Ser	Leu	Ile	Gly	Gly	Ser
		115					120						125		
Gly	Ala	Gly	Trp	Glu	Gly	Thr	Ala	Leu	Leu	His	His	Gly	Ser	Tyr	Ile
		130				135					140				
Lys	Leu	Gly	Cys	Leu	Gln	Phe	Val	Phe	Ser	Ile	Thr	Glu	Phe	Ala	Thr
145					150					155				160	
Lys	Gln	Pro	Lys	Gly	Asp	Ala	Ser	Leu	Leu	Gln	Asp	Gly	Val	Leu	Ala
				165					170					175	
Glu	Lys	Leu	Ser	Leu	Lys	Pro	His	Gln	Gly	Pro	Val	Leu	Arg	Ser	Asn
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Ser	Val	Pro													
		195													

<210> 3057

<211> 2169

<212> DNA

<213> Homo sapiens

<400> 3057
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120
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180
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240
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300
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360
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480
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540
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720
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<210> 3058

<211> 298

<212> PRT

<213> Homo sapiens

<400> 3058

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		20						25					30		
Ala	Arg	Arg	Ala	Arg	Lys	Val	Phe	Thr	Val	Ile	Glu	Pro	Val	Asp	Ile
		35				40					45				
Asn	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Gln	Ala	Gly	Ala	Arg	Glu	Lys	Val
	50				55					60					
Ala	Arg	Ser	Trp	Tyr	Cys	Asn	Arg	Gly	Leu	Val	Ser	Leu	Ser	Ala	Lys
65			70					75						80	
Ile	Asp	Arg	Lys	Gly	Tyr	Thr	Pro	Gly	Glu	Val	Ile	Pro	Val	Phe	Ala
		85						90					95		
Glu	Ile	Asp	Asn	Gly	Ser	Thr	Arg	Pro	Val	Leu	Pro	Arg	Ala	Ala	Val
		100						105					110		
Val	Gln	Thr	Gln	Thr	Phe	Met	Ala	Arg	Gly	Ala	Arg	Lys	Gln	Lys	Arg
	115				120							125			
Ala	Val	Val	Ala	Ser	Leu	Ala	Gly	Glu	Pro	Val	Gly	Pro	Gly	Gln	Arg
	130				135						140				
Ala	Leu	Trp	Gln	Gly	Arg	Ala	Leu	Arg	Ile	Pro	Pro	Val	Gly	Pro	Ser
145				150				155						160	
Ile	Leu	His	Cys	Arg	Val	Leu	His	Val	Asp	Tyr	Ala	Leu	Lys	Val	Cys
		165						170					175		
Val	Asp	Ile	Pro	Gly	Thr	Ser	Lys	Leu	Leu	Glu	Leu	Pro	Leu	Val	
		180						185				190			
Ile	Gly	Thr	Ile	Pro	Leu	His	Pro	Phe	Gly	Ser	Arg	Ser	Ser	Ser	Val

	195		200		205
Gly Ser His Ala Ser Phe Leu Leu Asp Trp Arg Leu Gly Ala Leu Pro					
210		215		220	
Glu Arg Pro Glu Ala Pro Pro Glu Tyr Ser Glu Val Val Ala Asp Thr					
225	230		235		240
Glu Glu Ala Ala Leu Gly Gln Ser Pro Phe Pro Leu Pro Gln Asp Pro					
	245		250		255
Asp Met Ser Leu Glu Gly Pro Phe Phe Ala Tyr Ile Gln Glu Phe Arg					
	260	265		270	
Tyr Arg Pro Pro Leu Tyr Ser Glu Glu Asp Pro Asn Pro Leu Leu					
	275	280		285	
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<210> 3059

<211> 1411

<212> DNA

<213> Homo sapiens

<400> 3059

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180
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240
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300
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360
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420
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480
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600
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660
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720
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780
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900
tcagtggaa ctagtgaagt gaaacaagca acttcaacat caggaccagc atcagcagtt
960
gctgatccac ccagtactga aaaagaaata gatcctacca gcacccctac tgctatcaag
1020

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 1140
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 1260
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 1380
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<210> 3060

<211> 334

<212> PRT

<213> Homo sapiens

<400> 3060

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Lys	Lys	Lys	His	Arg	Arg	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser
			20					25					30		
Arg	Thr	Tyr	Ser	Arg	Lys	Lys	Gly	Gly	Arg	Lys	Ser	Arg	Ser	Lys	Ser
			35				40					45			
Arg	Ser	Trp	Ser	Arg	Asp	Leu	Gln	Pro	Arg	Ser	His	Ser	Tyr	Asp	Arg
	50					55					60				
Arg	Arg	Arg	His	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Tyr	Gly	Ser	Arg	Arg
	65				70					75				80	
Lys	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Gly	Arg	Gly	Lys	Ser	Tyr	Arg	Val
			85						90					95	
Gln	Arg	Ser	Arg	Ser	Lys	Ser	Arg	Thr	Arg	Arg	Ser	Arg	Ser	Arg	Pro
			100					105					110		
Arg	Leu	Arg	Ser	His	Ser	Arg	Ser	Glu	Arg	Ser	Ser	His	Arg	Arg	
		115					120				125				
Thr	Arg	Ser	Arg	Ser	Arg	Asp	Arg	Glu	Arg	Arg	Lys	Gly	Arg	Asp	Lys
			130			135					140				
Glu	Lys	Arg	Glu	Lys	Glu	Lys	Asp	Lys	Gly	Lys	Asp	Lys	Glu	Leu	His
				150						155				160	
Asn	Ile	Lys	Arg	Gly	Glu	Ser	Gly	Asn	Ile	Lys	Ala	Gly	Leu	Glu	His
				165				170						175	
Leu	Pro	Pro	Ala	Glu	Gln	Ala	Lys	Ala	Arg	Leu	Gln	Leu	Val	Leu	Glu
			180					185					190		
Ala	Ala	Ala	Lys	Ala	Asp	Glu	Ala	Leu	Lys	Ala	Lys	Glu	Arg	Asn	Glu
			195				200					205			
Glu	Glu	Ala	Lys	Arg	Arg	Lys	Glu	Glu	Asp	Gln	Ala	Thr	Leu	Val	Glu
			210			215					220				
Gln	Val	Lys	Arg	Val	Lys	Glu	Ile	Glu	Ala	Ile	Glu	Ser	Asp	Ser	Phe
				230						235				240	
Val	Gln	Gln	Thr	Phe	Arg	Ser	Ser	Lys	Glu	Val	Lys	Lys	Ser	Val	Glu
				245					250					255	
Pro	Ser	Glu	Val	Lys	Gln	Ala	Thr	Ser	Thr	Ser	Gly	Pro	Ala	Ser	Ala

	260		265		270										
Val	Ala	Asp	Pro	Pro	Ser	Thr	Glu	Lys	Glu	Ile	Asp	Pro	Thr	Ser	Ile
	275		280		285										
Pro	Thr	Ala	Ile	Lys	Tyr	Gln	Asp	Asp	Asn	Ser	Leu	Ala	His	Pro	Asn
	290		295		300										
Leu	Phe	Ile	Glu	Lys	Ala	Asp	Ala	Glu	Glu	Lys	Trp	Phe	Lys	Arg	Leu
	305		310		315										
Ile	Ala	Leu	Arg	Gln	Glu	Arg	Leu	Met	Gly	Ser	Pro	Val	Ala		
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<210> 3061

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 3061

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1140

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<210> 3062

<211> 146

<212> PRT

<213> Homo sapiens

<400> 3062

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Phe	Lys	Met	Leu	Gln	Glu	Asn	Arg	Glu	Gly	Arg	Ala	Ala	Pro	Arg	Gln
			20					25					30		
Ser	Ser	Ser	Phe	Arg	Leu	Leu	Gln	Glu	Ala	Leu	Glu	Ala	Glu	Glu	Arg
			35				40					45			
Gly	Gly	Thr	Pro	Ala	Phe	Leu	Pro	Ser	Ser	Leu	Ser	Pro	Gln	Ser	Ser
	50				55						60				
Leu	Pro	Ala	Ser	Arg	Ala	Leu	Ala	Thr	Pro	Pro	Lys	Leu	His	Thr	Cys
	65				70					75				80	
Glu	Lys	Cys	Ser	Thr	Ser	Ile	Ala	Asn	Gln	Ala	Val	Arg	Ile	Gln	Glu
			85						90					95	
Gly	Arg	Tyr	Arg	His	Pro	Gly	Cys	Tyr	Thr	Cys	Ala	Asp	Cys	Gly	Leu
			100				105						110		
Asn	Leu	Lys	Met	Arg	Gly	His	Phe	Trp	Val	Gly	Asp	Glu	Leu	Tyr	Cys
		115				120						125			
Glu	Lys	His	Ala	Arg	Gln	Arg	Tyr	Ser	Ala	Pro	Ala	Thr	Leu	Ser	Ser
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Arg	Ala														
145															

<210> 3063

<211> 386

<212> DNA

<213> Homo sapiens

<400> 3063

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<210> 3064

<211> 128

<212> PRT

<213> Homo sapiens

<400> 3064

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Tyr	Gln	Cys	Ser	Arg	Pro	Ala	Pro	Leu	His	Ser	Arg	Asp	Leu	His	Ser
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Pro	Asp	Met	Leu	Asp	Glu	Lys	Asp	Tyr	Leu	Lys	Glu	Val	Leu	Glu	Ile
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<210> 3065

<211> 2104

<212> DNA

<213> Homo sapiens

<400> 3065

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tgca
2104

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<211> 183
<212> PRT
<213> Homo sapiens

<400> 3066
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35 40 45
Pro Val Gly Glu Glu Ser Ile Ser Asp Ala Glu Lys Val Ala Met Xaa
50 55 60
Ser Gln Gly Pro Xaa Thr Ala Pro Gly Ser Pro Cys Arg Ser Cys Gly
65 70 75 80
Thr Cys Cys Thr Arg Gly Thr Xaa Leu Lys Ser Lys Val Phe Leu Leu
85 90 95
Gln Glu Glu Leu Ala Tyr Tyr Lys Ser Glu Glu Met Glu Glu Glu Asn
100 105 110
Arg Ile Pro Gln Pro Pro Pro Ile Ala His Pro Arg Thr Ser Pro Gln
115 120 125
Pro Glu Ser Gly Ile Lys Arg Leu Phe Ser Phe Phe Ser Arg Asp Lys
130 135 140
Lys Arg Leu Ala Asn Thr Gln Arg Asn Val His Ile Gln Glu Ser Phe
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Gln Glu Ala Leu Gln His Leu
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<210> 3067
<211> 645
<212> DNA
<213> Homo sapiens

<400> 3067
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<210> 3068

<211> 204

<212> PRT

<213> Homo sapiens

<400> 3068

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			20				25					30		
Ser	Pro	Asn	Arg	Ala	Gln	Gly	Pro	Ser	Xaa	Val	Leu	Val	His	Gln
		35					40				45			
Arg	Glu	Pro	Thr	Ala	Gly	Ser	Pro	Pro	Cys	Ser	Leu	Pro	Arg	Pro
	50				55					60				
Leu	Gln	Pro	Pro	Ser	Thr	Pro	Pro	Pro	Val	His	Lys	Glu	Gln	Lys
	65				70				75				80	
Lys	Ser	Asp	Pro	Pro	Pro	Pro	Pro	Gly	Lys	Phe	Lys	Ser	Phe	Leu
			85					90					95	
Pro	Pro	Arg	Ser	Pro	Gly	Asn	Ser	Ala	Leu	Gly	Pro	Arg	Arg	Gly
			100					105					110	
Gly	Trp	Ile	Ala	Ala	Gly	Gly	Ala	Pro	Ala	Met	Pro	Arg	Pro	Pro
		115				120					125			
Gly	Ala	Gly	Asp	Arg	Glu	Ile	Pro	Arg	Asp	Leu	Ala	Cys	Ala	Pro
	130					135				140				
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			145			150				155				160
Arg	Arg	Cys	Gly	Ser	Lys	Glu	Pro	Glu	Ala	Ala	Ser	Arg	Pro	Pro
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<210> 3069

<211> 1561

<212> DNA

<213> Homo sapiens

<400> 3069

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 180

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<210> 3070

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3070

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Leu Gly Ser Ser Val Leu His Trp Gly Tyr Leu Pro Ser Lys Asp Asp
      35           40           45
Tyr Phe Gln Val Leu Cys Val Ala Asp Val Val Ile Ser Thr Ala Lys
 50           55           60
His Glu Phe Phe Gly Val Ala Met Leu Glu Ala Val Tyr Cys Gly Cys
65           70           75           80
Tyr Pro Leu Cys Pro Lys Asp Leu Val Tyr Pro Glu Ile Phe Pro Ala
      85           90           95
Glu Tyr Leu Tyr Ser Thr Pro Glu Gln Leu Ser Lys Arg Leu Gln Asn
      100          105          110
Phe Cys Lys Arg Pro Asp Ile Ile Arg Lys His Leu Tyr Lys Gly Glu
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<210> 3071

<211> 3343

<212> DNA

<213> Homo sapiens

<400> 3071

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780

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<211> 349

<212> PRT

<213> Homo sapiens

<400> 3072

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Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu Ala Ala			
195	200	205	
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245	250	255	
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260	265	270	
Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly			
275	280	285	
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Pro Asn Leu Leu Ser His Ser Lys Ile His Xaa Ser Asp Pro Arg Gly			
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<210> 3073

<211> 791

<212> DNA

<213> Homo sapiens

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<211> 263

<212> PRT

<213> Homo sapiens

<400> 3074

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 Ala Pro Gly Pro His Leu Pro Pro Arg Gly Ser Val Pro Gly Asp Pro
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 Val Arg Ile His Cys Asn Ile Thr Glu Ser Tyr Pro Ala Val Pro Pro
 65 70 75 80
 Ile Trp Ser Val Glu Ser Asp Asp Pro Asn Leu Ala Ala Val Leu Glu
 85 90 95
 Arg Leu Val Asp Ile Lys Lys Gly Asn Thr Leu Leu Leu Gln His Leu
 100 105 110
 Lys Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr Asn Leu Pro Gln His
 115 120 125
 Pro Asp Val Glu Met Leu Asp Gln Pro Leu Pro Ala Glu Gln Cys Thr
 130 135 140
 Gln Glu Asp Val Ser Ser Glu Asp Glu Asp Glu Glu Met Pro Glu Asp
 145 150 155 160
 Thr Glu Asp Leu Asp His Tyr Glu Met Lys Glu Glu Glu Pro Ala Glu
 165 170 175
 Gly Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys Glu Asn Leu Ala Ile
 180 185 190
 Leu Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp Tyr Leu Asn Gly Ala
 195 200 205
 Val Ser Gly Ser Val Gln Ala Thr Asp Arg Leu Met Lys Glu Leu Gln
 210 215 220
 Gly Tyr Ile Thr Xaa Ser Gln Ser Phe Lys Gly Gly Asn Tyr Xaa Ser
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 Ser Asn Ser Trp Asn Asp Ser Leu Tyr Gly Trp Asp Val Gln Leu Leu
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 Lys Val Asp Gln Gly Ser Val
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<210> 3075

<211> 603

<212> DNA

<213> Homo sapiens

<400> 3075

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<210> 3076

<211> 201

<212> PRT

<213> Homo sapiens

<400> 3076

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Val Gly Pro Gln Lys Lys Lys Lys Lys Lys Lys Val Leu Gly Gly
35     40     45
Gly Arg Phe Gly Gln Val His Arg Cys Thr Glu Lys Ser Thr Gly Leu
50     55     60
Ala Leu Ala Ala Lys Ile Ile Lys Val Lys Asn Val Lys Asp Arg Glu
65     70     75     80
Asp Val Lys Asn Glu Val Asn Ile Met Asn Gln Leu Ser His Val Asn
85     90     95
Leu Ile Gln Leu Tyr Asp Ala Phe Glu Ser Lys Ser Ser Phe Thr Leu
100    105    110
Ile Met Glu Tyr Val Asp Gly Gly Glu Leu Phe Asp Arg Ile Thr Asp
115    120    125
Glu Lys Tyr His Leu Thr Glu Leu Asp Val Val Leu Phe Thr Arg Gln
130    135    140
Ile Cys Glu Gly Val His Tyr Leu His Gln His Tyr Ile Leu His Leu
145    150    155    160
Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Ser Gln Thr Gly His Gln

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Lys Leu Lys Val Asn Phe Gly Thr Pro
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<210> 3077
<211> 1377
<212> DNA
<213> Homo sapiens

<400> 3077
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1260

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<210> 3078

<211> 310

<212> PRT

<213> Homo sapiens

<400> 3078

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 Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu
 35 40 45
 Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly
 50 55 60
 Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser
 65 70 75 80
 Leu Ala Leu Thr Ser Phe Lys Arg Gln Gln Glu Glu Ser Phe Gln Glu
 85 90 95
 Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu
 100 105 110
 Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu
 115 120 125
 Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala
 130 135 140
 Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu
 145 150 155 160
 Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala
 165 170 175
 Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro
 180 185 190
 Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp
 195 200 205
 Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr
 210 215 220
 Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe
 225 230 235 240
 Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala
 245 250 255
 His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln
 260 265 270
 Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu
 275 280 285
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 Gln Trp Ala Ser Leu Gln
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<210> 3079

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 3079

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<210> 3080

<211> 500

<212> PRT

<213> Homo sapiens

<400> 3080

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			20					25					30		
Val	Ser	Gln	Val	Gln	Pro	Pro	Pro	Ser	Lys	Ala	Ser	Ala	Pro	Glu	Pro
		35					40					45			
Pro	Ala	Glu	Glu	Val	Ala	Thr	Gly	Thr	Thr	Ser	Ala	Ser	Asp	Asp	
	50				55				60						
Leu	Glu	Ala	Leu	Gly	Thr	Leu	Ser	Leu	Gly	Thr	Glu	Glu	Lys	Ala	
	65			70					75				80		
Ala	Ala	Glu	Ala	Ala	Val	Pro	Arg	Thr	Ile	Gly	Ala	Glu	Leu	Met	Glu
			85					90					95		
Leu	Val	Arg	Arg	Asn	Thr	Gly	Leu	Ser	His	Glu	Leu	Cys	Arg	Val	Ala
		100						105					110		
Ile	Gly	Ile	Ile	Val	Gly	His	Ile	Gln	Ala	Ser	Val	Pro	Ala	Ser	Ser
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Pro	Val	Met	Glu	Gln	Val	Leu	Ser	Leu	Val	Glu	Gly	Lys	Asp	Leu	
	130				135					140					
Ser	Met	Ala	Leu	Pro	Ser	Gly	Gln	Val	Cys	His	Asp	Gln	Gln	Arg	Leu
	145			150					155					160	
Glu	Val	Ile	Phe	Ala	Asp	Leu	Ala	Arg	Arg	Lys	Asp	Asp	Ala	Gln	Gln
		165						170					175		
Arg	Ser	Trp	Ala	Leu	Tyr	Glu	Asp	Glu	Gly	Val	Ile	Arg	Cys	Tyr	Leu
		180					185						190		
Glu	Glu	Leu	Leu	His	Ile	Leu	Thr	Asp	Ala	Asp	Pro	Glu	Val	Cys	Lys
	195					200					205				
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Cys	Phe	Gly	Ala	Met	Cys	Ser	Leu	Asp	Ala	Ala	Ile	Ile	Ser	Thr	Leu
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Val	Ser	Ser	Val	Leu	Pro	Val	Glu	Leu	Ala	Arg	Asp	Met	Gln	Thr	Asp
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Thr	Gln	Asp	His	Gln	Lys	Leu	Cys	Tyr	Ser	Ala	Leu	Ile	Leu	Ala	Met
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Pro Leu Asp Thr Thr Glu Gln Leu Pro Asp Leu Cys Val Asn Leu Leu
      325              330              335
Leu Ala Leu Asn Leu His Leu Pro Ala Ala Asp Gln Asn Val Ile Met
      340              345              350
Ala Ala Leu Ser Lys His Ala Asn Val Lys Ile Phe Ser Glu Lys Leu
      355              360              365
Leu Leu Leu Leu Asn Arg Gly Asp Asp Pro Val Arg Ile Phe Lys His
      370              375              380
Glu Pro Gln Pro Pro His Ser Val Leu Lys Phe Leu Gln Asp Val Phe
385              390              395              400
Gly Ser Pro Ala Thr Ala Ala Ile Phe Tyr His Thr Asp Met Met Ala
      405              410              415
Leu Ile Asp Ile Thr Val Arg His Ile Ala Asp Leu Ser Pro Gly Asp
      420              425              430
Lys Gly Pro Phe Gly Ala Gly Gln Arg Pro Trp Pro Gly Val Pro Arg
      435              440              445
Leu Leu Glu Pro Gly Ser Thr Pro Ser Arg Glu Pro His Pro Val Glu
      450              455              460
Arg Ser Gly Val Pro Ala Leu Thr Ser Ser Trp Ala Ser Gly Cys Pro
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Arg Pro Leu His Pro Ala Leu Gln Leu Val Ile Asp Ser Ala Phe Gly
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Gly Arg Ser Val
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<210> 3081

<211> 1902

<212> DNA

<213> Homo sapiens

<400> 3081

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<210> 3082

<211> 414

<212> PRT

<213> Homo sapiens

<400> 3082

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Cys	His	Asp	Asp	Ala	Ala	Lys	Phe	Val	His	Leu	Leu	Met	Ser	Pro	Gly				
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Cys	Asn	Tyr	Leu	Val	Gln	Glu	Asp	Phe	Val	Pro	Phe	Leu	Gln	Asp	Val				
65										70					75				
Val	Asn	Thr	His	Pro	Gly	Leu	Ser	Phe	Leu	Lys	Glu	Ala	Ser	Glu	Phe				
85										90					95				
His	Ser	Arg	Tyr	Ile	Thr	Thr	Val	Ile	Gln	Arg	Ile	Phe	Tyr	Ala	Val				
100										105					110				
Asn	Arg	Ser	Trp	Ser	Gly	Arg	Ile	Thr	Cys	Ala	Glu	Leu	Arg	Arg	Ser				
115										120					125				
Ser	Phe	Leu	Gln	Asn	Val	Ala	Leu	Leu	Glu	Glu	Glu	Ala	Asp	Ile	Asn				
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Gln	Leu	Thr	Glu	Phe	Phe	Ser	Tyr	Glu	His	Phe	Tyr	Val	Ile	Tyr	Cys				
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Lys	Phe	Trp	Glu	Leu	Asp	Thr	Asp	His	Asp	Leu	Leu	Ile	Asp	Ala	Asp				
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Asp	Leu	Ala	Arg	His	Asn	Asp	His	Ala	Leu	Ser	Thr	Lys	Met	Ile	Asp				
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Arg	Ile	Phe	Ser	Gly	Ala	Val	Thr	Arg	Gly	Arg	Lys	Val	Gln	Lys	Glu				
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Gly	Lys	Ile	Ser	Tyr	Ala	Asp	Phe	Val	Trp	Phe	Leu	Ile	Ser	Glu	Glu				
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245										250					255				
Glu	Glu	Gln	Cys	Arg	Arg	Leu	Asp	Ser	Met	Ala	Ile	Glu	Ala	Leu	Pro				
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Phe	Gln	Asp	Cys	Leu	Cys	Gln	Met	Leu	Asp	Leu	Val	Lys	Pro	Arg	Thr				
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355										360					365				
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370										375					380				
Ala	Gln	Arg	Pro	Phe	Phe	Glu	Ala	Pro	Ser	Pro	Leu	Gly	Ala	Val	Asp				
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<210> 3083
<211> 610
<212> DNA
<213> Homo sapiens
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 agcaccttcc tgaaggacgc gccagggggag ttccctgctcc gagtcttctc taccggggcg
 420
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 480
 ccaaggcagg atttgggcac ttccctctg tggttgccag gtgccatgt gggaactgag
 540
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 gcagtggcca
 610

<210> 3084
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 3084
 Xaa Arg Pro Ser Cys Trp Glu Pro Val Arg Pro Ser Gly Ser Ser His
 1 5 10 15
 Leu Ser Trp His Arg Gly Pro Pro Cys Glu Val Tyr Ile Ala Val Leu
 20 25 30
 Gln Arg Ser Arg Leu His Ala Ala Asp Trp Ala Gly Arg Ala Arg Ala
 35 40 45
 Leu Val Gly Asp Ser His Thr Ser Trp Ser Pro Ala Ser Ile Pro Gly
 50 55 60
 Lys His Tyr Gln Ala Val Gly Leu His Leu Trp Lys Val Glu Lys Arg
 65 70 75 80
 Arg Val Asn Leu Pro Arg Val Leu Ser Met Pro Pro Val Ala Gly Thr
 85 90 95
 Ala Cys His Ala Tyr Asp Arg Glu Val His Leu Arg Cys Glu Leu Ser
 100 105 110
 Pro Gly Tyr Tyr Leu Ala Val Pro Ser Thr Phe Leu Lys Asp Ala Pro
 115 120 125
 Gly Glu Phe Leu Leu Arg Val Phe Ser Thr Gly Arg Val Ser Leu Arg
 130 135 140

<210> 3085
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 3085
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 120
 caaaagataa gaaaatggaa attaaggga atctgttcag caacaaagat cttgaggaat
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 tatgcagaca tatcaacaac agaaaccaag cagcacagca ttctcagaag cagtctactg
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 360
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 420
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 540
 ccatacaggc ctcacgttgc cattctgata caatcagact tgaataatt agtaacaaac
 600
 catacaagat accaaatata gaacttattc atcagagttc ccccttgctg aagagtggat
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 780
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<210> 3086
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 3086
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 Ala Tyr Met Xaa Asn Val Leu Ser Arg Ala Arg Trp Leu Thr Pro Val
 20 25 30
 Thr Pro Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Arg Gly Gln Glu
 35 40 45
 Ile Glu Thr Ile Leu Ala Asn Thr Val Lys
 50 55

<210> 3087

<211> 2329

<212> DNA

<213> Homo sapiens

<400> 3087

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180
atggagcgca cccatattca gcaactcctg gaacacttcc tccgccagct tcagagaaaa
240
gatccccatg gattttttgc ttttctctgc acggatgcaa ttgctctctg atattcaatg
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ataataaaac atcccatgga ttttggcacc atgaaagaca aaattgtagc taatgaatac
360
aagtcagtta cggaatttaa ggcagatttc aagctgatgt gtgataatgc aatgacatac
420
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480
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1320
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 1620
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 1800
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 1980
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 2160
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 2220
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 2329

<210> 3088

<211> 280

<212> PRT

<213> Homo sapiens

<400> 3088

Xaa Glu Lys His Leu Asp Asp Glu Glu Arg Arg Lys Arg Lys Glu Glu
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 Asp Asp Phe Asp Pro Gly Lys Lys Val Glu Val Glu Pro Pro Pro Asp
 35 40 45
 Arg Pro Val Arg Ala Cys Arg Thr Gln Gln Pro Glu Met Glu Arg Thr
 50 55 60
 His Ile Gln Gln Leu Leu Glu His Phe Leu Arg Gln Leu Gln Arg Lys
 65 70 75 80
 Asp Pro His Gly Phe Phe Ala Phe Pro Val Thr Asp Ala Ile Ala Pro
 85 90 95
 Gly Tyr Ser Met Ile Ile Lys His Pro Met Asp Phe Gly Thr Met Lys
 100 105 110
 Asp Lys Ile Val Ala Asn Glu Tyr Lys Ser Val Thr Glu Phe Lys Ala
 115 120 125
 Asp Phe Lys Leu Met Cys Asp Asn Ala Met Thr Tyr Asn Arg Pro Asp

130	135	140
Thr Val Tyr Tyr Lys	Leu Ala Lys Lys Ile	Leu His Ala Gly Phe Lys
145	150	155
Met Met Ser Lys	Gln Ala Ala Leu Leu Gly Asn	Glu Asp Thr Ala Val
	165	170
Glu Glu Pro Val	Pro Glu Val Val Pro Val Gln Val	Glu Thr Ala Lys
	180	185
Lys Ser Lys Lys	Pro Ser Arg Glu Val Ile Ser Cys Met Phe Glu Pro	
	195	200
Glu Gly Asn Ala Cys	Ser Leu Thr Asp Ser Thr Ala Glu Glu His Val	
	210	215
Leu Ala Leu Val Glu	His Ala Ala Asp Glu Ala Arg Asp Arg Ile Asn	
225	230	235
Arg Phe Leu Pro Gly	Gly Lys Met Gly Tyr Leu Lys Arg Asn Gly Asp	
	245	250
Gly Ser Leu Leu Tyr	Ser Val Val Asn Thr Ala Glu Pro Asn Ala Asp	
	260	265
Glu Glu Glu Thr His	Pro Val Thr	
	275	280

<210> 3089

<211> 722

<212> DNA

<213> Homo sapiens

<400> 3089

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 180
 tgggttaggt ctcaataaaa atcattatgc aacttggaag aaagtatcac gtcgtctggg
 240
 agagatgacc tagagagctt ccagcttgag ataagtggtt ttttaaaaga gatggcctgt
 300
 ccatactcgg tactcgtctc aggagacatt aaagagcgcc tcacaaagaa ggatgactgc
 360
 ttgaaacttc tgttgttttt aagtacagaa cttcaagctt tacaatatatt acagaacaa
 420
 aaacataaaa attctcaatt agataaaaat agtgaagttt atcaggaagt tcaagctatg
 480
 ttgtatacac ttgttatacc caagtcaaca acttctgaca ttcgcgatat gctaaaccaa
 540
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 600
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 720
 ca
 722

<210> 3090

<211> 240

<212> PRT

<213> Homo sapiens

<400> 3090

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Xaa Ala Leu Asp Gln Ala Thr Met Arg Gly Pro Glu Leu Gly Pro Glu
 1      5      10      15
Thr Ser Met Glu Gly Asp Val Leu Asp Thr Leu Glu Ala Leu Gly Tyr
      20      25      30
Lys Gly Pro Leu Leu Glu Glu Gln Ala Leu Thr Lys Ala Ala Glu Gly
      35      40      45
Gly Leu Ser Ser Pro Glu Phe Ser Glu Leu Cys Ile Trp Leu Gly Ser
      50      55      60
Gln Ile Lys Ser Leu Cys Asn Leu Glu Glu Ser Ile Thr Ser Ala Gly
65      70      75      80
Arg Asp Asp Leu Glu Ser Phe Gln Leu Glu Ile Ser Gly Phe Leu Lys
      85      90      95
Glu Met Ala Cys Pro Tyr Ser Val Leu Val Ser Gly Asp Ile Lys Glu
      100      105      110
Arg Leu Thr Lys Lys Asp Asp Cys Leu Lys Leu Leu Phe Leu Ser
      115      120      125
Thr Glu Leu Gln Ala Leu Gln Ile Leu Gln Asn Lys Lys His Lys Asn
      130      135      140
Ser Gln Leu Asp Lys Asn Ser Glu Val Tyr Gln Glu Val Gln Ala Met
145      150      155      160
Phe Asp Thr Leu Gly Ile Pro Lys Ser Thr Thr Ser Asp Ile Pro His
      165      170      175
Met Leu Asn Gln Val Glu Ser Lys Val Lys Asp Ile Leu Ser Lys Val
      180      185      190
Gln Lys Asn His Val Gly Lys Pro Leu Leu Lys Met Asp Leu Asn Ser
      195      200      205
Glu Gln Ala Glu Gln Leu Glu Arg Ile Asn Asp Ala Leu Ser Cys Glu
      210      215      220
Tyr Glu Cys Arg Arg Arg Met Leu Met Lys Arg Leu Asp Val Thr Val
225      230      235      240

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<210> 3091

<211> 333

<212> DNA

<213> Homo sapiens

<400> 3091

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acgcgtgaag gggcgagg ggaaggaagc cctggggagc agctgctcac ccctttgcca
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caccatcttg gcctggcagg ggtctgggac tgacaggagg caccacaggc ccttggtacc
120
ccagggcgca ccccttctgc caagtgtccc aaaatgattg ctaaatgcct ggctccccca
180
ctctttgact ccattctcttg gtccctcttt tctgctgcca gctccccaga ctcttccctg
240
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300
ttccataccc atccctgcct cctgctcg ccg
333

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<210> 3092

<211> 104

<212> PRT

<213> Homo sapiens

<400> 3092

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Met Gly Met Glu Glu Lys Gly Ile Cys Leu Ala Val Gly Ala Gly Glu
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Lys Gly Asp Thr Lys Arg Ser Pro Gln Gly Arg Val Gly Gly Ala Gly
      20             25             30
Ser Arg Lys Arg Glu Pro Arg Asp Gly Val Lys Glu Trp Gly Ser Gln
      35             40             45
Ala Phe Ser Asn His Phe Gly Thr Leu Gly Arg Arg Gly Arg Pro Gly
      50             55             60
Gly Thr Lys Gly Leu Gly Cys Ser Leu Ser Val Pro Asp Pro Cys Gln
      65             70             75             80
Ala Lys Met Val Trp Gln Arg Gly Glu Gln Leu Leu Pro Arg Ala Ser
      85             90             95
Phe Pro Ser Ala Pro Phe Thr Arg
      100

```

<210> 3093

<211> 720

<212> DNA

<213> Homo sapiens

<400> 3093

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nnaccggttt gtccaaggag gctggcctga ccacttacag cctgtccctg gctctggtgt'
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120
aggggggcag ctgtgggcag tgactctgtc tgtctttgga caggacaagg actgccatcc
180
accatggtga agctgggctg cagcttctct gggaagccag gtaaagacc tggggaccag
240
gatggggctg ccatggacag tgtgcctctg atcagcccct tggacatcag ccagctccag
300
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360
gaccagcaga atttccctga cctggagggc cagagggtga actgcagcca cccagaggaa
420
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480
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720

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<210> 3094

<211> 179

<212> PRT

<213> Homo sapiens

<400> 3094

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Met Val Lys Leu Gly Cys Ser Phe Ser Gly Lys Pro Gly Lys Asp Pro
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Gly Asp Gln Asp Gly Ala Ala Met Asp Ser Val Pro Leu Ile Ser Pro
      20          25          30
Leu Asp Ile Ser Gln Leu Gln Pro Leu Pro Asp Gln Val Val Ile
      35          40          45
Lys Thr Gln Thr Glu Tyr Gln Leu Ser Ser Pro Asp Gln Gln Asn Phe
      50          55          60
Pro Asp Leu Glu Gly Gln Arg Leu Asn Cys Ser His Pro Glu Glu Gly
      65          70          75          80
Arg Arg Leu Pro Thr Ala Arg Met Ile Ala Phe Ala Met Ala Leu Leu
      85          90          95
Gly Cys Val Leu Ile Met Tyr Lys Ala Ile Trp Tyr Asp Gln Phe Thr
      100          105          110
Cys Pro Asp Gly Phe Leu Leu Arg His Lys Ile Cys Thr Pro Leu Thr
      115          120          125
Leu Glu Met Tyr Tyr Thr Glu Met Asp Pro Glu Arg His Arg Ser Ile
      130          135          140
Leu Ala Ala Ile Gly Ala Tyr Pro Leu Ser Arg Lys His Gly Thr Glu
      145          150          155          160
Thr Pro Ala Ala Trp Gly Asp Gly Tyr Arg Ala Ala Lys Glu Glu Arg
      165          170          175

Lys Gly Pro

```

<210> 3095

<211> 519

<212> DNA

<213> Homo sapiens

<400> 3095

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120
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180
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360
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420
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519

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<210> 3096
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 3096
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 Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp Glu Val Phe Val Ile
 35 40 45
 Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg Met Leu Ala Ser Leu
 50 55 60
 Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp Ala Val Asp Gly Trp
 65 70 75 80
 Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly Val Asp Leu Leu Pro
 85 90 95
 Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu Thr Lys Gly Glu Val
 100 105 110
 Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu Glu Arg Ala Val Gln
 115 120 125
 Gly Thr Leu Leu Ala Thr Gly Pro Gly Gly Leu Leu Arg Pro Ala Pro
 130 135 140
 Ala Arg Cys Pro Tyr Pro Leu Cys Arg Gly Arg Val Ala Gln
 145 150 155

<210> 3097
 <211> 4953
 <212> DNA
 <213> Homo sapiens

<400> 3097
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 120
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2220

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<212> PRT

<213> Homo sapiens

<400> 3098

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Gln Leu Val Phe Tyr Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile		110
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<212> DNA

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Glu Glu Leu Asn Asp Leu Asp Met Gln Leu Tyr Asp Tyr Ala Lys Asp
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Leu Phe Gln Gln Arg Tyr Gln Tyr Lys Arg Gln Leu Glu Arg Arg Glu
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<212> DNA
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Cys Arg Leu Gln Val Leu Phe Leu Lys Lys Ala Gly Ser Glu Arg Pro
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<212> PRT

<213> Homo sapiens

<400> 3106

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<213> Homo sapiens

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 gtaaagcagg acccttcag acatgttgcc cagcacacag taggccccca ataaaagcca
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 2102

<210> 3108

<211> 517

<212> PRT

<213> Homo sapiens

<400> 3108

Met	Leu	Gln	Glu	Trp	Leu	Ala	Ala	Val	Gly	Asp	Asp	Tyr	Ala	Ala	Val
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Val	Trp	Arg	Pro	Glu	Gly	Glu	Pro	Arg	Phe	Tyr	Pro	Asp	Glu	Glu	Gly
		20						25					30		
Pro	Lys	His	Trp	Thr	Lys	Glu	Arg	His	Gln	Phe	Leu	Met	Glu	Leu	Lys
		35					40					45			
Gln	Glu	Ala	Leu	Thr	Phe	Ala	Arg	Asn	Trp	Gly	Ala	Asp	Tyr	Ile	Leu
	50					55				60					
Phe	Ala	Asp	Thr	Asp	Asn	Ile	Leu	Thr	Asn	Asn	Gln	Thr	Leu	Arg	Leu
	65				70				75					80	
Leu	Met	Gly	Gln	Gly	Leu	Pro	Val	Val	Ala	Pro	Met	Leu	Asp	Ser	Gln
			85					90					95		
Thr	Tyr	Tyr	Ser	Asn	Phe	Trp	Cys	Gly	Ile	Thr	Pro	Gln	Gly	Tyr	Tyr
		100					105						110		
Arg	Arg	Thr	Ala	Glu	Tyr	Phe	Pro	Thr	Lys	Asn	Arg	Gln	Arg	Arg	Gly
		115				120						125			
Cys	Phe	Arg	Val	Pro	Met	Val	His	Ser	Thr	Phe	Leu	Ala	Ser	Leu	Arg
	130				135					140					
Ala	Glu	Gly	Ala	Asp	Gln	Leu	Ala	Phe	Tyr	Pro	Pro	His	Pro	Asn	Tyr
	145				150				155					160	
Thr	Trp	Pro	Phe	Asp	Asp	Ile	Ile	Val	Phe	Ala	Tyr	Ala	Cys	Gln	Ala
			165					170						175	
Ala	Gly	Val	Ser	Val	His	Val	Cys	Asn	Glu	His	Arg	Tyr	Gly	Tyr	Met

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      180              185              190
Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn
195              200              205
Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln
210              215              220
Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly
225              230              235              240
Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg
245              250              255
Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val
260              265              270
Val Asp Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn
275              280              285
Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg
290              295              300
Thr Leu Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile
305              310              315              320
Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu
325              330              335
Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu
340              345              350
Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu
355              360              365
Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu
370              375              380
Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala
385              390              395              400
Leu Arg Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg
405              410              415
Arg Met Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His
420              425              430
Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala
435              440              445
Phe Ser Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp
450              455              460
Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp
465              470              475              480
Ser Gly Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser
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Pro Arg Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln
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<210> 3109

<211> 959

<212> DNA

<213> Homo sapiens

<400> 3109

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120

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cctggaatct ggaaggatct acttcaactcg atccctccac agtcagcagg acaactttat
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 420
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 660
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 780
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<210> 3110

<211> 207

<212> PRT

<213> Homo sapiens

<400> 3110

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Trp	His	Cys	Lys	Ile	Asp	Glu	Gly	Ser	Ala	Gly	Leu	Val	Ala	Ser	Cys
		20						25					30		
Trp	Ser	Pro	Asp	Gly	Arg	His	Ile	Leu	Asn	Thr	Thr	Glu	Phe	His	Leu
		35					40					45			
Arg	Ile	Thr	Val	Trp	Ser	Leu	Cys	Thr	Lys	Ser	Val	Ser	Tyr	Ile	Lys
		50				55					60				
Tyr	Pro	Lys	Ala	Cys	Leu	Gln	Gly	Ile	Thr	Phe	Thr	Arg	Asp	Gly	Arg
				70						75				80	
Tyr	Met	Ala	Leu	Ala	Glu	Arg	Arg	Asp	Cys	Lys	Asp	Tyr	Val	Ser	Ile
			85					90						95	
Phe	Val	Cys	Ser	Asp	Trp	Gln	Leu	Leu	Arg	His	Phe	Asp	Thr	Asp	Thr
			100					105					110		
Gln	Asp	Leu	Thr	Gly	Ile	Glu	Trp	Ala	Pro	Asn	Gly	Cys	Val	Leu	Ala
		115					120					125			
Val	Trp	Asp	Thr	Cys	Leu	Glu	Tyr	Lys	Ile	Leu	Leu	Tyr	Ser	Leu	Asp
		130				135					140				
Gly	Arg	Leu	Leu	Ser	Thr	Tyr	Ser	Ala	Xaa	Arg	Val	Val	Xaa	Leu	Gly

145		150		155		160									
Ile	Lys	Ser	Val	Ala	Trp	Ser	Pro	Ser	Ser	Gln	Phe	Leu	Ala	Val	Gly
			165						170					175	
Ser	Tyr	Asp	Gly	Lys	Val	Arg	Ile	Leu	Asn	His	Val	Thr	Trp	Lys	Met
			180						185					190	
Ile	Thr	Glu	Phe	Gly	His	Pro	Cys	Ser	Pro	Ile	Asn	Asp	Ser	Gln	
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<210> 3111

<211> 1269

<212> DNA

<213> Homo sapiens

<400> 3111

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180
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240
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300
tccatccaga gactgaaacc gtttctatcc ggtcagtggc aaaactgttg aaagggcaat
360
agttgaagct gttgggtttt atatatgtgt aactctgata aatattccta ccaggactaa
420
aacacagcac gctttgcggg catggctgac tcacaaagggt tgtaacaaac aagaactact
480
cttcaactga caccatggct cagaggccac cgagaagcac gagtgcactga cagctcctct
540
gcttacaaac gaatgaaacc caaagtggat gtcgttctca cagcactgaa agtgcttcag
600
gactcacact gatccaatac taactttctt ccctatttta cacatatttt tctactgttc
660
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720
aaatctgtga gaattctgct caatttaata caagatcact actttcttta gaatggtttc
780
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840
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960
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1020
tcttgatgca tacagctgca aggctggccc gtccttggtt gccagtcgct cttttctggg
1080
tgctggactg tgcgcacacc tctgcgctct tcccagtcct tccatggcct cccccggagc
1140
cccgtgtccc tggtccccct tcttccccct gtcttgacca ggctccttcc cccatctctg
1200

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 1269

<210> 3112
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 3112
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 Glu Gly Arg Arg Gly Ala Arg Thr Ala Gly Leu Arg Gly Arg Pro Trp
 35 40 45
 Arg Asp Trp Glu Glu Arg Arg Gly Val Thr Thr Val Gln His Pro Glu
 50 55 60
 Lys Ser Asp Trp Gln Thr Arg Thr Gly Gln Pro Cys Ser Cys Met Ile
 65 70 75 80
 Gln Glu Leu Ala Ser Glu Arg Glu Ser Val Ala Glu Ala Gly Gly Ser
 85 90 95
 Ala Arg Gln Lys Val Arg Gly Leu Val Leu Arg Arg Gly Lys Arg Gln
 100 105 110
 Ser Glu Ser Leu His Ala Pro Gly Leu His Gly Arg Ala Arg Ala Ser
 115 120 125
 Gln Lys Arg Val Asn Asp Pro Glu Cys Asp Trp Glu Gly Glu Leu Ile
 130 135 140
 Pro Tyr Gln Glu Thr Gly Ser
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<210> 3113
 <211> 631
 <212> DNA
 <213> Homo sapiens

<400> 3113
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 120
 ccaaaaggga aggagatagt aagcctgctg gaaagaaaca tcaccgtgac aatgtacatc
 180
 accatcgga cccggaactt gcagaaatat gtgagccgca cttegggtgt gtttgtctcc
 240
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 aggttttcat atgcaaatgc cagggatagg aaccagcgcc gactggggga tgcagcaaa
 360
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 420
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 480

ctgccctgcc ggcattcttt ccacaagtcc tgtgttgacc cctggcttct agaccatcgt
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<210> 3114
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 3114
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 35 40 45
 Leu Leu Glu Arg Asn Ile Thr Val Thr Met Tyr Ile Thr Ile Gly Thr
 50 55 60
 Arg Asn Leu Gln Lys Tyr Val Ser Arg Thr Ser Val Val Phe Val Ser
 65 70 75 80
 Ile Ser Phe Ile Val Leu Met Ile Ile Ser Leu Ala Trp Leu Val Phe
 85 90 95
 Tyr Tyr Ile Gln Arg Phe Arg Tyr Ala Asn Ala Arg Asp Arg Asn Gln
 100 105 110
 Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys Leu Gln Ile
 115 120 125
 Arg Thr Ile Lys Lys Gly Asp Lys Glu Thr Glu Ser Asp Phe Asp Asn
 130 135 140
 Cys Ala Val Cys Ile Glu Gly Tyr Lys Pro Asn Asp Val Val Arg Ile
 145 150 155 160
 Leu Pro Cys Arg His Leu Phe His Lys Ser Cys Val Asp Pro Trp Leu
 165 170 175
 Leu Asp His Arg Thr Cys Pro Met Cys Lys Met Asn Ile Leu Lys Ala
 180 185 190
 Leu Gly Ile Pro Pro Asn Ala Asp Cys Met Asp Asp Phe Ala Thr Asp
 195 200 205
 Phe Glu
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<210> 3115
 <211> 1366
 <212> DNA
 <213> Homo sapiens

<400> 3115
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 120
 gcagaaaaga tggaaaaaag gacatgtgca ctctgcccga aagatgtcga atataatgtc
 180

ctatactttg cacaatcaga gaatatagct gctcatgaga attgtttgct gtattcttca
 240
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 300
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 360
 ggagccaccg tgggatgtga tttaaaaaac tgtaacaaga attaccacct tttctgtgcc
 420
 aagaaggacg acgcagttcc acagtctgat ggagttcgag gaatttataa actgctttgc
 480
 cagcaacatg ctcaattccc gatcatcgct caaagtggta aattttcagg agtgaaaaga
 540
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 600
 tgtaatacat tcataagaca agtgaaagaa gagcatggca gacacacaga tgcaactgtg
 660
 aaagtctcct ttcttaagaa atgcaagnga agcaggactt cttaattact tacttgaaga
 720
 aatattagac aaagttcatt caattccaga aaaactcatg gatgagacta cttcagaatc
 780
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 900
 gaagggaagc attgagctac ttcaggactt aaaacaaacc ttgtgctcct ttcaagaaaa
 960
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 1020
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 1080
 aatccacaca tctttagaac tagtctgtct ctcttggcct cagcagctct tccctgttct
 1140
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 1366

<210> 3116

<211> 191

<212> PRT

<213> Homo sapiens

<400> 3116

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			20					25					30		
Leu	Leu	Tyr	Ser	Ser	Gly	Leu	Val	Glu	Cys	Glu	Asp	Gln	Asp	Pro	Leu
			35				40					45			
Asn	Pro	Asp	Arg	Ser	Phe	Asp	Val	Glu	Ser	Val	Lys	Lys	Glu	Ile	Gln

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Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr				
65	70	75	80	
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys				
85	90	95		
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile				
100	105	110		
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln				
115	120	125		
Ser Gly Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro				
130	135	140		
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr				
145	150	155		
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr				
165	170	175		
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Xaa Ser Arg Thr Ser				
180	185	190		

<210> 3117

<211> 1373

<212> DNA

<213> Homo sapiens

<400> 3117

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480
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600
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660
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720
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840
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900

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<210> 3118

<211> 312

<212> PRT

<213> Homo sapiens

<400> 3118

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			20						25				30		
Ala	Asp	Thr	Val	His	Leu	Ala	Val	Glu	Phe	Phe	Asn	Leu	Thr	His	Leu
			35				40					45			
Pro	Ala	Asn	Leu	Leu	Gln	Gly	Ala	Ser	Lys	Leu	Gln	Glu	Leu	His	Leu
			50			55					60				
Ser	Ser	Asn	Gly	Leu	Glu	Ser	Leu	Ser	Pro	Glu	Phe	Leu	Arg	Pro	Val
					70					75				80	
Pro	Gln	Leu	Arg	Val	Leu	Asp	Leu	Thr	Arg	Asn	Ala	Leu	Thr	Gly	Leu
				85					90					95	
Pro	Pro	Gly	Leu	Phe	Gln	Ala	Ser	Ala	Thr	Leu	Asp	Thr	Leu	Val	Leu
			100						105					110	
Lys	Glu	Asn	Gln	Leu	Glu	Val	Leu	Glu	Val	Ser	Trp	Leu	His	Gly	Leu
			115			120						125			
Lys	Ala	Leu	Gly	His	Leu	Asp	Leu	Ser	Gly	Asn	Arg	Leu	Arg	Lys	Leu
			130			135					140				
Pro	Pro	Gly	Leu	Leu	Ala	Asn	Phe	Thr	Leu	Leu	Arg	Thr	Leu	Asp	Leu
				150					155					160	
Gly	Glu	Asn	Gln	Leu	Glu	Thr	Leu	Pro	Pro	Asp	Leu	Leu	Arg	Gly	Pro
				165					170					175	
Leu	Gln	Leu	Glu	Arg	Leu	His	Leu	Glu	Gly	Asn	Lys	Leu	Gln	Val	Leu
			180					185					190		
Gly	Lys	Asp	Leu	Leu	Leu	Pro	Gln	Pro	Asp	Leu	Arg	Tyr	Leu	Phe	Leu
			195			200						205			
Ser	Gly	Asn	Lys	Leu	Ala	Arg	Val	Ala	Ala	Gly	Ala	Phe	Gln	Gly	Leu
			210			215					220				
Arg	Gln	Leu	Asp	Met	Leu	Asp	Leu	Ser	Asn	Asn	Ser	Leu	Ala	Ser	Val
				225		230				235				240	
Pro	Glu	Gly	Leu	Trp	Ala	Ser	Leu	Gly	Gln	Pro	Asn	Trp	Asp	Met	Arg

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                245                250                255
Asp Gly Phe Asp Ile Ser Gly Asn Pro Trp Ile Cys Asp Gln Asn Leu
                260                265                270
Ser Asp Leu Tyr Arg Trp Leu Gln Ala Gln Lys Asp Lys Met Phe Ser
                275                280                285
Gln Asn Asp Thr Arg Cys Ala Gly Pro Glu Ala Val Lys Gly Gln Thr
                290                295                300
Leu Leu Ala Val Ala Lys Ser Gln
305                310

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<210> 3119
 <211> 427
 <212> DNA
 <213> Homo sapiens

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<400> 3119
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120
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180
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240
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300
tccttcagcac tgctccagc tgccagggtg cctgctgccc ccacccctgt tgcctactat
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420
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427

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<210> 3120
 <211> 142
 <212> PRT
 <213> Homo sapiens

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<400> 3120
Val His Met Val Leu Asn Gln Gln Gly Arg Pro Ser Gly Asp Ala Phe
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Ile Gln Met Thr Ser Ala Glu Arg Ala Leu Ala Ala Ala Gln Arg Cys
20
His Lys Lys Val Met Lys Glu Arg Tyr Val Glu Val Val Pro Cys Ser
35
Thr Glu Glu Met Ser Arg Val Leu Met Gly Gly Thr Leu Gly Arg Ser
50         55         60
Gly Met Ser Pro Pro Pro Cys Lys Leu Pro Cys Leu Ser Pro Pro Thr
65         70         75         80
Tyr Thr Thr Phe Gln Ala Thr Pro Thr Leu Ile Pro Thr Glu Thr Ala
85         90         95
Ala Leu Tyr Pro Ser Ser Ala Leu Leu Pro Ala Ala Arg Val Pro Ala
100        105        110
Ala Pro Thr Pro Val Ala Tyr Tyr Pro Gly Pro Ala Thr Gln Leu Tyr

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      115              120              125
Leu Asn Tyr Thr Ala Tyr Tyr Pro Ser Pro Glu Asp Asn Ala
  130              135              140

<210> 3121
<211> 284
<212> DNA
<213> Homo sapiens

<400> 3121
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120
taagaggaaac atgaacctgg acgggggcagc ttccattgtc cctctcctgc tcctgctaata
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284

<210> 3122
<211> 91
<212> PRT
<213> Homo sapiens

<400> 3122
Met Ala Ala Gly Thr Ser Val Ser His Val Gly Ser Trp Ala Ala Pro
  1      5      10      15
Gly Pro Ser Glu Asp Phe Ser Thr Ser Ala Ala Thr Ser Ala Ala Ser
      20      25      30
Ser His Val Arg Arg Asn Lys Arg Asn Met Asn Leu Asp Gly Ala Ala
      35      40      45
Ser Ile Val Pro Leu Leu Leu Leu Met Asn Lys Ala Ser Pro Glu
      50      55      60
Tyr Glu Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Arg
      65      70      75      80
Gly Arg Phe Ser Leu Phe Trp Trp Thr Val Val
      85      90

<210> 3123
<211> 344
<212> DNA
<213> Homo sapiens

<400> 3123
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120
gcagcccagg tgaccttcag aaagacattg gagaagggaag caaagggaga ggagcccagc
180
atcgcagtc ccaagttcaa acagaggaag ggggagtcg acggggccta tatccaccgc
240

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atgcagcaag aggcccgca tgtgctgttc ctacagcaaga accaggccat ccggcagcca
 300
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 344

<210> 3124
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 3124
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 Lys Lys Ala Ala Gln Val Thr Phe Arg Lys Thr Leu Glu Lys Glu Ala
 20 25 30
 Lys Gly Glu Glu Pro Asp Ile Ala Val Pro Lys Phe Lys Lys Arg Lys
 35 40 45
 Gly Glu Ser Asp Gly Ala Tyr Ile His Arg Met Gln Gln Glu Ala Gln
 50 55 60
 His Val Leu Phe Leu Ser Lys Asn Gln Ala Ile Arg Gln Pro Glu Val
 65 70 75 80
 Gln Ala Ala Pro Lys Glu Lys Ser Glu Gln Lys Lys
 85 90

<210> 3125
 <211> 647
 <212> DNA
 <213> Homo sapiens

<400> 3125
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 ggtcagcagg cagtttagtt gtgggagtat ttccaatttg catgaatgaa acatggacaa
 180
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 240
 aaaactgcag cccatcctgg aattagggaa catcacaaaa cgtactgggg agaactcccc
 300
 atgtggcctc ggcccacgcc agaagccggg caaggtccca agtgccggct cgcccacaa
 360
 ctatggctaa gacagaaaaa caaaggaaaa aaagtctctc ccaaacacac acataagcaa
 420
 aacctatctt cctgtgttct ctgccaagag agctggagca aaagagatga gtttgagact
 480
 ctgattcatc catcaagaca aataaaactca gtctatggag gttagcaggg caatttgtga
 540
 agcaacaaaa agttgagttt tggaaagggg ctctgaagaa aatgaagatg acataccagg
 600
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 647

<210> 3126

<211> 116
 <212> PRT
 <213> Homo sapiens

<400> 3126
 Met Lys Leu Asn Ser Trp Tyr Val Ile Phe Ile Phe Phe Arg Ala Pro
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 Phe Gln Asn Ser Thr Phe Val Cys Phe Thr Asn Cys Pro Ala Asn Leu
 20 25 30
 His Arg Leu Ser Leu Phe Val Leu Met Asp Glu Ser Glu Ser Gln Thr
 35 40 45
 His Leu Phe Cys Ser Ser Ser Leu Gly Arg Glu His Arg Lys Met Gly
 50 55 60
 Phe Ala Tyr Val Cys Val Trp Gly Gly Leu Phe Phe Leu Cys Phe Ser
 65 70 75 80
 Val Leu Ala Ile Ala Cys Gly Arg Ala Gly Thr Trp Asp Leu Ala Arg
 85 90 95
 Leu Leu Ala Trp Ala Glu Ala Thr Trp Gly Val Leu Pro Ser Thr Phe
 100 105 110
 Cys Asp Val Pro
 115

<210> 3127
 <211> 2218
 <212> DNA
 <213> Homo sapiens

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 120
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 180
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 240
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 300
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 360
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 420
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 480
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 660
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 720
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<210> 3128

<211> 565

<212> PRT

<213> Homo sapiens

<400> 3128

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 20 25 30
 Gln Glu Gly Lys Ile Pro Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu
 35 40 45
 Gly Leu Phe Gly Leu Gln Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe
 50 55 60
 Ser Asn Thr Met Tyr Ser Arg Leu Gly Glu Ile Ile Ser Met Asp Gly
 65 70 75 80
 Ser Ile Thr Val Thr Leu Ala Ala His Gln Ala Ile Gly Leu Lys Gly
 85 90 95
 Ile Ile Leu Ala Gly Thr Glu Glu Gln Lys Ala Lys Tyr Leu Pro Lys
 100 105 110
 Leu Ala Ser Gly Glu His Ile Ala Ala Phe Cys Leu Thr Glu Pro Ala
 115 120 125
 Ser Gly Ser Asp Ala Ala Ser Ile Arg Ser Arg Ala Thr Leu Ser Glu
 130 135 140
 Asp Lys Lys His Tyr Ile Leu Asn Gly Ser Lys Val Trp Ile Thr Asn
 145 150 155 160
 Gly Gly Leu Ala Asn Ile Phe Thr Val Phe Ala Lys Thr Glu Val Val
 165 170 175
 Asp Ser Asp Gly Ser Val Lys Asp Lys Ile Thr Ala Phe Ile Val Glu
 180 185 190
 Arg Asp Phe Gly Gly Val Thr Asn Gly Lys Pro Glu Asp Lys Leu Gly
 195 200 205
 Ile Arg Gly Ser Asn Thr Cys Glu Val His Phe Glu Asn Thr Lys Ile
 210 215 220
 Pro Val Glu Asn Ile Leu Gly Glu Val Gly Asp Gly Phe Lys Val Ala
 225 230 235 240
 Met Asn Ile Leu Asn Ser Gly Arg Phe Ser Met Gly Ser Val Val Ala
 245 250 255
 Gly Leu Leu Lys Arg Leu Ile Glu Met Thr Ala Glu Tyr Ala Cys Thr
 260 265 270
 Arg Lys Gln Phe Asn Lys Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu
 275 280 285
 Lys Phe Ala Leu Met Ala Gln Lys Ala Tyr Val Met Glu Ser Met Thr
 290 295 300
 Tyr Leu Thr Ala Gly Met Leu Asp Gln Pro Gly Phe Pro Asp Cys Ser
 305 310 315 320
 Ile Glu Ala Ala Met Val Lys Val Phe Ser Ser Glu Ala Ala Trp Gln
 325 330 335
 Cys Val Ser Glu Ala Leu Gln Ile Leu Gly Gly Leu Gly Tyr Thr Arg
 340 345 350
 Asp Tyr Pro Tyr Glu Arg Ile Leu Arg Asp Thr Arg Ile Leu Leu Ile
 355 360 365
 Phe Glu Gly Thr Asn Glu Ile Leu Arg Met Tyr Ile Ala Leu Thr Gly
 370 375 380
 Leu Gln His Ala Gly Arg Ile Leu Thr Thr Arg Ile His Glu Leu Lys
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[illegible]

<210> 3129

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 3129

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300	gcagtataca	aacttgatat	taaatgacaa	attggaacaa	tctttctcta
360	cttttcatag	aggcatcaca	gtgagtcctt	taaagccttg	atctagggtg
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 1964

<210> 3130

<211> 273

<212> PRT

<213> Homo sapiens

<400> 3130

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			20					25				30			
Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	Val	Pro	Ala
			35					40				45			
Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	Ile	Gly	Phe	Phe
			50				55				60				
Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	His	Ser	Met	Val	Gln

65					70					75				80
Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	Thr	Asp	Ser	Glu	Val
				85						90			95	
Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	Ile	Cys	Leu	Phe	Arg	Leu
			100					105				110		
Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	Asp	Glu	Asp	Ile	Glu	Ser	Ile
		115					120				125			
Ala	Thr	Lys	Leu	Ser	Arg	Phe	Ile	Glu	Ile	Asn	Ser	Leu	His	Met
		130				135					140			
Thr	Glu	Tyr	Asn	Pro	Val	Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val
		145			150					155				160
Gln	Ile	His	Leu	Leu	Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr
			165						170					175
Glu	Asn	Met	His	Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly
		180					185						190	
Ile	Leu	Phe	Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys
	195					200					205			
Ile	Ser	Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala
	210				215					220				
Tyr	Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu
	225			230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
		245						250					255	
Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Lys	Arg	Lys	Thr	Pro	Lys	Val
		260					265					270		
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<210> 3131

<211> 1544

<212> DNA

<213> Homo sapiens

<400> 3131

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<210> 3132

<211> 283

<212> PRT

<213> Homo sapiens

<400> 3132

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Gly	Ser	Thr	Gly	Thr	Ala	Glu	Gly	Gly	Asn	Met	Ser	Arg	Leu	Ser	Leu
			20					25					30		
Thr	Arg	Ser	Pro	Val	Ser	Pro	Leu	Ala	Ala	Gln	Gly	Ile	Pro	Leu	Pro
			35				40				45				
Ala	Gln	Leu	Thr	Lys	Ser	Asn	Ala	Pro	Val	His	Ile	Asp	Val	Gly	Gly
			50			55					60				
His	Met	Tyr	Thr	Ser	Ser	Leu	Ala	Thr	Leu	Thr	Lys	Tyr	Pro	Glu	Ser
			65			70				75				80	
Arg	Ile	Gly	Arg	Leu	Phe	Asp	Gly	Thr	Glu	Pro	Ile	Val	Leu	Asp	Ser
			85					90					95		
Leu	Lys	Gln	His	Tyr	Phe	Ile	Asp	Arg	Asp	Gly	Gln	Met	Phe	Arg	Tyr
			100				105						110		
Ile	Leu	Asn	Phe	Leu	Arg	Thr	Ser	Lys	Leu	Leu	Ile	Pro	Asp	Asp	Phe

115	120	125
Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala Lys Tyr Phe Gln Leu Gln		
130	135	140
Pro Met Leu Leu Glu Met Glu Arg Trp Lys Gln Asp Arg Glu Thr Gly		
145	150	155
Arg Phe Ser Arg Pro Cys Glu Cys Leu Val Val Arg Val Ala Pro Asp		
165	170	175
Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp Lys Ser Leu Ile Glu Glu		
180	185	190
Val Phe Pro Glu Ile Gly Asp Val Met Cys Asn Ser Val Asn Ala Gly		
195	200	205
Trp Asn His Asp Ser Thr His Val Ile Arg Phe Pro Leu Asn Gly Tyr		
210	215	220
Cys His Leu Asn Ser Val Gln Val Leu Glu Arg Leu Gln Gln Arg Gly		
225	230	235
Phe Glu Ile Val Gly Ser Cys Gly Gly Gly Val Asp Ser Ser Gln Phe		
245	250	255
Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg Arg Thr Pro Arg Val Pro		
260	265	270
Ser Val Ile Arg Ile Lys Gln Glu Pro Leu Asp		
275	280	

<210> 3133

<211> 621

<212> DNA

<213> Homo sapiens

<400> 3133

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<212> PRT

<213> Homo sapiens

<400> 3134

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Trp Thr Pro Gln Ser Asn Val Ser Asn Glu Thr Ser Thr Gly Lys Thr
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Phe Gln Arg Thr Ile Ser Ala Gln Asp Ala Leu Ala Tyr Ala Thr Ala
      915              920              925
Leu Leu Asn Glu Lys Glu Gln Ser Gly Ser Ser Asn Gly Ser Glu Ser
      930              935              940
Ser Pro Ala Asn Glu Asn Gly Asp Arg His Leu Gln Gln Gly Ser Glu
      945              950              955              960
Ser Pro Met Met Ile Gly Glu Leu Arg Ser Asp Leu Asp Asp Val Asp
      965              970              975
Pro

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<210> 3139

<211> 503

<212> DNA

<213> Homo sapiens

<400> 3139

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120
acctccccgc tgctatggta cttctactca gccctgcccc gcggcctggg ctgcagcctg
180
ctcttcaccc ccttgggctt ggtagacaga aggacgcacg cggcgacggg gctggcactg
240
ggcttcacgg cactctactc cctcctgccca cacaaggagc tacgcttcat catctatgcc
300
ttccccatgc tcaacatcac ggctgccaga ggctgctcct acctgtgagt gctctttttg
360
tgacatgcac ttttatagtt tcattggaaa cagggttact gatttactgt tgggggggatg
420
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503

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<210> 3140

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3140

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Arg Gln Leu Thr Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val
      20      25      30
Leu Asn Lys Ser Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe
      35      40      45
Tyr Ser Ala Leu Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro
      50      55      60
Leu Gly Leu Val Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu

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65		70		75		80									
Gly	Phe	Met	Ala	Leu	Tyr	Ser	Leu	Leu	Pro	His	Lys	Glu	Leu	Arg	Phe
			85					90					95		
Ile	Ile	Tyr	Ala	Phe	Pro	Met	Leu	Asn	Ile	Thr	Ala	Ala	Arg	Gly	Cys
			100					105					110		
Ser	Tyr	Leu													
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<210> 3141

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 3141

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120
gcattccgct caagaggcga agagagcgcg cgctcccac gtctctgcgt cctgggtgcc
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240
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300
gagttctgga aacagctgtg cgcgagcat ggtatcagcc ccgagggcat cgtggaggag
360
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420
tacatcccc gggcgtgct getggacttg gaacccggg tgatccactc catcctcaac
480
tccccctatg ccaagctcta caaccagag aacatctacc tgctggaaca tggaggagga
540
gctggcaaca actggggccag cggattctcc cagggtgaga aaattcatga ggacattttt
600
gacatcatag accgggaggc agatggtagt gacagtctag agggcctttg gctgtgtcac
660
tccattgctg gggggacagg ctctggactg ggctcctacc tcttagaacg gctgaatgac
720
aggtatccta agaagctggt gcagacatac tcagtgtttc ccaaccagga cgagatgagc
780
gatgtgtgtg tccagcctta caattcactc ctacactca agaggctgac gcagaatgca
840
gactgtgttg tgggtctgga caacacagcc ctgaaccgga ttgccacaga ccgctgcac
900
atccagaacc catccttctc ccagatcaac cagctggtgt ctaccatcat gtcagccagc
960
accaccacc tgcgctacc tggtacatg aacaatgacc tcactcgccct catcgctctg
1020
ctcattccca cccacggct ccaattcctc atgaccggct acaccccgct cactacagac
1080
cagtcagtgg ccagcgtgag gaagaccacg gtcttgatg tcatgaggcg gctgtgcag
1140
cccaagaacg tgatggtgtc cacaggcga gaccgccaga ccaaccactg ctacatcgcc
1200

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 1260
 atccgggaac gcaagttggc caacttcacg ccgtggggcc ccgccagcat ccaggtggcc
 1320
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 1380
 aaccacacca gcattctctc gctcttcgag agaacctgtc gccagtatga caagctgcgt
 1440
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 1500
 gagatggaca catccaggga gattgtgcag cagctcatcg atgagtacca tgcggccaca
 1560
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 1620
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 1680
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 1800
 aaaaaaaaaa aaaaa
 1815

<210> 3142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 3142

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 1 5 10 15
 Ile Gly Phe Glu Phe Trp Lys Gln Leu Cys Ala Glu His Gly Ile Ser
 20 25 30
 Pro Glu Gly Ile Val Glu Glu Phe Ala Thr Glu Gly Thr Asp Arg Lys
 35 40 45
 Asp Val Phe Phe Tyr Gln Ala Asp Asp Glu His Tyr Ile Pro Arg Ala
 50 55 60
 Val Leu Leu Asp Leu Glu Pro Arg Val Ile His Ser Ile Leu Asn Ser
 65 70 75 80
 Pro Tyr Ala Lys Leu Tyr Asn Pro Glu Asn Ile Tyr Leu Ser Glu His
 85 90 95
 Gly Gly Gly Ala Gly Asn Asn Trp Ala Ser Gly Phe Ser Gln Gly Glu
 100 105 110
 Lys Ile His Glu Asp Ile Phe Asp Ile Ile Asp Arg Glu Ala Asp Gly
 115 120 125
 Ser Asp Ser Leu Glu Gly Phe Val Leu Cys His Ser Ile Ala Gly Gly
 130 135 140
 Thr Gly Ser Gly Leu Gly Ser Tyr Leu Leu Glu Arg Leu Asn Asp Arg
 145 150 155 160
 Tyr Pro Lys Lys Leu Val Gln Thr Tyr Ser Val Phe Pro Asn Gln Asp
 165 170 175
 Glu Met Ser Asp Val Val Val Gln Pro Tyr Asn Ser Leu Leu Thr Leu
 180 185 190
 Lys Arg Leu Thr Gln Asn Ala Asp Cys Val Val Val Leu Asp Asn Thr


```

      195              200              205
Ala Leu Asn Arg Ile Ala Thr Asp Arg Leu His Ile Gln Asn Pro Ser
  210              215              220
Phe Ser Gln Ile Asn Gln Leu Val Ser Thr Ile Met Ser Ala Ser Thr
  225              230              235              240
Thr Thr Leu Arg Tyr Pro Gly Tyr Met Asn Asn Asp Leu Ile Gly Leu
      245              250              255
Ile Ala Ser Leu Ile Pro Thr Pro Arg Leu His Phe Leu Met Thr Gly
      260              265              270
Tyr Thr Pro Leu Thr Thr Asp Gln Ser Val Ala Ser Val Arg Lys Thr
      275              280              285
Thr Val Leu Asp Val Met Arg Arg Leu Leu Gln Pro Lys Asn Val Met
      290              295              300
Val Ser Thr Gly Arg Asp Arg Gln Thr Asn His Cys Tyr Ile Ala Ile
  305              310              315              320
Leu Asn Ile Ile Gln Gly Glu Val Asp Pro Thr Gln Val His Lys Ser
      325              330              335
Leu Gln Arg Ile Arg Glu Arg Lys Leu Ala Asn Phe Ile Pro Trp Gly
      340              345              350
Pro Ala Ser Ile Gln Val Ala Leu Ser Arg Lys Ser Pro Tyr Leu Pro
      355              360              365
Ser Ala His Arg Val Ser Gly Leu Met Met Ala Asn His Thr Ser Ile
      370              375              380
Ser Ser Leu Phe Glu Arg Thr Cys Arg Gln Tyr Asp Lys Leu Arg Lys
  385              390              395              400
Arg Glu Ala Phe Leu Glu Gln Phe Arg Lys Glu Asp Met Phe Lys Asp
      405              410              415
Asn Phe Asp Glu Met Asp Thr Ser Arg Glu Ile Val Gln Gln Leu Ile
      420              425              430
Asp Glu Tyr His Ala Ala Thr Arg Pro Asp Tyr Ile Ser Trp Gly Thr
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Gln Glu Gln
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<210> 3143

<211> 356

<212> DNA

<213> Homo sapiens

<400> 3143

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  120
caggcctgag ctccctggctg gtgggaaggg gaggctgctg gtccacagtg tgggggtgct
  180
tcacgggttaa ccaagccatc ccccatgctg ggcgtgaggc actagcggaa ttgagagcct
  240
cagaaaccca ggtgctgctg tgtgaggctg tcgcagccac gaagatgacc atgactgcaa
  300
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  356

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<210> 3144

<211> 81
 <212> PRT
 <213> Homo sapiens

<400> 3144
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 20 25 30
 Ala Trp Leu Thr Val Lys His Pro His Thr Val Asp Gln Gln Pro Pro
 35 40 45
 Leu Pro Thr Ser Gln Glu Leu Arg Pro Ala Ala Gln Pro Lys Gln Gln
 50 55 60
 Pro His His Ser Gln Thr Pro Pro Gln Arg Val Cys Leu Arg Ala Pro
 65 70 75 80
 Ser

<210> 3145
 <211> 436
 <212> DNA
 <213> Homo sapiens

<400> 3145
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 120
 ctccgaggag cccgctccac ctgccctcag gaggggtgtt aaaacggagg ttgcacccgt
 180
 ttacgcacct gccctcagt ccagggcccc cgagcctggt ttgtcagact ctgcagccgc
 240
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 300
 gctccaggog ccctcgga aa ctgccctggc ctgctcacc ccgatgcagt gcctgtcccc
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 cgaatgtagt gaggacccgt cgcagactca cccccgccg gggctgggga accagctaag
 420
 tcccacagcg gttgct
 436

<210> 3146
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 3146
 Met Glu Lys Leu Arg Ser Lys Thr Pro Leu Gly Leu His Pro Lys Ser
 1 5 10 15
 Pro Ile Thr Ser Cys Ser Gly Gly Pro Ser Arg Thr Gly Gly Gly Gln
 20 25 30
 Thr Pro Arg Ser Pro Leu His Leu Pro Ser Gly Gly Cys Leu Lys Arg
 35 40 45
 Arg Leu Pro Pro Phe Thr His Leu Pro Ser Val Pro Gly Pro Pro Ser

50		55		60
Leu Val Cys Gln Thr Leu Gln Pro Pro Ala Ser Gly His Ser Ala Arg				
65	70	75	80	
Gln Met Thr Ser Gly Gly Glu Pro His Ile Ser Thr Gly Ser Arg Arg				
85	90	95		
Pro Arg Lys Leu Pro Trp Pro Ala His Pro Arg Cys Ser Ala Cys Pro				
100	105	110		
Pro Asn Val Val Ser Ser Arg Arg Arg Leu Thr Pro Arg Arg Gly Trp				
115	120	125		
Gly Thr Ser				
130				

<210> 3147

<211> 3106

<212> DNA

<213> Homo sapiens

<400> 3147

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 120
 gcgagcgcg aggtgtcggg gccacacctc agctgggagg agattcagaa gcataacctg
 180
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 240
 cagcaccggg ggggccagcg ggtcatcggg cactacgctg gagaagatgc aacggatgcc
 300
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 360
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 aagtggaaac acctgtgcca caaattcgtc attggccact taaaggggtc ctctgccaac
 720
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 780
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 840
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 900
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 960
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 1020
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 1080

cactgggtttg tgtgggtcac acagatgaat cacatcgtca tggagattga ccaggaggcc
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 3000
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 3106

<210> 3148

<211> 444

<212> PRT

<213> Homo sapiens

<400> 3148

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Ser	Val	Pro	Thr	Phe	Ser	Trp	Glu	Glu	Ile	Gln	Lys	His	Asn	Leu	Arg
			20					25					30		
Thr	Asp	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	Ile	Thr	Lys
			35					40				45			
Trp	Ser	Ile	Gln	His	Pro	Gly	Gln	Arg	Val	Ile	Gly	His	Tyr	Ala	
	50					55				60					
Gly	Glu	Asp	Ala	Thr	Asp	Ala	Phe	Arg	Ala	Phe	His	Pro	Asp	Leu	Glu
	65				70				75					80	
Phe	Val	Gly	Lys	Phe	Leu	Lys	Pro	Leu	Leu	Ile	Gly	Glu	Leu	Ala	Pro
			85						90				95		
Glu	Glu	Pro	Ser	Gln	Asp	His	Gly	Lys	Asn	Ser	Lys	Ile	Thr	Glu	Asp
		100						105					110		
Phe	Arg	Ala	Leu	Arg	Lys	Thr	Ala	Glu	Asp	Met	Asn	Leu	Phe	Lys	Thr
		115					120					125			
Asn	His	Val	Phe	Phe	Leu	Leu	Leu	Ala	His	Ile	Ile	Ala	Leu	Glu	
	130					135				140					
Ser	Ile	Ala	Trp	Phe	Thr	Val	Phe	Tyr	Phe	Gly	Asn	Gly	Trp	Ile	Pro
	145				150				155					160	
Thr	Leu	Ile	Thr	Ala	Phe	Val	Leu	Ala	Thr	Ser	Gln	Ala	Gln	Ala	Gly
			165						170					175	
Trp	Leu	Gln	His	Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	Arg	Lys	Pro	Lys
		180					185						190		
Trp	Asn	His	Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	Leu	Lys	Gly	Ala
		195					200					205			
Ser	Ala	Gln	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	His	Ala	Lys	Pro
	210					215				220					
Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His	Val	Phe	Val
	225				230					235				240	
Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	Lys	Leu	Lys	Tyr
			245					250					255		
Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	Pro	Pro

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                260                265                270
Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met Thr Met Ile
275                280                285
Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile
290                295                300
Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu
305                310                315                320
Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp
325                330                335
Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr
340                345                350
Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
355                360                365
Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
370                375                380
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala
385                390                395                400
Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu
405                410                415
Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys
420                425                430
Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys
435                440

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<210> 3149

<211> 1006

<212> DNA

<213> Homo sapiens

<400> 3149

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120
gtgtgccact ccgcgtctga ggaggtgcgg gagctcgagg gcaagaccgg cttctcatcg
180
gatcagatcg agcagctcca tcggagattt aagcagctga gtggagatca gcctaccatt
240
cgcaaggaga acttcaacaa tgtcccggac ctggagctca accccatccg atccaaaatt
300
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360
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420
gacgaggaac aggtggagct gtcccgaag gagaagctga gatttctgtt ccacatgtac
480
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600
ccatgatgga ggcggccagc gtgtgcatgg ggcagatgga gctgatcag gtgtacaggg
660
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720

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 840
 ggcggagacg ctcttctctgc agcgccggta catagccaag gctcgtctgc gcaccttgtg
 900
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 1006

<210> 3150
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 3150
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 Ala Pro Ala Ala Gly Thr Met Gly Ala Ala His Ser Ala Ser Glu Glu
 35 40 45
 Val Arg Glu Leu Glu Gly Lys Thr Gly Phe Ser Ser Asp Gln Ile Glu
 50 55 60
 Gln Leu His Arg Arg Phe Lys Gln Leu Ser Gly Asp Gln Pro Thr Ile
 65 70 75 80
 Arg Lys Glu Asn Phe Asn Asn Val Pro Asp Leu Glu Leu Asn Pro Ile
 85 90 95
 Arg Ser Lys Ile Val Arg Ala Phe Phe Asp Asn Arg Asn Leu Arg Lys
 100 105 110
 Gly Pro Ser Gly Leu Ala Asp Glu Ile Asn Phe Glu Asp Phe Leu Thr
 115 120 125
 Ile Met Ser Tyr Phe Arg Pro Ile Asp Thr Thr Met Asp Glu Glu Gln
 130 135 140
 Val Glu Leu Ser Arg Lys Glu Lys Leu Arg Phe Leu Phe His Met Tyr
 145 150 155 160
 Asp Ser Asp Ser Asp Gly Arg Ile Thr Leu Glu Glu Tyr Arg Asn Val
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 Lys Trp Ser Arg Ser Cys Cys Arg Glu Thr Leu Thr Ser Arg Arg Ser
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 Pro Leu Ala Pro Ser Pro Thr Gly Pro
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<210> 3151
 <211> 2079
 <212> DNA
 <213> Homo sapiens

<400> 3151
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240
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300
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360
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480
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1740

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 1920
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 1980
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 2040
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 2079

<210> 3152

<211> 214

<212> PRT

<213> Homo sapiens

<400> 3152

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 1 5 10 15
 Phe Lys Gln Cys Leu Asp Glu Lys Glu Glu Val Leu Leu Asp Pro Tyr
 20 25 30
 Ile Ala Ser Trp Lys Gly Leu Val Arg Phe Leu Asn Ser Leu Gly Thr
 35 40 45
 Ile Phe Ser Phe Ile Ser Lys Asp Val Val Ser Lys Leu Arg Ile Met
 50 55 60
 Glu Arg Leu Arg Gly Gly Pro Gln Ser Glu His Tyr Arg Ser Leu Gln
 65 70 75 80
 Ala Met Val Ala His Glu Leu Ser Asn Arg Leu Val Asp Leu Glu Gly
 85 90 95
 Arg Ser His His Pro Glu Ser Gly Cys Arg Thr Val Leu Arg Leu His
 100 105 110
 Arg Ala Leu His Trp Leu Gln Leu Phe Leu Glu Gly Leu Arg Thr Ser
 115 120 125
 Pro Glu Asp Ala Arg Thr Ser Ala Leu Cys Ala Asp Ser Tyr Asn Ala
 130 135 140
 Ser Leu Ala Ala Tyr His Pro Trp Val Val Arg Arg Ala Val Thr Val
 145 150 155 160
 Ala Phe Cys Thr Leu Pro Thr Arg Glu Val Phe Leu Glu Ala Met Asn
 165 170 175
 Val Gly Pro Pro Glu Gln Ala Val Gln Met Leu Gly Glu Ala Leu Pro
 180 185 190
 Phe Ile Gln Arg Val Tyr Asn Val Ser Gln Lys Leu Tyr Ala Glu His
 195 200 205
 Ser Leu Leu Asp Leu Pro
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<210> 3153

<211> 1498

<212> DNA

<213> Homo sapiens

<400> 3153

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ccactcagc aaccaacaag gaggaagacc cccgcagtgc tcggccagtg ccgcgccatc
180
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240
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300
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720
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<210> 3154

<211> 65

<212> PRT

<213> Homo sapiens

<400> 3154

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Thr Asp Thr Ala Pro Trp Ala Ala Leu Pro Val Gly His Leu Ser Leu
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Cys Pro Gly Ala Gly Ile Ala Ser Arg Arg Pro Arg Gln Gln Gly Asp
           20           25           30
Ser Gly His Arg Trp Gly Ile Thr Leu Pro Thr Arg Asp Ser Arg His
           35           40           45
Gly Leu Leu Gly Leu Gln Ala Pro Trp Gly Ser Arg Gly Lys Pro Gln
 50           55           60
Gly
65

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<210> 3155

<211> 551

<212> DNA

<213> Homo sapiens

<400> 3155

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120
actaactgtg actcttcttc agaaggactg gaaaaggaca cagcaacaca gagaagtgc
180
cagacttgcc tagaaccatc atgttcatgt tcttctgaaa atcaggaatg ccagactgct
240
gccagccctg gggaaattct ggaattttg aagaaaggga aggcatttgt tttagatatt
300
gacttggatt ttttttcagt caagaatccc ttcaaaaaa tggtcactca ggaagagtac
360
aaaatcttac aagagctgta ccaatttaag aaacctggca ccaacctaac agaggaagat
420
ttggtagata ttgttgatac tcgaattcat caattagagg atttagaagc cactttcgct
480
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<210> 3156

<211> 178

<212> PRT

<213> Homo sapiens

<400> 3156

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Met Val Lys Pro Tyr Lys Leu Cys Asn Asn Gln Glu Glu Asn Asp Ala
 1           5           10           15
Val Ser Ser Ala Lys Lys Pro Lys Leu Ala Leu Glu Asp Ser Glu Asn
           20           25           30
Thr Ala Ser Thr Asn Cys Asp Ser Ser Ser Glu Gly Leu Glu Lys Asp
           35           40           45
Thr Ala Thr Gln Arg Ser Asp Gln Thr Cys Leu Glu Pro Ser Cys Ser

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50	55	60
Cys Ser Ser Glu Asn Gln Glu Cys Gln Thr Ala Ala Ser Pro Gly Glu		
65	70	75
Ile Leu Glu Ile Leu Lys Lys Gly Lys Ala Phe Val Leu Asp Ile Asp		80
	85	90
Leu Asp Phe Phe Ser Val Lys Asn Pro Phe Lys Lys Met Phe Thr Gln		95
	100	105
Glu Glu Tyr Lys Ile Leu Gln Glu Leu Tyr Gln Phe Lys Lys Pro Gly		110
	115	120
Thr Asn Leu Thr Glu Glu Asp Leu Val Asp Ile Val Asp Thr Arg Ile		125
	130	135
His Gln Leu Glu Asp Leu Glu Ala Thr Phe Ala Asp Leu Cys Asp Gly		140
	145	150
Asp Asp Glu Glu Thr Val Gln Gly Trp Ala Ser Asn Pro Gly Met Glu		155
	160	165
	170	175
Ser Leu		

<210> 3157

<211> 903

<212> DNA

<213> Homo sapiens

<400> 3157

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120
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240
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300
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420
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480
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780
cgctggcgct cccccagggg ccggagccgg ggcgcgcccc gcactggggg cggggtgtgt
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cac
903

<210> 3158
<211> 92
<212> PRT
<213> Homo sapiens

<400> 3158
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Val Leu Ser Glu Lys Met Glu Pro Ser Ser Phe Gln Pro Leu Pro Glu
20 25 30
Thr Glu Pro Pro Thr Pro Glu Pro Gly Pro Lys Thr Pro Pro Arg Thr
35 40 45
Met Gln Glu Ser Pro Leu Gly Leu Gln Val Lys Glu Glu Ser Glu Val
50 55 60
Thr Glu Asp Ser Asp Phe Leu Glu Ser Gly Pro Leu Ala Ala Thr Gln
65 70 75 80
Glu Ser Val Pro Thr Leu Leu Pro Glu Glu Ala Gln
85 90

<210> 3159
<211> 2408
<212> DNA
<213> Homo sapiens

<400> 3159
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240
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780

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2160
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2220
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2280
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2340
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2400

tgccatta
2408

<210> 3160
<211> 431
<212> PRT
<213> Homo sapiens

<400> 3160

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          20          25          30
Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu Trp Trp Ile
          35          40          45
Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn Asp Met Gln Ser
          50          55          60
Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln Val Tyr Pro Thr Ala
65          70          75          80
Ser Asn Met Glu Tyr Met Thr Trp Asp Val Glu Leu Glu Arg Ser Ala
          85          90          95
Glu Ser Trp Ala Glu Ser Cys Leu Trp Glu His Gly Pro Ala Ser Leu
          100          105          110
Leu Pro Ser Ile Gly Gln Asn Leu Gly Ala His Trp Gly Arg Tyr Arg
          115          120          125
Pro Pro Thr Phe His Val Gln Ser Trp Tyr Asp Glu Val Lys Asp Phe
          130          135          140
Ser Tyr Pro Tyr Glu His Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys
145          150          155          160
Ser Gly Pro Val Cys Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser
          165          170          175
Asn Arg Ile Gly Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp
          180          185          190
Gly Gln Ile Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro
          195          200          205
Lys Gly Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys
210          215          220
Ser Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys
225          230          235          240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu Thr
          245          250          255
Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His Val Arg
          260          265          270
Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser Ala Gln Gln
          275          280          285
Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg Asp Gln Cys Lys
          290          295          300
Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala Gly Cys Leu Asp Ser
305          310          315          320
Lys Ala Lys Val Ile Gly Ser Val His Tyr Glu Met Gln Ser Ser Ile
          325          330          335
Cys Arg Ala Ala Ile His Tyr Gly Ile Ile Asp Asn Asp Gly Gly Trp
          340          345          350
Val Asp Ile Thr Arg Gln Gly Arg Lys His Tyr Phe Ile Lys Ser Asn

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          355              360              365
Arg Asn Gly Ile Gln Thr Ile Gly Lys Tyr Gln Ser Ala Asn Ser Phe
   370              375              380
Thr Val Ser Lys Val Thr Val Gln Ala Val Thr Cys Glu Thr Thr Val
   385              390              395              400
Asp Ser Ser Val His Phe Ile Ser Leu Leu His Ile Ala Gln Glu Tyr
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Thr Val Leu Val Thr Val Cys Lys Gln Ile His Ile Met Leu Val
          420              425              430

<210> 3161
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 3161
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240
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420
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1080
gggtaccagg tgtccaatca gtgtatggca ctggtccgtg atgagtgttt gctgccatgc
1140

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1197

<210> 3162

<211> 386

<212> PRT

<213> Homo sapiens

<400> 3162

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			20					25					30		
Ile	Thr	Ala	Ser	Ser	Asn	Lys	Ser	Leu	Asn	Leu	Leu	Lys	Ile	Lys	His
		35				40					45				
Gly	Asp	Leu	Leu	Phe	Leu	Phe	Pro	Ser	Ser	Leu	Ala	Gly	Pro	Ser	Ser
	50					55					60				
Glu	Met	Glu	Thr	Ser	Val	Pro	Pro	Gly	Phe	Lys	Val	Phe	Gly	Ala	Pro
65					70					75				80	
Asn	Val	Val	Glu	Asp	Glu	Ile	Asp	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Gly
				85					90					95	
Lys	Ile	Tyr	Arg	Ser	Arg	Asp	Pro	Gln	Leu	Cys	Arg	His	Gly	Pro	Leu
			100				105						110		
Gly	Lys	Cys	Val	His	Cys	Val	Pro	Leu	Glu	Pro	Phe	Asp	Glu	Asp	Tyr
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Leu	Asn	His	Leu	Glu	Pro	Pro	Val	Lys	His	Met	Ser	Phe	His	Ala	Tyr
	130					135					140				
Ile	Arg	Lys	Leu	Thr	Gly	Gly	Ala	Asp	Lys	Gly	Lys	Phe	Val	Ala	Leu
145					150					155				160	
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			165						170					175	
Trp	Pro	Asn	Gly	Ile	Cys	Thr	Lys	Cys	Gln	Pro	Ser	Ala	Ile	Thr	Leu
			180						185				190		
Asn	Arg	Gln	Lys	Tyr	Arg	His	Val	Asp	Asn	Ile	Met	Phe	Glu	Asn	His
		195				200						205			
Thr	Val	Ala	Asp	Arg	Phe	Leu	Asp	Phe	Trp	Arg	Lys	Thr	Gly	Asn	Gln
	210					215						220			
His	Phe	Gly	Tyr	Leu	Tyr	Gly	Arg	Tyr	Thr	Glu	His	Lys	Asp	Ile	Pro
225				230						235				240	
Leu	Gly	Ile	Arg	Ala	Glu	Val	Ala	Ala	Ile	Tyr	Glu	Pro	Pro	Gln	Ile
			245						250					255	
Gly	Thr	Gln	Asn	Ser	Leu	Glu	Leu	Leu	Glu	Asp	Pro	Lys	Ala	Glu	Val
		260					265						270		
Val	Asp	Glu	Ile	Ala	Ala	Lys	Leu	Gly	Leu	Arg	Lys	Val	Gly	Trp	Ile
	275					280						285			
Phe	Thr	Asp	Leu	Val	Ser	Glu	Asp	Thr	Arg	Lys	Gly	Thr	Val	Arg	Tyr
	290					295					300				
Ser	Arg	Asn	Lys	Asp	Thr	Tyr	Phe	Leu	Ser	Ser	Glu	Glu	Cys	Ile	Thr
305					310					315				320	
Ala	Gly	Asp	Phe	Gln	Asn	Lys	His	Pro	Asn	Met	Cys	Arg	Leu	Ser	Pro
			325						330					335	
Asp	Gly	His	Phe	Gly	Ser	Lys	Phe	Val	Thr	Ala	Val	Ala	Thr	Gly	Gly
		340					345						350		
Pro	Asp	Asn	Gln	Val	His	Phe	Glu	Gly	Tyr	Gln	Val	Ser	Asn	Gln	Cys

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          355                      360                      365
Met Ala Leu Val Arg Asp Glu Cys Leu Leu Pro Cys Lys Asp Ala Pro
      370                      375                      380
Val Cys
385

<210> 3163
<211> 1075
<212> DNA
<213> Homo sapiens

<400> 3163
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120
tgggggctac cagtggaccc actgactcct ggacatcagg atgtctctgcc atggcaaaag
180
tggttatcatc catgttcttc gtcttcagtt cctcctcggc aggcctcgcg ctcaccggct
240
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300
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360
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480
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540
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600
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660
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720
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780
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840
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960
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<210> 3164
<211> 94
<212> PRT
<213> Homo sapiens

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<400> 3164

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His Gln Asp Ala Leu Pro Trp Gln Arg Cys Tyr His Pro Cys Ser Ser
      20           25           30
Ser Ser Val Pro Pro Arg Gln Ala Cys Ala Ser Pro Ala Ser Cys Ser
      35           40           45
Ser Ser Ala Ala Xaa Ala Ser Ala Ser Thr Gly Pro Trp His Ser Gly
      50           55           60
Cys Gly Ser Ser Cys Gly Ser Cys Cys Cys Trp Gly Ser Pro Ser Ala
65           70           75           80
Ser Val Gly Val Gly Ala Gly Ala Ile Arg Ser Arg Thr Val
      85           90

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<210> 3165

<211> 2413

<212> DNA

<213> Homo sapiens

<400> 3165

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120
ggaaagtgcg ttaaagggaa agggtcgttg ccactctcgg cccacggcat cgtggtcgcc
180
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240
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300
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360
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420
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480
gtaaatattc cggattggat tgttgacctt cgccatgagt tgaccacaa gaaaatgccc
540
catataaatg actgccgag aggctgctac ttgtctctgg attggctcca gaagacctat
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660
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720
cagaaaccag agcctcagga tgatgggaaa agtacggagt cagatgtaaa ggccgatgga
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900
gagaaattta ggtatttacc taaggccatt aaggcgtgga ataaccgctc cccacgtgta
960
gaatgtgtcc tggcagagct caagggcggt acatgcgaga acagggaggc tgtgctggat
1020

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gcttttctgg atgatggctt ccttgctccc acatttgaac agttggcagc tttgcagata
 1080
 gaatatgaag aaaacgtgga ctggaatgac gtectggtgc caaagccgtt ctctcagttc
 1140
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 1200
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<210> 3166

<211> 717

<212> PRT

<213> Homo sapiens

<400> 3166

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 20           25           30
Ser Leu Pro Leu Ser Ala His Gly Ile Val Val Ala Trp Leu Ser Arg
 35           40           45
Ala Glu Trp Asp Gln Val Thr Val Tyr Leu Phe Cys Asp Asp His Lys
 50           55           60
Leu Gln Arg Tyr Ala Leu Asn Arg Ile Thr Val Trp Arg Ser Arg Ser
 65           70           75           80
Gly Asn Glu Leu Pro Leu Ala Val Ala Ser Thr Ala Asp Leu Ile Arg
 85           90           95
Cys Lys Leu Leu Asp Val Thr Gly Gly Leu Gly Thr Asp Glu Leu Arg
 100          105          110
Leu Leu Tyr Gly Met Ala Leu Val Arg Phe Val Asn Leu Ile Ser Glu
 115          120          125
Arg Lys Thr Lys Phe Ala Lys Val Pro Leu Lys Cys Leu Ala Gln Glu
 130          135          140
Val Asn Ile Pro Asp Trp Ile Val Asp Leu Arg His Glu Leu Thr His
 145          150          155          160
Lys Lys Met Pro His Ile Asn Asp Cys Arg Arg Gly Cys Tyr Phe Val
 165          170          175
Leu Asp Trp Leu Gln Lys Thr Tyr Trp Cys Arg Gln Leu Glu Asn Ser
 180          185          190
Leu Arg Glu Thr Trp Glu Leu Glu Phe Arg Glu Gly Ile Glu Glu
 195          200          205
Glu Asp Gln Glu Glu Asp Lys Asn Ile Val Val Asp Asp Ile Thr Glu
 210          215          220
Gln Lys Pro Glu Pro Gln Asp Asp Gly Lys Ser Thr Glu Ser Asp Val
 225          230          235          240
Lys Ala Asp Gly Asp Ser Lys Gly Ser Glu Glu Val Asp Ser His Cys
 245          250          255
Lys Lys Ala Leu Ser His Lys Glu Leu Tyr Glu Arg Ala Arg Glu Leu
 260          265          270
Leu Val Ser Tyr Glu Glu Glu Gln Phe Thr Val Leu Glu Lys Phe Arg
 275          280          285
Tyr Leu Pro Lys Ala Ile Lys Ala Trp Asn Asn Pro Ser Pro Arg Val
 290          295          300
Glu Cys Val Leu Ala Glu Leu Lys Gly Val Thr Cys Glu Asn Arg Glu
 305          310          315          320
Ala Val Leu Asp Ala Phe Leu Asp Asp Gly Phe Leu Val Pro Thr Phe
 325          330          335
Glu Gln Leu Ala Ala Leu Gln Ile Glu Tyr Glu Glu Asn Val Asp Leu
 340          345          350
Asn Asp Val Leu Val Pro Lys Pro Phe Ser Gln Phe Trp Gln Pro Leu
 355          360          365
Leu Arg Gly Leu His Ser Gln Asn Phe Thr Gln Ala Leu Leu Glu Arg
 370          375          380
Met Leu Ser Glu Leu Pro Ala Leu Gly Ile Ser Gly Ile Arg Pro Thr
 385          390          395          400
Tyr Ile Leu Arg Trp Thr Val Glu Leu Ile Val Ala Asn Thr Lys Thr
 405          410          415
Gly Arg Asn Ala Arg Arg Phe Ser Ala Gly Gln Trp Glu Ala Arg Arg

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Gly Trp Arg Leu Phe Asn Cys Ser Ala Ser Leu Asp Trp Pro Arg Met
          435                      440                      445
Val Glu Ser Cys Leu Gly Ser Pro Cys Trp Ala Ser Pro Gln Leu Leu
          450                      455                      460
Arg Ile Ile Phe Lys Ala Met Gly Gln Gly Leu Pro Asp Glu Glu Gln
          465                      470                      475                      480
Glu Lys Leu Leu Arg Ile Cys Ser Ile Tyr Thr Gln Ser Gly Glu Asn
          485                      490                      495
Ser Leu Val Gln Glu Gly Ser Glu Ala Ser Pro Ile Gly Lys Ser Pro
          500                      505                      510
Tyr Thr Leu Asp Ser Leu Tyr Trp Ser Val Lys Pro Ala Ser Ser Ser
          515                      520                      525
Phe Gly Ser Glu Ala Lys Ala Gln Gln Gln Glu Glu Gln Gly Ser Val
          530                      535                      540
Asn Asp Val Lys Glu Glu Glu Lys Glu Glu Lys Glu Val Leu Pro Asp
          545                      550                      555                      560
Gln Val Glu Glu Glu Glu Asn Asp Asp Gln Glu Glu Glu Glu Glu
          565                      570                      575
Asp Glu Asp Asp Glu Asp Asp Glu Glu Glu Asp Arg Met Glu Val Gly
          580                      585                      590
Pro Phe Ser Thr Gly Gln Glu Ser Pro Thr Ala Glu Asn Ala Arg Leu
          595                      600                      605
Leu Ala Gln Lys Arg Gly Ala Leu Gln Gly Ser Ala Trp Gln Val Ser
          610                      615                      620
Ser Glu Asp Val Arg Trp Asp Thr Phe Pro Leu Gly Arg Met Pro Gly
          625                      630                      635                      640
Gln Thr Glu Asp Pro Ala Glu Leu Met Leu Glu Asn Tyr Asp Thr Met
          645                      650                      655
Tyr Leu Leu Asp Gln Pro Val Leu Glu Gln Arg Leu Glu Pro Ser Thr
          660                      665                      670
Cys Lys Thr Asp Thr Leu Gly Leu Ser Cys Gly Val Gly Ser Gly Asn
          675                      680                      685
Cys Ser Asn Ser Ser Ser Ser Asn Phe Glu Gly Leu Leu Trp Ser Gln
          690                      695                      700
Gly Gln Leu His Gly Leu Lys Thr Gly Leu Glu Leu Phe
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<210> 3167

<211> 2730

<212> DNA

<213> Homo sapiens

<400> 3167

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gcgggcacgg tggcctacct agccctgcgt atttcgtact cgctcttcac ggcctccgg
180
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240
acaggtagta ctgatggaat tggaaaatca tatgcagaag agttagcaaa gcatggaatg
300

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aaggttgctc ttatcagcag atcaaaggat aaacttgacc aggtttccag tgaataaaaa
360
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gataaaatta aaacaggcct ggctggctct gaaatcgcca tcttagtgaa caacgtggga
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<210> 3168

<211> 312

<212> PRT

<213> Homo sapiens

<400> 3168

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 20 25 30
 Ala Leu Arg Val Trp Gly Val Gly Asn Glu Ala Gly Val Gly Pro Gly
 35 40 45
 Leu Gly Glu Trp Ala Val Val Thr Gly Ser Thr Asp Gly Ile Gly Lys
 50 55 60
 Ser Tyr Ala Glu Glu Leu Ala Lys His Gly Met Lys Val Val Leu Ile
 65 70 75 80
 Ser Arg Ser Lys Asp Lys Leu Asp Gln Val Ser Ser Glu Ile Lys Glu
 85 90 95
 Lys Phe Lys Val Glu Thr Arg Thr Ile Ala Val Asp Phe Ala Ser Glu
 100 105 110
 Asp Ile Tyr Asp Lys Ile Lys Thr Gly Leu Ala Gly Leu Glu Ile Gly
 115 120 125
 Ile Leu Val Asn Asn Val Gly Met Ser Tyr Glu Tyr Pro Glu Tyr Phe
 130 135 140
 Leu Asp Val Pro Asp Leu Asp Asn Val Ile Lys Lys Met Ile Asn Ile


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Val Glu Arg Ser Lys Gly Ala Ile Leu Asn Ile Ser Ser Gly Ser Gly
              180              185              190
Met Leu Pro Val Pro Leu Leu Thr Ile Tyr Ser Ala Thr Lys Thr Phe
              195              200              205
Val Asp Phe Phe Ser Gln Cys Leu His Glu Glu Tyr Arg Ser Lys Gly
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Val Phe Val Gln Ser Val Leu Pro Tyr Phe Val Ala Thr Lys Leu Ala
225              230              235              240
Lys Ile Arg Lys Pro Thr Leu Asp Lys Pro Ser Pro Glu Thr Phe Val
              245              250              255
Lys Ser Ala Ile Lys Thr Val Gly Leu Gln Ser Arg Thr Asn Gly Tyr
              260              265              270
Leu Ile His Ala Leu Met Gly Ser Ile Ile Ser Asn Leu Pro Ser Trp
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Ile Tyr Leu Lys Ile Val Met Asn Met Asn Lys Ser Thr Arg Ala His
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<210> 3169

<211> 5945

<212> DNA

<213> Homo sapiens

<400> 3169

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780

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<211> 412

<212> PRT

<213> Homo sapiens

<400> 3170

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			20					25					30		
Ala	Tyr	Gln	Gly	Ile	Thr	Gln	Glu	Lys	Ile	Asn	Glu	Met	Arg	Val	Ala
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Pro	Glu	Gln	Gln	Met	Ile	Ala	Asp	Ile	His	Cys	Met	Ile	Ala	Ala	Gly
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Gln	Asp	Leu	Asp	Trp	Ile	Asp	Ala	Gln	Gly	Ala	Thr	Leu	Leu	His	Ile
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Gly	Val	Arg	Val	Asp	Val	Lys	Asp	Trp	Asp	Gly	Trp	Glu	Pro	Leu	His
			100					105					110		
Ala	Ala	Ala	Phe	Trp	Gly	Gln	Met	Gln	Met	Ala	Glu	Leu	Leu	Val	Ser
			115					120					125		
His	Gly	Ala	Ser	Leu	Ser	Ala	Arg	Thr	Ser	Met	Asp	Glu	Met	Pro	Ile
			130					135					140		
Asp	Leu	Cys	Glu	Glu	Glu	Glu	Phe	Lys	Val	Leu	Leu	Leu	Glu	Leu	Lys
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His	Lys	His	Asp	Val	Ile	Met	Lys	Ser	Gln	Leu	Arg	His	Lys	Ser	Ser
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Ser	Thr	Tyr	Asn	Gly	Asp	Ile	Arg	Glu	Thr	Arg	Thr	Asp	Gln	Glu	Asn
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Lys	Asp	Pro	Asn	Pro	Arg	Leu	Glu	Lys	Pro	Val	Leu	Leu	Ser	Glu	Phe
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Pro	Thr	Lys	Ile	Pro	Arg	Gly	Glu	Leu	Asp	Met	Pro	Val	Glu	Asn	Gly
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Leu	Arg	Ala	Pro	Val	Ser	Ala	Tyr	Gln	Tyr	Ala	Leu	Ala	Asn	Gly	Asp

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Pro Gly Val Ala Asp Ala Thr Pro Pro Trp Ser Ser Tyr Lys Glu Gln		
305	310	315
Ser Pro Gln Thr Leu Leu Glu Leu Lys Arg Gln Arg Ala Ala Ala Lys		
325	330	335
Leu Leu Ser His Pro Phe Leu Ser Thr His Leu Gly Ser Ser Met Ala		
340	345	350
Arg Thr Gly Glu Ser Ser Ser Glu Gly Lys Ala Xaa Leu Ile Gly Gly		
355	360	365
Arg Thr Ser Pro Tyr Ser Ser Asn Gly Thr Ser Val Tyr Tyr Thr Val		
370	375	380
Thr Ser Gly Asp Pro Pro Leu Leu Lys Phe Lys Ala Pro Ile Glu Glu		
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<210> 3171

<211> 753

<212> DNA

<213> Homo sapiens

<400> 3171

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<210> 3172

<211> 228

<212> PRT

<213> Homo sapiens

<400> 3172

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Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val Val Gly Asp
35      40      45
Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser Thr Leu Leu
50      55      60
Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly Asp Ile Ile
65      70      75      80
Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg Tyr Asp Phe
85      90      95
Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu Gly Thr Val
100     105     110
Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg Asp Arg Lys
115     120     125
Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys Gln Gln Leu
130     135     140
Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala Ala Glu Asp
145     150     155     160
Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala Ile Asn Ala
165     170     175
Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly Leu Ser Pro
180     185     190
Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu Ile Arg Lys
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Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Trp His Glu Val Cys
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Lys Lys Pro Leu
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<210> 3173

<211> 573

<212> DNA

<213> Homo sapiens

<400> 3173

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<210> 3174
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 3174
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 Val Ala Gln Tyr Phe Arg Glu Lys Tyr Thr Leu Gln Leu Lys Tyr Pro
 50 55 60
 His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys His Thr Tyr Leu
 65 70 75 80
 Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg Cys Ile Lys Lys
 85 90 95
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 100 105 110
 Ala Pro Asp Arg Gln Glu Glu Ile Ser Arg Leu Val Arg Ser Ala Asn
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<210> 3175
 <211> 948
 <212> DNA
 <213> Homo sapiens

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<210> 3176

<211> 92

<212> PRT

<213> Homo sapiens

<400> 3176

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			20					25					30		
Pro	Asp	Ala	Trp	Gly	Leu	Pro	Thr	Pro	Gln	Gln	Ala	Arg	Gly	Lys	Ala
		35					40				45				
Arg	Gly	Asn	Glu	Tyr	Gln	Pro	Ser	Asn	Ile	Lys	Arg	Lys	Asn	Lys	His
	50				55					60					
Gly	Trp	Val	Arg	Arg	Leu	Ser	Thr	Pro	Ala	Gly	Val	Gln	Val	Ile	Leu
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<210> 3177

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 3177

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<210> 3178

<211> 273

<212> PRT

<213> Homo sapiens

<400> 3178

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Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu
 65           70           75           80
Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
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Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val Glu
100           105           110
Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro Val Ile
115           120           125
Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys Ala Ser Trp
130           135           140
Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val Met Cys Thr Leu
145           150           155           160
Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe Leu Leu Tyr Arg His
165           170           175
Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu Cys Ala Ser Val
180           185           190
His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu Thr Arg Pro Leu
195           200           205
Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His Arg Gly Tyr Gln
210           215           220
Ser Leu Ser Asp Ser Pro Pro Gly Ala Arg Val Phe Thr Glu Ser Glu
225           230           235           240
Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu Val Ser Pro Val
245           250           255
Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val
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<210> 3179

<211> 3447

<212> DNA

<213> Homo sapiens

<400> 3179

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180

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360
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420
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<210> 3180

<211> 127

<212> PRT

<213> Homo sapiens

<400> 3180

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Met Ser Phe Thr Asn Lys Ser Arg Gln Val Ser Gln Pro Glu Ile Ser
 1           5           10           15
Thr Gln Thr Asp Gly Arg Asp Val Asn Ser Cys Leu Lys Leu Arg Cys
          20           25           30
Ala Phe Thr Pro Thr Gly Lys Val Lys Leu Thr Phe Val Phe Leu Phe
          35           40           45
Asn Asn Phe Met Ile Asn Lys Glu Leu Gln Leu Glu Thr Lys Ala Asn
          50           55           60
Ser Arg Asn Ser Leu Thr Pro Ser Cys Pro Met Val Phe Met Ile Ala
65           70           75           80
Cys Tyr Gln Asn Glu Ala Leu Cys Ser Thr Leu Tyr Ser Lys Ala Phe
          85           90           95
Tyr Ala Pro Thr Arg Pro Ser Gly Ile Pro Glu Ser Ala Leu His Thr
          100          105          110
Gly Arg Lys Thr Ala Ser Ser Tyr Arg Leu Cys Glu Asn Thr Gln
          115          120          125
```

<210> 3181

<211> 287

<212> DNA

<213> Homo sapiens

<400> 3181

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180
tacactctt caggctgtgt cctctgtgca ggtcctgagc ttttgcctcc aaaaggtctg
240
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287
```

<210> 3182

<211> 95

<212> PRT

<213> Homo sapiens

<400> 3182

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Met Ala Ser Ser Pro Ala Val Asp Val Ser Cys Arg Arg Arg Gly Glu
 1           5           10           15
Arg Arg Gln Leu Asp Ala Arg Arg Asn Lys Cys Arg Ile Arg Leu Gly
          20           25           30
Gly His Met Lys Gln Gly Gly Leu Leu Lys Asp Gly Trp Ala Ser Pro
```

35					40					45				
Cys	Thr	Arg	Ser	Ser	Pro	Ser	Ser	Cys	Trp	Thr	Gly	Thr	Leu	Gln
50						55					60			
Ala	Val	Ser	Ser	Val	Gln	Val	Leu	Ser	Phe	Cys	Leu	Gln	Lys	Val
65					70					75				Cys
Ser	Ile	Trp	Cys	Ser	Cys	Leu	Met	Pro	His	Thr	Gly	Asp	Ala	Pro
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<210> 3183
<211> 1457
<212> DNA
<213> Homo sapiens
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400> 3183

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120	aaagtgtctc	ctgagagctg	cagggtgtcc	tggaatctcc	tcggggatga	ggcagctgcc
180	gagctggccc	aggtgctgcc	gcagatgggc	cggtgaaga	gagtggacct	ggagaagaat
240	cagatcacag	ctttgggggc	ctggctcctg	gctgaaggac	tggcccaggg	gtctagcatc
300	caagtcatcc	gcctctggaa	taaccccatt	cctgtcgaca	tggcccagca	cctgaagagc
360	caggagccca	ggctggacct	tgccctcttt	gacaaccagc	cccaggcccc	ttggggctact
420	tgtgggcccc	ctcaagacct	ttggaatcca	gccaagtgat	gcacccaaat	gatccacctt
480	tcgcccactg	ggataaatga	ctcaggaaa	aagagcctcg	gcagggcgct	ctgcactcca
540	cccaggagga	aggatacgtg	tgtcctgctg	cagtcctcag	ggagaacctt	tttgggaacc
600	aggagctggg	tctggacaaa	ggagtaccct	gcattacgtg	ggatatgtgt	gatcaattgg
660	ggacatgcga	cacacaatga	gggtgtcatg	acaatgcatg	acacgtacgg	ttatatgtgg
720	cagtggtgac	ccttgacatg	tggcggttca	tgaaagtcat	tgtggcacgt	gttctgtggc
780	atgggtgctg	gcatcccaag	tggcaggata	catgattgtt	ggtctatata	tgacacatga
840	caaattgtcca	tgtcacagga	ctcatggctg	gccagatgac	ctcaggctgg	cccaagatct
900	aatttattaa	tttttaaaag	aaatacatat	ttatagattg	tgtgtatgga	gcagctaagt
960	caggaaaaag	cttcgccccc	agctggggag	ggagagtgtc	catgcaactga	ccagtcacagg
1020	ggctcaaggg	ccagggtctc	ggaacaagcc	agggactcag	ccattaagtc	ccctcctgcc
1080	tcaatcccca	gcctacccat	ctataaaact	gatgactcct	cccttactta	catactagct
1140	tccaaggaca	ggtggaggta	gggccagcct	ggcgggagtg	gagaagccca	gtctgtccta
1200						

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 1320
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 1440
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<210> 3184

<211> 140

<212> PRT

<213> Homo sapiens

<400> 3184

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			20					25					30		
Gln	Thr	Gln	Leu	Leu	Val	Pro	Lys	Lys	Val	Leu	Pro	Glu	Ser	Cys	Arg
		35					40					45			
Leu	Ser	Trp	Asn	Leu	Leu	Gly	Asp	Glu	Ala	Ala	Ala	Glu	Leu	Ala	Gln
	50					55			60						
Val	Leu	Pro	Gln	Met	Gly	Arg	Leu	Lys	Arg	Val	Asp	Leu	Glu	Lys	Asn
65				70					75					80	
Gln	Ile	Thr	Ala	Leu	Gly	Ala	Trp	Leu	Leu	Ala	Glu	Gly	Leu	Ala	Gln
			85					90						95	
Gly	Ser	Ser	Ile	Gln	Val	Ile	Arg	Leu	Trp	Asn	Asn	Pro	Ile	Pro	Cys
			100					105					110		
Asp	Met	Ala	Gln	His	Leu	Lys	Ser	Gln	Glu	Pro	Arg	Leu	Asp	Phe	Ala
		115					120					125			
Phe	Phe	Asp	Asn	Gln	Pro	Gln	Ala	Pro	Trp	Gly	Thr				
	130					135					140				

<210> 3185

<211> 1433

<212> DNA

<213> Homo sapiens

<400> 3185

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 120
 cctggtaacc tgaggagggtg tagagcacc cagaaggagg gtaaaagcag ggggcaaaagc
 180
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 240
 gtagctttca gggctggcca caccctaagc cttgcaaaag ggctcctcgc aagggtctggc
 300
 ccatgggggc ccacacctcc cagccagtga ggtagcatg gttaggagtc cacatgtgtg
 360

caagtgccttg tgtggaggct catgtatgca tgtgtgtata tgcaaagctg cacatgacaa
 420
 tgtgcatgcc agtccagagt tagatgtacc tatgcagttg ccctcaagcg aagggtcata
 480
 ttggaaaca aggatggctc taaacatgta agcgtgcatg tgggcatgta tgtatctggg
 540
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 600
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 660
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 720
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 780
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 840
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 900
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 960
 aagtcacga gccctgtatg ccaactcctc ggtttgtcca ggtaacaggg gtgccccgcc
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 1320
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 1380
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 1433

<210> 3186

<211> 112

<212> PRT

<213> Homo sapiens

<400> 3186

Met Pro Leu Leu Trp Phe Val Gln Val Thr Gly Val Pro Arg Pro Leu
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 His Asp Gln His Pro Val Val Gly Gln Leu Leu Gln Val Leu Lys Ala
 20 25 30
 Gly Leu Thr His Gly Val Leu Val Ser Ile Tyr Asn Gln Ser Trp Ser
 35 40 45
 Leu Arg Gly Arg Ile Gly Gly Trp Gly Arg Val Asn Arg Thr Cys His
 50 55 60
 Ser Ile Pro Ser Pro Pro His Phe Ser Leu Phe Leu Gly Pro Pro His
 65 70 75 80
 Met Arg Glu Arg Asp Lys Leu Ala Gln Trp Val Gly Ala Gln Ile Gly

```

      85              90              95
Val  Cys  Pro  Arg  Thr  Gln  Phe  Ser  Thr  Gly  Leu  Gly  Thr  Val  Val  Cys
      100              105              110

<210> 3187
<211> 860
<212> DNA
<213> Homo sapiens

<400> 3187
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120
aagtgggtcct cccgcctcgg cctcctgagt agctgggatt acagatatgt tcctaaaaca
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240
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720
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<210> 3188
<211> 120
<212> PRT
<213> Homo sapiens

<400> 3188
Thr  Pro  Gly  Leu  Lys  Trp  Ser  Ser  Arg  Leu  Gly  Leu  Leu  Ser  Ser  Trp
1      5      10      15
Asp  Tyr  Arg  Tyr  Val  Pro  Lys  Thr  Ser  Leu  Ser  Ser  Pro  Pro  Trp  Pro
20      25      30
Glu  Val  Val  Leu  Pro  Asp  Pro  Val  Glu  Glu  Thr  Arg  His  His  Ala  Glu
35      40      45
Val  Val  Lys  Lys  Val  Asn  Glu  Met  Ile  Val  Thr  Gly  Gln  Tyr  Gly  Arg

```

```

      50              55              60
Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val Thr Ser
65              70              75              80
Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly Glu
      85              90              95
Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe Thr
      100              105              110
Leu Leu Gly Lys Pro Leu Leu Gly
      115              120

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<210> 3189
 <211> 440
 <212> DNA
 <213> Homo sapiens

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<400> 3189
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120
gactccctt ctgggcagtg gctgccctgc tttctctgtc tctttcaggg tgtgctgtcc
180
gacctcacca aagtgaccog gatgcatgga atcgaccctg tgggtgctgt cctgatgggt
240
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300
tgcttgctca actttgtgag tggccacaga gacaagagtg ggatatgatg caatggggta
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420
ctcccccctat ggcccctgcc
440

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<210> 3190
 <211> 111
 <212> PRT
 <213> Homo sapiens

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<400> 3190
Gly His Gly Trp Gly Arg Thr Leu Ala Trp Leu Ser Thr Arg Gly Leu
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Ser Leu Gly Lys Gln Val Pro Val Phe Ser Thr Thr Cys Ile Pro Gln
      20              25              30
Gly Ser Ile Leu Asp Ser Pro Ser Gly Pro Val Leu Pro Cys Phe Leu
      35              40              45
Cys Leu Phe Gln Gly Val Leu Ser Asp Leu Thr Lys Val Thr Arg Met
      50              55              60
His Gly Ile Asp Pro Val Val Leu Val Leu Met Val Gly Met Val Met
      65              70              75              80
Phe Thr Leu Gly Phe Ala Gly Cys Val Gly Ala Leu Arg Glu Asn Ile
      85              90              95
Cys Leu Leu Asn Phe Val Ser Gly His Arg Asp Lys Ser Gly Ile
      100              105              110

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<210> 3191
 <211> 266
 <212> DNA
 <213> Homo sapiens

<400> 3191
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 120
 aacagcagga caatccacac ttccgtagcc tcctgggggc ggccgccgag ccagcccggg
 180
 gcccgccgc ccagcaccgc ttgcagggca gaaaagagaa gagagttgac aacatcgaga
 240
 tacagaaatt catctcccaa aaagcg
 266

<210> 3192
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 3192
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 Cys Asn Gly Cys Trp Gly Gly Gly Pro Arg Ala Gly Ser Ala Ala Asp
 20 25 30
 Pro Arg Arg Leu Arg Lys Cys Gly Leu Ser Cys Cys Ser Leu Arg Ser
 35 40 45
 Arg Glu Ser Lys Asp Asp Pro Trp Gln Phe Ser Asp Cys Arg Lys Arg
 50 55 60
 Ser Arg Ser Met Ala Gln Val Ala Asp Thr Glu Gln Gly Thr Ile Ser
 65 70 75 80
 Pro Ser Ala Ser

<210> 3193
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 3193
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 acagccctgcc tgagtgttca gatccaggct ctgccagag ctggatgtaa atttatgacc
 120
 tggagtgagt tgttttgcc ctctgagcct cagttttctcc atctgtgaaa tggggacaac
 180
 agcagttcct tccaggaggg taaaaggagg agaaaaagaa tgcagatcca gcctcgcca
 240
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 360

gctggcctcg tgattcctct ctttccctgc aggccacggt tcacctactt ccccttctcc
 420
 ctgggccacc gctctgcat cgggcagcag ttgtctcaga tggagggtgaa ggtggtcatg
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 gagcaggcca cactcaagcc actggac
 567

<210> 3194
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 3194
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 Gly Leu Val Ile Pro Leu Phe Pro Cys Arg Pro Arg Phe Thr Tyr Phe
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 Pro Phe Ser Leu Gly His Arg Ser Cys Ile Gly Gln Gln Phe Ala Gln
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 Met Glu Val Lys Val Val Met Ala Lys Leu Gln Arg Leu Glu Phe
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 <212> DNA
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<211> 153

<212> PRT

<213> Homo sapiens

<400> 3196

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Ala	Ile	Arg	Lys	Pro	Gln	Thr	Pro	Thr	Ser	Leu	Ala	Gly	Ser	Ala	Lys
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Glu	Ala	Asn	Arg	Ser	Phe	Leu	Ser	Gly	Ile	Lys	Thr	Ile	Leu	Lys	Lys
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<211> 833

<212> PRT

<213> Homo sapiens

<400> 3198

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Val	Lys	Pro	Gln	Val	Phe	Gln	Ser	His	Cys	Glu	Arg	Arg	His	Gly	Ser
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Thr	Ser	Leu	Val	Gln	Val	Lys	Thr	Lys	Ala	Cys	Leu	Ser	Gly	His	His
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Pro	Asn	Leu	Val	Lys	Ala	Asp	Gly	Ala	Asn	Val	Lys	Met	Asn	Ser	Thr
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Ser Gly Arg Thr Ser Leu Pro Gly Gly Pro Ala Asp Ile Val Arg Gln
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Ser Leu Ala Leu His Ala Gly Asp Leu Ser Leu Ala Ser His Asn Ala
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<210> 3199

<211> 777

<212> DNA

<213> Homo sapiens

<400> 3199

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<211> 92

<212> PRT

<213> Homo sapiens

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			20					25					30		
Asp	Thr	Leu	Phe	Gly	Ala	Leu	Arg	Phe	Leu	Ala	Ser	Pro	Ser	Phe	Trp
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Val	Ser	Pro	Arg	Ser	Pro	Val	Pro	Ala	Val	Gly	Ala	Ala	Cys	Cys	Met
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<213> Homo sapiens

<400> 3201

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 120
 gaagccgaca gcctttggga ccgaggtcag cagctgcacc ggcgcaagaa ttccaaacac
 180
 agctgtggct gaagggcctg ggggtgtgca ggtcccaaac ccagtgagc ctgatccccg
 240
 catgggtcct gtctcctggg ggccaccttt gtgtcccggt gtggtgacc ctgagagggg
 300
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 360
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 390

<210> 3202

<211> 116

<212> PRT

<213> Homo sapiens

<400> 3202

Met Gly Thr Arg Lys Gln Leu Pro Ser Arg Leu Pro Gln Ala Gly Arg

1	5	10	15
Lys Gly His Ala Ala Gly Val Ser Thr Ala Lys Pro Thr Ala Phe			
	20	25	30
Gly Thr Glu Val Ser Ser Cys Thr Gly Ala Arg Ile Asn Thr Ala			
	35	40	45
Val Ala Glu Gly Pro Gly Gly Val Gln Val Pro Asn Pro Ser Glu Pro			
	50	55	60
Asp Pro Asp Met Gly Pro Val Ser Trp Gly Pro Leu Cys Pro Val			
	65	70	75
Val Ala Asp Pro Glu Arg Glu Gly Cys Gly Asp Ala His Met Thr Leu			
	85	90	95
Gly Ser Gln Arg Gln Pro Leu Leu Thr Leu Arg Val Pro Gly Ala Ser			
	100	105	110
Gln Glu Gly Arg			
115			

<210> 3203

<211> 1906

<212> DNA

<213> Homo sapiens

<400> 3203

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120
cacgggtggca gcattgagag ttggacaccc gggtccttga agtgatctct aggccccagc
180
cccaaatccg ccaccattcc gtgctgcggg gacaccatgg ctccagaaga ggacgctgga
240
ggggaggcct tagggggcag tttctgggag gctggcaact acaggcgcac ggtacagcgg
300
gtggaaggacg ggcaccggct gtgcggggac ctggtcagct gcttccagga gcgcgcccgc
360
atcgagaagg cttatgccca gcagtgggct gactggggcc gaaagtggag ggggaccgtg
420
gagaaggggcc ccagtatgg cactctggag aaggcctggc atgccttttt cacggcggtc
480
gagcggctga gcgcgctgca cctggagggt cgggagaagc tgcaagggca ggacagtga
540
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600
agccggggcg ccgaggacgg cttccgcaag gcccagaagc cctgggtgaa gaggtgaa
660
gaggttgagg cttccaagaa aagctaccac gcagcccgga aggatgagaa gaccgcccag
720
acgagggaga gccacgcaaa ggcagacagc gccgtctccc aggagcagct gcgcaactg
780
cagggaacggg tggaacgctg tgccaaggag gccgagaaga caaaagctca gtatgagcag
840
acgtggcgag agctgcatcg ctacactcca cgctacatgg aggacatgga acaggccttt
900
gagacctgcc aggccgccga gcgccagcgg cttcttttct tcaaggatat gctgctcacc
960

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ttacaccagc acctggacct ttccagcagt gagaagttcc atgaactcca ccgtgacttg
 1020
 caccagggga tttaggcagc cagtgcagaa gaggatctgc gctggtggcg cagcaccac
 1080
 gggccaggca tggccatgaa ctggccacag ttcgaggagt ggtccttgga cacacagagg
 1140
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 1200
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 1320
 agggcactct atgactacgc tggccaggaa gctgatgagc tgagcttccg agcaggggag
 1380
 gagctgctga agatgagtga ggaggacgag cagggtggtt gccaaaggcca gttgcagagt
 1440
 ggccgcattg gcctgtaccc tgccaactac gtggagtgtg tgggcgcctg agtgcctga
 1500
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 1560
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 1680
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 1740
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 1800
 ttgggggtgag ttagttctg gcctagcagc accctcttgt ggcctgttct agcgtgtatt
 1860
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 1906

<210> 3204

<211> 424

<212> PRT

<213> Homo sapiens

<400> 3204

Met Ala Pro Glu Glu Asp Ala Gly Gly Glu Ala Leu Gly Gly Ser Phe
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 20 25 30
 His Arg Leu Cys Gly Asp Leu Val Ser Cys Phe Gln Glu Arg Ala Arg
 35 40 45
 Ile Glu Lys Ala Tyr Ala Gln Gln Leu Ala Asp Trp Ala Arg Lys Trp
 50 55 60
 Arg Gly Thr Val Glu Lys Gly Pro Gln Tyr Gly Thr Leu Glu Lys Ala
 65 70 75 80
 Trp His Ala Phe Phe Thr Ala Ala Glu Arg Leu Ser Ala Leu His Leu
 85 90 95
 Glu Val Arg Glu Lys Leu Gln Gly Gln Asp Ser Glu Arg Val Arg Ala
 100 105 110
 Trp Gln Arg Gly Ala Phe His Arg Pro Val Leu Gly Gly Phe Arg Glu

```

115          120          125
Ser Arg Ala Ala Glu Asp Gly Phe Arg Lys Ala Gln Lys Pro Trp Leu
130          135          140
Lys Arg Leu Lys Glu Val Glu Ala Ser Lys Lys Ser Tyr His Ala Ala
145          150          155          160
Arg Lys Asp Glu Lys Thr Ala Gln Thr Arg Glu Ser His Ala Lys Ala
165          170          175
Asp Ser Ala Val Ser Gln Glu Gln Leu Arg Lys Leu Gln Glu Arg Val
180          185          190
Glu Arg Cys Ala Lys Glu Ala Glu Lys Thr Lys Ala Gln Tyr Glu Gln
195          200          205
Thr Leu Ala Glu Leu His Arg Tyr Thr Pro Arg Tyr Met Glu Asp Met
210          215          220
Glu Gln Ala Phe Glu Thr Cys Gln Ala Ala Glu Arg Gln Arg Leu Leu
225          230          235          240
Phe Phe Lys Asp Met Leu Leu Thr Leu His Gln His Leu Asp Leu Ser
245          250          255
Ser Ser Glu Lys Phe His Glu Leu His Arg Asp Leu His Gln Gly Ile
260          265          270
Glu Ala Ala Ser Asp Glu Glu Asp Leu Arg Trp Trp Arg Ser Thr His
275          280          285
Gly Pro Gly Met Ala Met Asn Trp Pro Gln Phe Glu Glu Trp Ser Leu
290          295          300
Asp Thr Gln Arg Thr Ile Ser Arg Lys Glu Lys Gly Gly Arg Ser Pro
305          310          315          320
Asp Glu Val Thr Leu Thr Ser Ile Val Pro Thr Arg Asp Gly Thr Ala
325          330          335
Pro Pro Pro Gln Ser Pro Gly Ser Pro Gly Thr Gly Gln Asp Glu Glu
340          345          350
Trp Ser Asp Glu Glu Ser Pro Arg Lys Ala Ala Thr Gly Val Arg Val
355          360          365
Arg Ala Leu Tyr Asp Tyr Ala Gly Gln Glu Ala Asp Glu Leu Ser Phe
370          375          380
Arg Ala Gly Glu Glu Leu Lys Met Ser Glu Glu Asp Glu Gln Gly
385          390          395          400
Trp Cys Gln Gly Gln Leu Gln Ser Gly Arg Ile Gly Leu Tyr Pro Ala
405          410          415
Asn Tyr Val Glu Cys Val Gly Ala
420

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<210> 3205

<211> 1482

<212> DNA

<213> Homo sapiens

<400> 3205

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120
ctgttgaccc ccacaggaga gccccggagc tatgtggagt ctgtggcacg gacagcggtg
180
gctggacccc gagctcagga ctctgagccc aagagcttta gtgctccagc caccagggcc
240

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tatggccatg agataccctt gaggaacggg accctgggtg gtcctttgt cteccccage
 300
 cccctctcca ccagcagccc catcctcagt gctgacagca cttcagtgagg gagtttcccg
 360
 tcggggagaga gcagtgacca ggggtcccg acgcccaccc agcctctgtt ggagttctggc
 420
 ttccgctcag gcagcctggg acagcccagc cgtctgccc agagaaacta ccagagctct
 480
 tctctctccc cgactgtggg cagtagctac agcagccccg actactcact tcagcatttc
 540
 agctcctctc cggaaagcca ggctcgagct cagttcagtg tggctggcgt ccacacggtg
 600
 cctggggagcc ctccagcgcg tcacagaaca gtgggcacca acactcccc tagtctggc
 660
 ttccgctggc gggccatcaa tcccagcatg gctgccccca gcagtcaccg tttgagccat
 720
 caccagatga tgggtccacc aggcactggc ttccatggta gcactgtctc cagccccag
 780
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 840
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 900
 caccctgggg ctccaccaag caacctggcc tccggtcttc atagcaatgc aatagccagc
 960
 cctggaagcc ccagcctggg ccgtcacctc ggagggtctg gatctgtggt tcccggcagc
 1020
 ccctgcttgg accggcatgt ggcctatggc ggctattcta ccccgaggga tcggagaccc
 1080
 aactgtctcc ggcagagcag tgcctctggc taccaggctc cttccacgcc ctccttcct
 1140
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 1260
 ggagaccggg caggcagcct cccaactat gccaccatca atgggaaggt gtcttcgct
 1320
 gtcgccagcg gcatgtccag tccagtgagg ggcagcaccg tctcctctc ccacactctg
 1380
 cccgacttct ccaagtactc catgccagac aacagcccg agacgcgggc taaagtgaag
 1440
 tttgtccagg acacttctaa gtattgttac aagcctaaga tc
 1482

<210> 3206

<211> 494

<212> PRT

<213> Homo sapiens

<400> 3206

Xaa Glu Met Glu Gly Thr Ser Pro Ser Ser Pro Pro Pro Ser Gly Val
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 Arg Ser Pro Pro Gly Leu Ala Lys Thr Pro Leu Ser Ala Leu Gly Leu
 20 25 30
 Lys Pro His Asn Pro Ala Asp Ile Leu Leu His Pro Thr Gly Glu Pro

35										40										45										
Arg	Ser	Tyr	Val	Glu	Ser	Val	Ala	Arg	Thr	Ala	Val	Ala	Gly	Pro	Arg															
50						55					60																			
Ala	Gln	Asp	Ser	Glu	Pro	Lys	Ser	Phe	Ser	Ala	Pro	Ala	Thr	Gln	Ala															
65					70					75					80															
Tyr	Gly	His	Glu	Ile	Pro	Leu	Arg	Asn	Gly	Thr	Leu	Gly	Gly	Ser	Phe															
			85						90					95																
Val	Ser	Pro	Ser	Pro	Leu	Ser	Thr	Ser	Ser	Pro	Ile	Leu	Ser	Ala	Asp															
			100					105					110																	
Ser	Thr	Ser	Val	Gly	Ser	Phe	Pro	Ser	Gly	Glu	Ser	Ser	Asp	Gln	Gly															
			115				120					125																		
Pro	Arg	Thr	Pro	Thr	Gln	Pro	Leu	Leu	Glu	Ser	Gly	Phe	Arg	Ser	Gly															
			130			135					140																			
Ser	Leu	Gly	Gln	Pro	Ser	Pro	Ser	Ala	Gln	Arg	Asn	Tyr	Gln	Ser	Ser															
145					150					155					160															
Ser	Pro	Leu	Pro	Thr	Val	Gly	Ser	Ser	Tyr	Ser	Ser	Pro	Asp	Tyr	Ser															
			165						170					175																
Leu	Gln	His	Phe	Ser	Ser	Ser	Pro	Glu	Ser	Gln	Ala	Arg	Ala	Gln	Phe															
			180					185						190																
Ser	Val	Ala	Gly	Val	His	Thr	Val	Pro	Gly	Ser	Pro	Gln	Ala	Arg	His															
			195				200							205																
Arg	Thr	Val	Gly	Thr	Asn	Thr	Pro	Pro	Ser	Pro	Gly	Phe	Gly	Trp	Arg															
			210			215					220																			
Ala	Ile	Asn	Pro	Ser	Met	Ala	Ala	Pro	Ser	Ser	Pro	Ser	Leu	Ser	His															
225					230					235					240															
His	Gln	Met	Met	Gly	Pro	Pro	Gly	Thr	Gly	Phe	His	Gly	Ser	Thr	Val															
			245						250					255																
Ser	Ser	Pro	Gln	Ser	Ser	Ala	Ala	Thr	Thr	Pro	Gly	Ser	Pro	Ser	Leu															
			260					265					270																	
Cys	Arg	His	Pro	Ala	Gly	Val	Tyr	Gln	Val	Ser	Gly	Leu	His	Asn	Lys															
			275				280					285																		
Val	Ala	Thr	Thr	Pro	Gly	Ser	Pro	Ser	Leu	Gly	Arg	His	Pro	Gly	Ala															
			290			295					300																			
His	Gln	Gly	Asn	Leu	Ala	Ser	Gly	Leu	His	Ser	Asn	Ala	Ile	Ala	Ser															
305					310					315					320															
Pro	Gly	Ser	Pro	Ser	Leu	Gly	Arg	His	Leu	Gly	Gly	Ser	Gly	Ser	Val															
			325						330					335																
Val	Pro	Gly	Ser	Pro	Cys	Leu	Asp	Arg	His	Val	Ala	Tyr	Gly	Gly	Tyr															
			340				345						350																	
Ser	Thr	Pro	Glu	Asp	Arg	Arg	Pro	Thr	Leu	Ser	Arg	Gln	Ser	Ser	Ala															
			355				360					365																		
Ser	Gly	Tyr	Gln	Ala	Pro	Ser	Thr	Pro	Ser	Phe	Pro	Val	Ser	Pro	Ala															
			370			375					380																			
Tyr	Tyr	Pro	Gly	Leu	Ser	Ser	Pro	Ala	Thr	Ser	Pro	Ser	Pro	Asp	Ser															
385					390					395					400															
Ala	Ala	Phe	Arg	Gln	Gly	Ser	Pro	Thr	Pro	Ala	Leu	Pro	Glu	Lys	Arg															
			405						410					415																
Arg	Met	Ser	Val	Gly	Asp	Arg	Ala	Gly	Ser	Leu	Pro	Asn	Tyr	Ala	Thr															
			420				425						430																	
Ile	Asn	Gly	Lys	Val	Ser	Ser	Pro	Val	Ala	Ser	Gly	Met	Ser	Ser	Pro															
			435				440					445																		
Ser	Gly	Gly	Ser	Thr	Val	Ser	Phe	Ser	His	Thr	Leu	Pro	Asp	Phe	Ser															
			450			455					460																			
Lys	Tyr	Ser	Met	Pro	Asp	Asn	Ser	Pro	Glu	Thr	Arg	Ala	Lys	Val	Lys															

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465                               470                               475                               480
Phe Val Gln Asp Thr Ser Lys Tyr Trp Tyr Lys Pro Lys Ile
                               485                               490

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<210> 3207

<211> 495

<212> DNA

<213> Homo sapiens

<400> 3207

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120
ctgtcgcgca agctgcataa gatcctggag acgcggtcgg acaacgcaca ggagatgtta
180
gaagctctca aggcactttc aacctttttt gttgaaaata gtctcgcgac tcgaagaaat
240
ttacgtggag atattgaacg taaaagttta gccatcaatg aagaatttgt aagcattttc
300
aagggaagtga aggaggaact tgaagcata agcgaagatg ttcaagcaat gagcaactgt
360
tgtcaagata tgacaagtcg cctacaggca gcaaaggaac agactcaaga tttaatagta
420
aataccacta agcttcaatc tgaaagccaa aaattagaga taagagctca agttgcagat
480
gccttcttat ccaag
495

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<210> 3208

<211> 107

<212> PRT

<213> Homo sapiens

<400> 3208

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Met Leu Glu Ala Leu Lys Ala Leu Ser Thr Phe Phe Val Glu Asn Ser
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Leu Arg Thr Arg Arg Asn Leu Arg Gly Asp Ile Glu Arg Lys Ser Leu
20          25          30
Ala Ile Asn Glu Glu Phe Val Ser Ile Phe Lys Glu Val Lys Glu Glu
35          40          45
Leu Glu Ser Ile Ser Glu Asp Val Gln Ala Met Ser Asn Cys Cys Gln
50          55          60
Asp Met Thr Ser Arg Leu Gln Ala Ala Lys Glu Gln Thr Gln Asp Leu
65          70          75          80
Ile Val Asn Thr Thr Lys Leu Gln Ser Glu Ser Gln Lys Leu Glu Ile
85          90          95
Arg Ala Gln Val Ala Asp Ala Phe Leu Ser Lys
100          105

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<210> 3209

<211> 346

<212> DNA

<213> Homo sapiens

<400> 3209
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 tgcgtccagc cttgtccctt ctgacctggg ccctaccac ggggaaatgt tcccatagca
 120
 gaagaatcag cccacacatg caggggtgtg ttagtgggga acgggctctg ggctcctgtg
 180
 ggaaccaggg accccctatc ttggtaccgg tcattggatg tatccccagc tcatgcctgt
 240
 gtctgtcttg gccctgtgg tcacctgtg ttcattctctc tccagccat ggcctctcaa
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 346

<210> 3210
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 3210
 Met Arg Pro Ala Leu Ser Leu Leu Thr Trp Ala Leu Pro Thr Gly Lys
 1 5 10 15
 Cys Ser His Ser Arg Arg Ile Ser Pro Thr Val Gln Gly Cys Val Ser
 20 25 30
 Gly Glu Arg Ala Leu Gly Ser Cys Gly Asn Gln Gly Pro Ile Leu
 35 40 45
 Val Pro Val Ile Gly Cys Ile Pro Ser Ser Cys Leu Cys Leu Ser Trp
 50 55 60
 Pro Val Trp Ser Pro Cys Val His Leu Ser Pro Ser His Gly Leu Ser
 65 70 75 80
 Asn Trp Gly Phe Arg Leu Pro Met Arg Gly Ser Trp Tyr Val Arg
 85 90 95

<210> 3211
 <211> 1728
 <212> DNA
 <213> Homo sapiens

<400> 3211
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 120
 gtttctcttg ccatcgtgca agccagtcgg aaggaccagg gactctatta ctgctgcac
 180
 aagaacagct acggaaaagt gactgctgaa tttaacctca cagctgaagt tctcaaacag
 240
 ctgtcaagtc acacagaata ctaaaggatg tgaagagatt gaattcagcc aactcatctt
 300
 caaagaagac ttctccatg acagctactt tggggggcgc ctgcgtgggc agatcgccac
 360
 ggaggagctg cactttggag aaggggttca ccgcaaagcc ttccgcagca cagtgatgca
 420

cggcctcatg cctgttctca aacctggcca tgctgtgtg ctaaggtgc acaatgccat
 480
 tgccattggg accagaaata atgatgagct catccaaagg aactacaaac tcgctgccca
 540
 ggaatgctat gttcaaaata ctgccaggta ttatgccaaag atctacgctg ctgaagcaca
 600
 gcctctggaa ggctttggag aagtacctga gatcattcct atttttctta tccatcggcc
 660
 tgagaacaat atcccgatg ctacagtggg ggaggagctg attggagaat ttgtgaagta
 720
 ttccatcagg gatgggaaag aaataaaact cttgagaaga gaatcagaag ctggtcagaa
 780
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 900
 caagggattt aaaggcaact gttccatgac cttcattgat cagttaaag cactacacca
 960
 gtgtaacaa tattgcaaaa tgctgggact gaaatccctt caaaacaaca accagaaaaa
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 gaagcagcgg agcattggga aaagcaaagt tcaacaaaac tctatgacag taaagaaggc
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 1140
 ggctagcagc acacaatctc gccagggaaa atctgaggcc acacaggaga gaatatacag
 1200
 cctgcagaga gtgcgtggca atccttactc ccagccgact gtgcgccaag atgcttctaa
 1260
 acccatcacc tgctgtcttc actcaaatga ttgcagaaca ggatttgcca ccagggttat
 1320
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 1380
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 1500
 ctgggatttc tagacacatc ctgctgtgat gtaaacagaa atcacgaatt cgctcactgg
 1560
 atcaagttgt tccactgggt tctaatacgc tattgttgcc ggagggtgggt tctgtgacgt
 1620
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 1680
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 1728

<210> 3212

<211> 87

<212> PRT

<213> Homo sapiens

<400> 3212

Ser Gly Asn Ile Lys Leu Ser Tyr Gln Phe Ser Glu Ile His Glu Asp

1

5

10

15

Ser Thr Val Cys Trp Thr Lys Asp Ser Lys Ser Ile Ala Gln Ala Lys

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                20                25                30
Lys Ser Ala Gly Asp Asn Ser Ser Val Ser Leu Ala Ile Val Gln Ala
   35                40                45
Ser Pro Lys Asp Gln Gly Leu Tyr Tyr Cys Cys Ile Lys Asn Ser Tyr
   50                55                60
Gly Lys Val Thr Ala Glu Phe Asn Leu Thr Ala Glu Val Leu Lys Gln
   65                70                75                80
Leu Ser Ser His Thr Glu Tyr
                85

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<210> 3213
 <211> 348
 <212> DNA
 <213> Homo sapiens

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<400> 3213
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tctaccgtca tcatggctaa tgaggactgt cccaaggctg ctgatagatcc tttttcatca
120
gataaacatg cccaactcat ctggcccaa atcaataaga tgagaaatgg acagcatttc
180
tgtgatgtgc agctgcaagt tggacaggaa agttttaaag ctcatcggtt ggttttgggt
240
gccagcagtc cttactttgc agctttgttc actggaggaa tgaaagagtc ctcaaaagat
300
gttgtaccga ttctaggaat tgaagcagga atctttcaga tactttcta
348

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<210> 3214
 <211> 92
 <212> PRT
 <213> Homo sapiens

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<400> 3214
Met Ala Asn Glu Asp Cys Pro Lys Ala Ala Asp Ser Pro Phe Ser Ser
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Asp Lys His Ala Gln Leu Ile Leu Ala Gln Ile Asn Lys Met Arg Asn
20        25        30
Gly Gln His Phe Cys Asp Val Gln Leu Gln Val Gly Gln Glu Ser Phe
35        40        45
Lys Ala His Arg Leu Val Leu Ala Ala Ser Ser Pro Tyr Phe Ala Ala
50        55        60
Leu Phe Thr Gly Gly Met Lys Glu Ser Ser Lys Asp Val Val Pro Ile
65        70        75        80
Leu Gly Ile Glu Ala Gly Ile Phe Gln Ile Leu Leu
                85                90

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<210> 3215
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 3215

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 120
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 180
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 240
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 300
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 420
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<210> 3216

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3216

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Ile	Leu	Asn	Val	Cys	Asn	Thr	Gly	Asp	Lys	Met	Val	Glu	Cys	Gln	Leu
		20						25					30		
Glu	Thr	His	Asn	His	Lys	Met	Val	Thr	Phe	Lys	Phe	Asp	Leu	Asp	Gly
		35					40					45			
Asp	Ala	Pro	Asp	Glu	Ile	Ala	Thr	Tyr	Met	Val	Glu	His	Asp	Phe	Ile
	50				55					60					
Leu	Gln	Ala	Glu	Arg	Glu	Thr	Phe	Ile	Glu	Gln	Met	Lys	Asp	Val	Met
65				70					75					80	
Asp	Lys	Ala	Glu	Asp	Met	Leu	Ser	Glu	Asp	Thr	Asp	Ala	Asp	Arg	Gly
		85						90						95	
Ser	Asp	Pro	Gly	Thr	Ser	Pro	Pro	His	Leu	Ser	Thr	Cys	Gly	Leu	Gly
		100				105						110			
Thr	Gly	Glu	Glu	Ser	Arg	Gln	Ser	Gln	Ala	Asn	Ala	Pro	Val	Tyr	Gln
	115					120						125			
Gln	Asn	Val	Leu	His	Thr	Gly	Lys	Arg	Trp	Phe	Ile	Ile	Cys	Pro	Val
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Pro	Glu	Pro	Pro	Ala	Pro	Glu	Gly	Pro							
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<210> 3217

<211> 2570

<212> DNA

<213> Homo sapiens

<400> 3217

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120
accatacca ggcactatga gctttacagg cgctgcaaac tggaggaaat gggctttaca
180
gatgtgggcc cagaaaacaa gccagtcagt gttcaagaga cctatgaagc caaaagacat
240
gagttccatg gtgaacgtca gaggaaggaa gaagaaatga aacagatgtt tgtgcagcga
300
gtaaaggaga aagaagccat attgaaagaa gctgagagag agctacaggc caaatttgag
360
caccttaaga gacttcacca agaagagaga atgaagcttg aagaacaaag aagacttttg
420
gaagaagaaa taattgcttt ctctaaaaag aaagctacct ccgagatatt tcacagccag
480
tcctttctgg caacaggcag caacctgagt aaggacaagg accataagaa ctccaatttt
540
ttgtaaaaca gaagtccag agcacagaag gtcacatca caagcaaact ttattaaaaa
600
aaaactagaa gtgtgctttg attttgctgt tatttgtttt atcacttcta tatttggtga
660
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720
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780
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840
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960
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1020
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1080
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1140
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1200
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1380
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1440
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1560
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1620

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 1680
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 1980
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 2040
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 2280
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 2340
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 2460
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<210> 3218

<211> 181

<212> PRT

<213> Homo sapiens

<400> 3218

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Glu	Asn	His	Cys	Asp	Phe	Val	Lys	Leu	Arg	Glu	Met	Leu	Ile	Cys	Thr
		20						25					30		
Asn	Met	Glu	Asp	Leu	Arg	Glu	Gln	Thr	His	Thr	Arg	His	Tyr	Glu	Leu
		35				40						45			
Tyr	Arg	Arg	Cys	Lys	Leu	Glu	Met	Gly	Phe	Thr	Asp	Val	Gly	Pro	
	50				55				60						
Glu	Asn	Lys	Pro	Val	Ser	Val	Gln	Glu	Thr	Tyr	Glu	Ala	Lys	Arg	His
65				70					75				80		
Glu	Phe	His	Gly	Glu	Arg	Gln	Arg	Lys	Glu	Glu	Met	Lys	Gln	Met	
			85					90					95		
Phe	Val	Gln	Arg	Val	Lys	Glu	Lys	Glu	Ala	Ile	Leu	Lys	Glu	Ala	Glu
		100					105					110			
Arg	Glu	Leu	Gln	Ala	Lys	Phe	Glu	His	Leu	Lys	Arg	Leu	His	Gln	Glu

	115		120		125	
Glu	Arg	Met	Lys	Leu	Glu	Gln
	130		135		140	
Ile	Ala	Phe	Ser	Lys	Lys	Ala
	145		150		155	
Ser	Phe	Leu	Ala	Thr	Gly	Ser
			165		170	
Asn	Ser	Asn	Phe	Leu		
			180			

<210> 3219

<211> 1241

<212> DNA

<213> Homo sapiens

<400> 3219

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120
gagcggggaga cagacatcct ggacgatgaa ttgccaaacc aggatgggtca cagtgcgggc
180
agcatgggca cactctcttc tctggacggg gtcaccaaca tcagtggagg gggctaccca
240
gaggccctgt cccactgac caacggtctg gacaagtcct accccatgga gcctatggtc
300
aatggaggag gctaccacct cagatctgac agccggggcg ggctgtccca tgctggccac
360
acggccccca tgcggccctc ctactctgca caggagggtt tagctggcta ccagagggag
420
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480
ggtatgttcc gctctcaatc cttttcggaa gctgaacccc agctgcccc agctccggtc
540
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600
cagcagcagc agcagcctcg cccacctcca cgccagcagg aaagagccca cttggagagt
660
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720
gagttccccc gagcagcctc ccagcaggag attgaacagt ccatacgaac actcaatatg
780
ctgatgtggt acctggagcc agcctccgct gctgccccac tacacaagtc ccagagtgtc
840
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900
cagtcctcct cactgaccca gtccagatct ggctatatcc ccagtgggca ttcgttggga
960
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1020
ccttatgact atcagccatg ttggtgtggg cctaaccagg atttcattc aaagagccca
1080
gcctcttctt ccttgctctg ctctcttccg accaccacaa gccctccagg gcctcagcaa
1140

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 1241

<210> 3220

<211> 413

<212> PRT

<213> Homo sapiens

<400> 3220

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Leu	Gly	Cys	Ala	Ser	Ser	Gly	Arg	His	Val	Val	Pro	Ala	Gln	Val	His
			20				25						30		
Val	Asn	Gly	Gly	Xaa	Val	Thr	Ser	Glu	Arg	Glu	Thr	Asp	Ile	Leu	Asp
			35				40					45			
Asp	Glu	Leu	Pro	Asn	Gln	Asp	Gly	His	Ser	Ala	Gly	Ser	Met	Gly	Thr
			50			55					60				
Leu	Ser	Ser	Leu	Asp	Gly	Val	Thr	Asn	Ile	Ser	Glu	Gly	Gly	Tyr	Pro
65				70					75					80	
Glu	Ala	Leu	Ser	Pro	Leu	Thr	Asn	Gly	Leu	Asp	Lys	Ser	Tyr	Pro	Met
				85					90					95	
Glu	Pro	Met	Val	Asn	Gly	Gly	Gly	Tyr	Pro	Tyr	Glu	Ser	Ala	Ser	Arg
			100					105					110		
Ala	Gly	Pro	Ala	His	Ala	Gly	His	Thr	Ala	Pro	Met	Arg	Pro	Ser	Tyr
			115				120					125			
Ser	Ala	Gln	Glu	Gly	Leu	Ala	Gly	Tyr	Gln	Arg	Glu	Gly	Pro	His	Pro
			130			135					140				
Ala	Trp	Pro	Gln	Pro	Val	Thr	Thr	Ser	His	Tyr	Ala	His	Asp	Pro	Ser
145					150					155				160	
Gly	Met	Phe	Arg	Ser	Gln	Ser	Phe	Ser	Glu	Ala	Glu	Pro	Gln	Leu	Pro
				165					170					175	
Pro	Ala	Pro	Val	Arg	Gly	Gly	Ser	Ser	Arg	Glu	Ala	Val	Gln	Arg	Gly
			180					185					190		
Leu	Asn	Ser	Trp	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Arg	Pro
			195				200						205		
Pro	Pro	Arg	Gln	Gln	Glu	Arg	Ala	His	Leu	Glu	Ser	Leu	Val	Ala	Ser
					210		215				220				
Arg	Pro	Ser	Pro	Gln	Pro	Leu	Ala	Glu	Thr	Pro	Ile	Pro	Ser	Leu	Pro
225					230					235				240	
Glu	Phe	Pro	Arg	Ala	Ala	Ser	Gln	Gln	Glu	Ile	Glu	Gln	Ser	Ile	Glu
				245					250					255	
Thr	Leu	Asn	Met	Leu	Met	Leu	Asp	Leu	Glu	Pro	Ala	Ser	Ala	Ala	Ala
				260			265					270			
Pro	Leu	His	Lys	Ser	Gln	Ser	Val	Pro	Gly	Ala	Trp	Pro	Gly	Ala	Ser
			275				280					285			
Pro	Leu	Ser	Ser	Gln	Pro	Leu	Ser	Gly	Ser	Ser	Arg	Gln	Ser	His	Pro
					290		295				300				
Leu	Thr	Gln	Ser	Arg	Ser	Gly	Tyr	Ile	Pro	Ser	Gly	His	Ser	Leu	Gly
305					310					315				320	
Thr	Pro	Glu	Pro	Ala	Pro	Arg	Ala	Ser	Leu	Glu	Ser	Val	Pro	Pro	Gly
				325				330						335	
Arg	Ser	Tyr	Ser	Pro	Tyr	Asp	Tyr	Gln	Pro	Cys	Leu	Ala	Gly	Pro	Asn

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          340          345          350
Gln Asp Phe His Ser Lys Ser Pro Ala Ser Ser Ser Leu Pro Ala Phe
      355          360          365
Leu Pro Thr Thr His Ser Pro Pro Gly Pro Gln Gln Pro Pro Ala Ser
      370          375          380
Leu Pro Gly Leu Thr Ala Gln Pro Leu Leu Ser Pro Lys Glu Ala Thr
      385          390          395          400
Ser Asp Pro Ser Arg Thr Pro Glu Glu Glu Pro Leu Asn
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<210> 3221

<211> 1585

<212> DNA

<213> Homo sapiens

<400> 3221

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120
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gaacaagaca attcagtaac atctattcct gagattcttc gatggggatc acagagcacg
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960
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1080
gcagaggggt ccttgctcgc gagtccccgt ctttgggctc tagtgatgca tagggaaaca
1140

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 1260
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 1320
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 1380
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 1440
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 1560
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 1585

<210> 3222

<211> 331

<212> PRT

<213> Homo sapiens

<400> 3222

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 Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Trp His Ile
 20 25 30
 Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys
 35 40 45
 His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu Val Leu
 50 55 60
 Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala
 65 70 75 80
 Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro Gly Thr
 85 90 95
 Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val Thr Cys
 100 105 110
 Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly Asp Val
 115 120 125
 Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys Ala Glu
 130 135 140
 Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu Cys Ala
 145 150 155 160
 Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr Ser Gly
 165 170 175
 Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg Arg Pro
 180 185 190
 Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro Ile Arg
 195 200 205
 Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln Asp Asn
 210 215 220
 Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln Ser Thr
 225 230 235 240
 Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala Thr Ile

245										250					255				
Thr	Pro	Ser	Gly	Ser	Val	Ile	Ser	Lys	Phe	Asn	Ser	Thr	Thr	Ser	Ser				
260										265					270				
Ala	Thr	Pro	Gln	Ala	Phe	Asp	Ser	Ser	Ser	Ala	Val	Val	Phe	Ile	Phe				
275										280					285				
Val	Ser	Thr	Ala	Val	Val	Val	Leu	Val	Ile	Leu	Thr	Met	Thr	Val	Leu				
290										295					300				
Gly	Leu	Val	Lys	Leu	Cys	Phe	His	Glu	Ser	Pro	Ser	Ser	Gln	Pro	Arg				
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<210> 3223
<211> 985
<212> DNA
<213> Homo sapiens
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120
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<210> 3224

<211> 224

<212> PRT

<213> Homo sapiens

<400> 3224

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 20           25           30
Val Ile Gly Val Ile Leu Gly Ala Glu Ala Ser Arg Arg Tyr Lys Lys
 35           40           45
Val Ile Pro Gly Ala Glu Pro Leu Ile Cys Ala Ser Ser Leu Leu Ala
 50           55           60
Thr Ala Pro Cys Leu Tyr Leu Ala Leu Val Leu Ala Pro Thr Thr Leu
 65           70           75           80
Leu Ala Ser Tyr Val Phe Leu Gly Leu Gly Glu Leu Leu Leu Ser Cys
 85           90           95
Asn Trp Ala Val Val Ala Asp Ile Leu Leu Ser Val Val Val Pro Arg
100           105           110
Cys Arg Gly Thr Ala Glu Ala Leu Gln Ile Thr Val Gly His Ile Leu
115           120           125
Gly Asp Ala Gly Ser Pro Tyr Leu Thr Gly Leu Ile Ser Ser Val Leu
130           135           140
Arg Pro Gly Ala Leu Thr Pro Leu Gln Arg Phe Arg Ser Leu Gln Gln
145           150           155           160
Ser Phe Leu Cys Cys Ala Phe Val Ile Ala Leu Gly Gly Gly Cys Phe
165           170           175
Leu Leu Thr Ala Leu Tyr Leu Glu Arg Asp Glu Thr Arg Ala Trp Gln
180           185           190
Pro Val Thr Gly Thr Pro Asp Ser Asn Asp Val Asp Ser Asn Asp Leu
195           200           205
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<210> 3225

<211> 506

<212> DNA

<213> Homo sapiens

<400> 3225

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240
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300
aagtggaacc acagcctcaa cccacacaga ggatggaacc acctcttgca gctaaaaata
360
accacaccgc ctttgaggtg agccacccaa gatgcaggtg gggctgtatg aaactccacg
420

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aacatgggat gagtttcatt ttcaggggttc cgagggggcca tgagtgggtac caagatccct
 480
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 506

<210> 3226

<211> 137

<212> PRT

<213> Homo sapiens

<400> 3226

Met	Lys	Val	Ile	Phe	Pro	Lys	Leu	Lys	Gln	Arg	Asn	Ile	Leu	Asn	Gly
1				5				10					15		
Leu	Arg	Pro	Cys	Thr	Phe	Phe	Ile	Gln	Glu	Ala	Thr	Lys	Asn	Ser	Ala
			20					25				30			
Cys	Phe	Pro	Val	Pro	Lys	Met	Pro	Val	Pro	Cys	Ala	Leu	Gly	Glu	Glu
			35				40				45				
Leu	Val	Pro	Cys	His	Arg	Gly	Thr	Gly	Pro	Ala	Val	Val	Trp	Pro	Ala
			50			55				60					
Gln	Pro	Gln	Gln	Gly	Glu	Val	Glu	Pro	Gln	Pro	Gln	Pro	Thr	Gln	Arg
65				70				75					80		
Met	Glu	Pro	Pro	Ser	Ala	Ala	Lys	Asn	Asn	His	Thr	Ala	Phe	Glu	Val
				85				90					95		
Ser	His	Pro	Arg	Cys	Arg	Trp	Gly	Cys	Met	Lys	Leu	His	Glu	His	Gly
			100				105				110				
Met	Ser	Phe	Ile	Phe	Arg	Val	Pro	Arg	Gly	His	Glu	Trp	Tyr	Gln	Asp
		115				120					125				
Pro	Trp	Arg	Cys	Pro	Trp	Phe	Pro	Met							
		130				135									

<210> 3227

<211> 1623

<212> DNA

<213> Homo sapiens

<400> 3227

nngtgtaggg gtagatttcc gctgcagtg tccccagacc tgtagtagcgc agcgcccggg
 60
 agactgagag aggaaggat agaggaagtg ctgccctagg ctgcatgagt cgaagcaagc
 120
 gtgtttcctt ccgcaccagg aagtgccctt agaaaccggg ccccgccccc ttcttgccct
 180
 gcattcccat cccctctccc gggcgaggagg tgaggacctc cttggttctct ttggttctgt
 240
 cagtgcagccc cttccttgcc catgaagctc gtgaggaaga acatcgagaa ggacaatgag
 300
 ggccagggtga ccctggtccc cgaggagcct gaggacatgt ggcacacctta caacctcggtg
 360
 caggtggggcg acagcctgag cgcctccacc atccgcaagg tacagacaga gtcctccagc
 420
 ggcagcgtgg gcagcaaccg ggtccgcact accctcactc tctgcgtgga ggccatcgac
 480
 ttgcactctc aagcctgcca gctgcggggt aaggggacca acatccaaga gaatgagtat
 540

gtcaagatgg gggcttacca caccatcgag ctggagccca accgccagtt caccctggcc
 600
 aagaagcagt gggatagtgt ggtactggag cgcacgcagc aggcctgtga cccagcctgg
 660
 agcgcctgatg tggcggctgt ggtcatgcag gaaggcctcg cccatatctg cttagtcaat
 720
 cccagcatga cccctactcg ggccaagggt gaggtgaaca tccctaggaa aaggaaaggc
 780
 aattgtcttc agcatgaccg ggccttggag cggttctatg aacagggtgt ccagggtatc
 840
 cagcgccaca tacactttga tgttgtaaaag tgcacccctgg tggccagccc aggatttgtg
 900
 agggagcagt tctgcgacta catgtttcaa caagcagtga agaccgacaa caaactgctc
 960
 ctggaaaacc ggtccaaatt tcttcaggta catgcctcct ccggacacaa gtactccctg
 1020
 aaagaggccc tttgtgaccc tactgtggct agccgccttt cagacacata agctgctggg
 1080
 gaagtcaaaag ccttggtatga cttctataaa atgttacagc atgaaccgga tcgagctttc
 1140
 tatggactca agcagggtga gaaggccaat gaagccatgg caattgacac attgctcatc
 1200
 agcgatgagc tcttcaggca tcaggatgta gccacacgga gccggtatgt gaggctgggtg
 1260
 gacagtgtga aagagaatgc aggcaccgtt aggatattct ctagtcttca cgtttctggg
 1320
 gaacagctca gccagttgac tggggtagct gccattctcc gcttccctgt tcccgaactt
 1380
 tctgaccaag aggggtgattc cagtctctga gaggattaat gattgaaact taaaattgag
 1440
 acaatcttgt gtttcctaaa ctgttacagt acatttctca gcacccctgt gacagaaagc
 1500
 tgcaagaatg gcactttttg attcatacag ggatttctta tgtctttggc tacactagat
 1560
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 1620
 aaa
 1623

<210> 3228

<211> 385

<212> PRT

<213> Homo sapiens

<400> 3228

Met	Lys	Leu	Val	Arg	Lys	Asn	Ile	Glu	Lys	Asp	Asn	Ala	Gly	Gln	Val
1				5				10					15		
Thr	Leu	Val	Pro	Glu	Glu	Pro	Glu	Asp	Met	Trp	His	Thr	Tyr	Asn	Leu
			20					25					30		
Val	Gln	Val	Gly	Asp	Ser	Leu	Arg	Ala	Ser	Thr	Ile	Arg	Lys	Val	Gln
		35				40					45				
Thr	Glu	Ser	Ser	Thr	Gly	Ser	Val	Gly	Ser	Asn	Arg	Val	Arg	Thr	Thr
	50				55				60						
Leu	Thr	Leu	Cys	Val	Glu	Ala	Ile	Asp	Phe	Asp	Ser	Gln	Ala	Cys	Gln

```

65              70              75              80
Leu Arg Val Lys Gly Thr Asn Ile Gln Glu Asn Glu Tyr Val Lys Met
85              90              95
Gly Ala Tyr His Thr Ile Glu Leu Glu Pro Asn Arg Gln Phe Thr Leu
100             105             110
Ala Lys Lys Gln Trp Asp Ser Val Val Leu Glu Arg Ile Glu Gln Ala
115             120             125
Cys Asp Pro Ala Trp Ser Ala Asp Val Ala Ala Val Val Met Gln Glu
130             135             140
Gly Leu Ala His Ile Cys Leu Val Thr Pro Ser Met Thr Leu Thr Arg
145             150             155             160
Ala Lys Val Glu Val Asn Ile Pro Arg Lys Arg Lys Gly Asn Cys Ser
165             170             175
Gln His Asp Arg Ala Leu Glu Arg Phe Tyr Glu Gln Val Val Gln Ala
180             185             190
Ile Gln Arg His Ile His Phe Asp Val Val Lys Cys Ile Leu Val Ala
195             200             205
Ser Pro Gly Phe Val Arg Glu Gln Phe Cys Asp Tyr Met Phe Gln Gln
210             215             220
Ala Val Lys Thr Asp Asn Lys Leu Leu Leu Glu Asn Arg Ser Lys Phe
225             230             235             240
Leu Gln Val His Ala Ser Ser Gly His Lys Tyr Ser Leu Lys Glu Ala
245             250             255
Leu Cys Asp Pro Thr Val Ala Ser Arg Leu Ser Asp Thr Lys Ala Ala
260             265             270
Gly Glu Val Lys Ala Leu Asp Asp Phe Tyr Lys Met Leu Gln His Glu
275             280             285
Pro Asp Arg Ala Phe Tyr Gly Leu Lys Gln Val Glu Lys Ala Asn Glu
290             295             300
Ala Met Ala Ile Asp Thr Leu Leu Ile Ser Asp Glu Leu Phe Arg His
305             310             315             320
Gln Asp Val Ala Thr Arg Ser Arg Tyr Val Arg Leu Val Asp Ser Val
325             330             335
Lys Glu Asn Ala Gly Thr Val Arg Ile Phe Ser Ser Leu His Val Ser
340             345             350
Gly Glu Gln Leu Ser Gln Leu Thr Gly Val Ala Ala Ile Leu Arg Phe
355             360             365
Pro Val Pro Glu Leu Ser Asp Gln Glu Gly Asp Ser Ser Ser Glu Glu
370             375             380

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Asp
385

<210> 3229
<211> 1008
<212> DNA
<213> Homo sapiens

<400> 3229
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cctgcactgg gcgcgcgaga gctgctaggg cggtttctct gcctcgggcc tgttgggcag
120
ggccggctaa ggtgcgcgtg ctgcgtggtt ctaacccttc tgttgggcgt ttctgctgag
180

```

aggcgggagg cgctgagagt ctgtgcggag gtccgtggac agactgcttt gctcgttggt
240
gtctctcgga ggcgcgatc ccgaagcg agctgaaata cggtgcagg ctacaatttg
300
cagccgacca ttatggaaga cggaagcgg gagaggtggc ccacctcat ggagcgcttg
360
tgctcgatg gttcgcatt tcccaatac ccattaaac cgtatcatct gaagaggatc
420
cacagagctg tttactgtg taatctggag gaactgaagt acctctctgt cacgtattat
480
gacatcaata agagagacag gaaggaaagg accgccctac atttggcctg tgccactggc
540
caaccggaaa tggtagatct cctggtgtcc agaagatgtg agcttaacct ctgcgaccgt
600
gaagacagga cacctctgat caagcgtgta caactgaggc aggaggcttg tgcaactctt
660
ctgctgcaaa atggcgccga tccaaatatt acggatgtct ttggaaggac tgctctgcac
720
tacgctgtgt ataatgaaga tacatccatg atagaaaaac ttctttcaca tggtagaaat
780
attgaagaat gcagcaagaa tgaatatcag cactgtttac ttgctgtgag tgaagaaaa
840
gtgaaaatgg tggatttttt attaaagaaa aaagcaaatg taaatgccat tgattatctt
900
ggcagatcag cctcatact tgctgttact ctggagaaaa aagatatagt cattctcttt
960
ctgcagcaca atattgatgt gttttctcga gatgtgatg gaaagctt
1008

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<210> 3230

<211> 232

<212> PRT

<213> Homo sapiens

<400> 3230

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Met Glu Asp Gly Lys Arg Glu Arg Trp Pro Thr Leu Met Glu Arg Leu
1      5      10      15
Cys Ser Asp Gly Phe Ala Phe Pro Gln Tyr Pro Ile Lys Pro Tyr His
20     25     30
Leu Lys Arg Ile His Arg Ala Val Leu Arg Gly Asn Leu Glu Glu Leu
35     40     45
Lys Tyr Leu Leu Leu Thr Tyr Tyr Asp Ile Asn Lys Arg Asp Arg Lys
50     55     60
Glu Arg Thr Ala Leu His Leu Ala Cys Ala Thr Gly Gln Pro Glu Met
65     70     75     80
Val His Leu Leu Val Ser Arg Arg Cys Glu Leu Asn Leu Cys Asp Arg
85     90     95
Glu Asp Arg Thr Pro Leu Ile Lys Ala Val Gln Leu Arg Gln Glu Ala
100    105    110
Cys Ala Thr Leu Leu Leu Gln Asn Gly Ala Asp Pro Asn Ile Thr Asp
115    120    125
Val Phe Gly Arg Thr Ala Leu His Tyr Ala Val Tyr Asn Glu Asp Thr
130    135    140
Ser Met Ile Glu Lys Leu Leu Ser His Gly Thr Asn Ile Glu Glu Cys

```

145		150		155		160									
Ser	Lys	Asn	Glu	Tyr	Gln	Pro	Leu	Leu	Leu	Ala	Val	Ser	Arg	Arg	Lys
				165					170					175	
Val	Lys	Met	Val	Glu	Phe	Leu	Leu	Lys	Lys	Ala	Asn	Val	Asn	Ala	
				180					185				190		
Ile	Asp	Tyr	Leu	Gly	Arg	Ser	Ala	Leu	Ile	Leu	Ala	Val	Thr	Leu	Gly
				195					200				205		
Glu	Lys	Asp	Ile	Val	Ile	Leu	Leu	Leu	Gln	His	Asn	Ile	Asp	Val	Phe
				210					215				220		
Ser	Arg	Asp	Val	Tyr	Gly	Lys	Leu								
225					230										

<210> 3231

<211> 1367

<212> DNA

<213> Homo sapiens

<400> 3231

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nnacgcgtga aggggaagtt tcgcctcaga aggcgcctc gctggtccga attcggtggc
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gccacgtccg ccgcgtccg cctcttgcac cgcggtctcg gcggcttcca cctagacacc
120
taacagtgcg ggagccggcc gcgtcgtgag ggggtcggca cggggagtgc ggcggtcttg
180
tgcatcttgg ctacctgtgg gtccaagatg tcggacatcg gagactgggt caggagcatc
240
ccggcgatca cgcgtattg gttcgcgcgc accgtgcgcg tgcccttggt cgggcaaac
300
ggcctcatca gcccgcccta cctcttcttc tggcccgaa ccttcttcta tcgctttcag
360
atttggaggc caatcactgc caccttttat ttccctgtgg gtccaggaac tggatttctt
420
tatttggcca atttatattt cttatatcag tattctacgc gacttgaaac aggagctttt
480
gatggggagg cagcagacta ttattcatg ctctcttcta actggatttg catcgtgatt
540
actggccttag caatggatat gcagttgctg atgattcttc tgatcatgtc agtactttat
600
gtctggggccc agctgaacag agacatgatt gtatcatttt ggtttggaac acgatttaag
660
gctcgtattt taccctgggt tacccttgga ttcaactata tcacggagg ctcggtaata
720
aatgagctta ttggaatctt ggttggacat ctttattttt tcctaattgt cagataccca
780
atggacttgg gaggaagaaa tttctatccc acacctcagt ttttgtaccg ctggctgccc
840
agtaggagag gaggagtatc aggatttggg gtgccccctg ctacgatgag gcgagctgct
900
gatcagaatg gcggaggcgg gagacacaac tggggccagg gctttcgact tggagaccag
960
tgaaggggcg gcctcgggca gccgtctctc tcaagccaca tttctctcca gtgctgggtg
1020
cacttaacaa ctgcgttctg gctaacactg ttggacctga ccacactga atgtagtctt
1080

```

tcagtacgag acaaagtctt ttaaatcccg aagaaaaata taagtgtcc acaagtcttca
 1140
 cgattctcat tcaagtcctt actgctgtga agaacaaata ccaactgtgc aaattgcгаа
 1200
 actgactaca ttttttggtg tttttttttt tcccccttcc gttctgaata atgggttttta
 1260
 gcgggtccta gtctgctggc attgagctgg ggctgggtca ccaaaccctt cccaaaagga
 1320
 cccttatctc tttcttgac acatgctct ctccccctt cagcgcg
 1367

<210> 3232

<211> 251

<212> PRT

<213> Homo sapiens

<400> 3232

Met	Ser	Asp	Ile	Gly	Asp	Trp	Phe	Arg	Ser	Ile	Pro	Ala	Ile	Thr	Arg
1			5						10					15	
Tyr	Trp	Phe	Ala	Ala	Thr	Val	Ala	Val	Pro	Leu	Val	Gly	Lys	Leu	Gly
			20					25					30		
Leu	Ile	Ser	Pro	Ala	Tyr	Leu	Phe	Leu	Trp	Pro	Glu	Ala	Phe	Leu	Tyr
		35					40					45			
Arg	Phe	Gln	Ile	Trp	Arg	Pro	Ile	Thr	Ala	Thr	Phe	Tyr	Phe	Pro	Val
		50				55				60					
Gly	Pro	Gly	Thr	Gly	Phe	Leu	Tyr	Leu	Val	Asn	Leu	Tyr	Phe	Leu	Tyr
65					70					75				80	
Gln	Tyr	Ser	Thr	Arg	Leu	Glu	Thr	Gly	Ala	Phe	Asp	Gly	Arg	Pro	Ala
			85					90						95	
Asp	Tyr	Leu	Phe	Met	Leu	Leu	Phe	Asn	Trp	Ile	Cys	Ile	Val	Ile	Thr
			100					105					110		
Gly	Leu	Ala	Met	Asp	Met	Gln	Leu	Leu	Met	Ile	Pro	Leu	Ile	Met	Ser
		115					120					125			
Val	Leu	Tyr	Val	Trp	Ala	Gln	Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe
		130				135					140				
Trp	Phe	Gly	Thr	Arg	Phe	Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu
145					150					155				160	
Gly	Phe	Asn	Tyr	Ile	Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly
			165					170					175		
Asn	Leu	Val	Gly	His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met
			180					185					190		
Asp	Leu	Gly	Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg
		195				200						205			
Trp	Leu	Pro	Ser	Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro
	210					215					220				
Ala	Ser	Met	Arg	Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His
225					230					235					240
Asn	Trp	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Asp	Gln					
			245						250						

<210> 3233

<211> 975

<212> DNA

<213> Homo sapiens

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<400> 3233
naccggtacg tgggtggagct ctgcgtgttt actatttttg gaaatgaaga aaatggaaag
60
accgttggtt accttggtggc ttcccatctg ttctttgtta tgtttgtatg gtcctattgg
120
atgacaattt tcacatctcc cgcttcccc tccaaagagt tctactgtgc caattctgaa
180
aagggaacgt atgaaaaaga attcagccaa gaaagacaac aagaaatttt gagaagagca
240
gcaagagctt tacctatcta taccacatca gcttcaaaaa ctatcagata ttgtgaaaaa
300
tgtcagctga ttaaacctga tcgggcgcac cactgctcag cctgtgactc atgtattctt
360
aagatggatc atccctgtcc ttgggtgaat aactgtgtgg gattttctaa ttacaaattc
420
ttcctgctgt tttattgtta ttccctatta tattgccttt tcgtggccgc acagttttag
480
agtacttaaa aaatttttga cgaagaacac gacaaaaacc cgggccaaaa ttccacgtac
540
ttttttcttt tctttgtgtc tgcaatgttc ttcatcagcg tcctctcact tttcagctac
600
cactgctggc tttaaacagc attgtccaca gctccgtctg cagggtcagg gcatggcctc
660
tctccgtgtt cctgtgaaga gccttcattg gaatcatccc gggacatata gcttgaatgt
720
gctgtctggc tagccctccc acaagtcggt cactctgcac aagggaatccg agagctcatc
780
aaggatcagc acggtctggg gccaggtgg ggtggaacac gcacggtcca caagcaattc
840
tgtctttctc aaggcttttt cttgtgcagt atgaaatcct tcataattca tatgaagtat
900
gtgcctcttg gggcactgag ctcagggaact ccaaaaagac cccttcgggc cggatcccg
960
cttcaaggct gcccc
975

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<210> 3234

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3234

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Xaa Ala Tyr Val Val Glu Leu Cys Val Phe Thr Ile Phe Gly Asn Glu
1          5          10          15
Glu Asn Gly Lys Thr Val Val Tyr Leu Val Ala Phe His Leu Phe Phe
20          25          30
Val Met Phe Val Trp Ser Tyr Trp Met Thr Ile Phe Thr Ser Pro Ala
35          40          45
Ser Pro Ser Lys Glu Phe Tyr Leu Ser Asn Ser Glu Lys Glu Arg Tyr
50          55          60
Glu Lys Glu Phe Ser Gln Glu Arg Gln Gln Glu Ile Leu Arg Arg Ala
65          70          75          80
Ala Arg Ala Leu Pro Ile Tyr Thr Thr Ser Ala Ser Lys Thr Ile Arg

```

	85		90		95
Tyr Cys Glu Lys Cys Gln Leu Ile Lys Pro Asp Arg Ala His His Cys					
	100		105		110
Ser Ala Cys Asp Ser Cys Ile Leu Lys Met Asp His Pro Cys Pro Trp					
	115		120		125
Val Asn Asn Cys Val Gly Phe Ser Asn Tyr Lys Phe Phe Leu Leu Phe					
	130		135		140
Leu Leu Tyr Ser Leu Leu Tyr Cys Leu Phe Val Ala Ala Gln Phe					
145	150		155		

<210> 3235

<211> 551

<212> DNA

<213> Homo sapiens

<400> 3235

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ntggaaactg agcttcaaac atataagcat tctcgtcagg ggctagatga aatgtacaat
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gaagccagaa ggagccttcg agatgaatct cagttacgac aggatgtaga gaatgaagcta
120
gcagtacaag ttagtatgaa gcatgagatt gaacttgcca tgaagtgtct ggagaaaagat
180
atccatgaga aacaagatag tctgataggc ctctgcacaac aactagagga agttaaagca
240
attaacatag agatgtatca aaagttgcag gggtctgaag atggccttgaa agaaaaaaat
300
gaaataattg ccgactaga agaaaaaac aataaaatta ctgcagccat gaggcagctg
360
gaacaaagat tgacgaagc agagaaggcg caaatggaag ctgaagatga ggatgagaaa
420
tatctacaag aatgtctcag taaatctgat agtctgcaga acaaatctc ccaaaaggag
480
aaacagctgg tgcaactgga aactgacttg aagattgaga aggaatggag gcagactttg
540
caggaagatc t
551

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<210> 3236

<211> 183

<212> PRT

<213> Homo sapiens

<400> 3236

Xaa Glu Thr Glu Leu Gln Thr Tyr Lys His Ser Arg Gln Gly Leu Asp					
1	5		10		15
Glu Met Tyr Asn Glu Ala Arg Arg Gln Leu Arg Asp Glu Ser Gln Leu					
	20		25		30
Arg Gln Asp Val Glu Asn Glu Leu Ala Val Gln Val Ser Met Lys His					
	35		40		45
Glu Ile Glu Leu Ala Met Lys Leu Leu Glu Lys Asp Ile His Glu Lys					
	50		55		60
Gln Asp Thr Leu Ile Gly Leu Arg Gln Gln Leu Glu Glu Val Lys Ala					
65	70		75		80
Ile Asn Ile Glu Met Tyr Gln Lys Leu Gln Gly Ser Glu Asp Gly Leu					

	85		90		95										
Lys	Glu	Lys	Asn	Glu	Ile	Ile	Ala	Arg	Leu	Glu	Glu	Lys	Thr	Asn	Lys
	100		105		110										
Ile	Thr	Ala	Ala	Met	Arg	Gln	Leu	Glu	Gln	Arg	Leu	Gln	Gln	Ala	Glu
	115		120		125										
Lys	Ala	Gln	Met	Glu	Ala	Glu	Asp	Glu	Lys	Tyr	Leu	Gln	Glu		
	130		135		140										
Cys	Leu	Ser	Lys	Ser	Asp	Ser	Leu	Gln	Lys	Gln	Ile	Ser	Gln	Lys	Glu
	145		150		155									160	
Lys	Gln	Leu	Val	Gln	Leu	Glu	Thr	Asp	Leu	Lys	Ile	Glu	Lys	Glu	Trp
	165		170		175										
Arg	Gln	Thr	Leu	Gln	Glu	Asp									
	180														

<210> 3237

<211> 1323

<212> DNA

<213> Homo sapiens

<400> 3237

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cgggcgctgt ggaccatggc tccgcccgcg gcgcctggcc gggacogctgt gggccgtgag
120
gatgaggacc gttgggaagt acggggggac cgcaaggccc ggaagccctt ggtggagaag
180
aagcgacgcg gcgcgatcaa cgagagtctt caggagtgc ggtcgtctgt ggcggggcgc
240
gaggtgcagg ccaagctgga gaacgccgaa gtgctggagc tgacggtgcg gcgggtccag
300
ggtgtgctgt gggggccggc gcgcgagcgc gacgagctgc aggcggaagc gagcgagcgc
360
ttcgctgccg gctacatcca gtgcatgcac gagggtgcaca cgttcgtgtc cacgtgccag
420
gccatcgacg ctaccgtcgc tgcgagctgc ctgaaccatc tgctcgagtc catgcccgtg
480
cgtgagggca gcagcttcca ggatctgctg ggggacgccc tggcggggccc acctagagcc
540
cctggacgga gtggttgccc tgcggggggc gctccgggat ccccaatacc cagcccccg
600
ggtcctgggg acgacctgtg ctccgacctg gaggaggccc ctgaggctga actgagtcag
660
gctcctgctg agggggcccga cttggtgccc gcagccctgg gcagcctgac cacagcccaa
720
attgcccgga gtgtctggag gccttggtga ccaatgccag ccagagtctt gcgggggttg
780
gccggccct ccttgatct cctccctct cccaggggtt cagatgtggt ggggtagggc
840
cctggaagtc tccaggtct tcctccctc ctctgatgga tggcttgtag ggcagccct
900
ggtaaccagc ccagtcaggc ccagccccc ttcttaaga aacttttagg gacctgcag
960
ctctggagtg ggtggaggga gggagctacg ggcaggagga agaattttgt agagctgcca
1020

```


gcgctctccc aggttcaccc acccaggctt caccagccct gtgcgggctc tgggggcaga
 1080
 ggtggcagaa atggtgctgg gcactagtgt tccaggcagc cctgggctaa acaaaagctt
 1140
 gaacttgcca cttcagcggg gagatgagag gcaggtgcac tcagctgcac tgcccagagc
 1200
 tgtgatgctc tgtacatctt gttttagca cacttgagtt tgtgtattcc attgacatca
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 1320
 acg
 1323

<210> 3238

<211> 249

<212> PRT

<213> Homo sapiens

<400> 3238

Xaa	Leu	Gly	Cys	Asp	Leu	Pro	Arg	Arg	Gly	Val	Cys	Thr	Lys	Ala	Leu
1			5						10					15	
Gly	Ala	Gly	Leu	Arg	Ala	Leu	Trp	Thr	Met	Ala	Pro	Pro	Ala	Ala	Pro
			20						25				30		
Gly	Arg	Asp	Arg	Val	Gly	Arg	Glu	Asp	Glu	Asp	Arg	Trp	Glu	Val	Arg
		35					40					45			
Gly	Asp	Arg	Lys	Ala	Arg	Lys	Pro	Leu	Val	Glu	Lys	Lys	Arg	Arg	Ala
		50				55					60				
Arg	Ile	Asn	Glu	Ser	Leu	Gln	Glu	Leu	Arg	Leu	Leu	Leu	Ala	Gly	Ala
65					70					75				80	
Glu	Val	Gln	Ala	Lys	Leu	Glu	Asn	Ala	Glu	Val	Leu	Glu	Leu	Thr	Val
				85					90					95	
Arg	Arg	Val	Gln	Gly	Val	Leu	Arg	Gly	Arg	Ala	Arg	Glu	Arg	Glu	Gln
			100					105					110		
Leu	Gln	Ala	Glu	Ala	Ser	Glu	Arg	Phe	Ala	Ala	Gly	Tyr	Ile	Gln	Cys
		115				120						125			
Met	His	Glu	Val	His	Thr	Phe	Val	Ser	Thr	Cys	Gln	Ala	Ile	Asp	Ala
		130				135						140			
Thr	Val	Ala	Ala	Glu	Leu	Leu	Asn	His	Leu	Leu	Glu	Ser	Met	Pro	Leu
145					150					155				160	
Arg	Glu	Gly	Ser	Ser	Phe	Gln	Asp	Leu	Leu	Gly	Asp	Ala	Leu	Ala	Gly
			165					170					175		
Pro	Pro	Arg	Ala	Pro	Gly	Arg	Ser	Gly	Trp	Pro	Ala	Gly	Gly	Ala	Pro
			180					185					190		
Gly	Ser	Pro	Ile	Pro	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Asp	Leu	Cys	Ser
		195				200						205			
Asp	Leu	Glu	Glu	Ala	Pro	Glu	Ala	Glu	Leu	Ser	Gln	Ala	Pro	Ala	Glu
		210				215					220				
Gly	Pro	Asp	Leu	Val	Pro	Ala	Ala	Leu	Gly	Ser	Leu	Thr	Thr	Ala	Gln
					230					235				240	
Ile	Ala	Arg	Ser	Val	Trp	Arg	Pro	Trp							
				245											

<210> 3239

<211> 432

<212> DNA

<213> Homo sapiens

<400> 3239

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agaaaacttg tgagaaataa gctggcagtg attacgcgtc tccttcagaa tctgatcatg
120
ggtttgttcc tccttttctt cgttctgcgg gtccgaagca atgtgctaaa ggggtctatc
180
caggaccgcg taggtctcct ttaccagttt gtgggcgcca ccccgtagac aggcagctg
240
aacgctgtga atctgtttcc cgtgctgcga gctgtcagcg accaggagag tcaggacggc
300
ctctaccaga agtggcagat gatgctggcc tatgctactgc acgtcctccc cttcagcggt
360
gttgccacca tgattttcag cagtgtgtgc tactggagcg tgggcttaca tctgagggtt
420
gccccgattg gt
432

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<210> 3240

<211> 144

<212> PRT

<213> Homo sapiens

<400> 3240

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Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu Gly Val Leu Leu
1      5      10      15
Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu Ala Val Ile Thr
20     25     30
Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu Leu Phe Val
35     40     45
Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile Gln Asp Arg Val
50     55     60
Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Tyr Thr Gly Met Leu
65     70     75     80
Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val Ser Asp Gln Glu
85     90     95
Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met Leu Ala Tyr Ala
100    105    110
Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met Ile Phe Ser Ser
115    120    125
Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val Ala Arg Leu Gly
130    135    140

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<210> 3241

<211> 492

<212> DNA

<213> Homo sapiens

<400> 3241

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gtggaatttt tttagacaaa gtctcaaaaa acaaacaaac aaacaaaagg taagataaat
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acgaaatata aaataagagg caggaagagc ccaaagcatc agaaatgtgc cagttataat
 120
 gggccaaaaat cccctcttgt gtctccagaa gtatttgaaa aatacgtag gatctgcctc
 180
 acagacatgc tcccaggaca ctgcacagca aggaggtag gcgggcccag ccagccaagg
 240
 cagaggagga catcactgcc acagcagggg gcctgactgg cagcaaaagg gacgactccg
 300
 gcgaaaagtc agcaggaaac aggacagggg ctggaccaat ggcctccctc agccccacac
 360
 cccacccagg caggagcggg gcctggcccg gggcaggcgg gtgggagagc tcaactgagt
 420
 ggcagcagg catggccct gatgctgcag gtaccaggc tgcagctgca gaaacctcag
 480
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 492

<210> 3242

<211> 107

<212> PRT

<213> Homo sapiens

<400> 3242

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Leu	Gly	Ser	Ala	Ser	Gln	Thr	Cys	Ser	Gln	Asp	Thr	Arg	Gln	Gln	Gly
			20					25					30		
Gly	Thr	Ala	Gly	Pro	Ala	Ser	Gln	Gly	Arg	Gly	Gly	His	His	Cys	His
		35				40					45				
Ser	Arg	Gly	Pro	Asp	Trp	Gln	Gln	Lys	Gly	Arg	Leu	Arg	Arg	Lys	Val
50					55					60					
Ser	Arg	Lys	Gln	Asp	Arg	Gly	Trp	Thr	Asn	Gly	Leu	Pro	Gln	Pro	His
65				70				75					80		
Thr	Pro	Pro	Arg	Gln	Glu	Arg	Cys	Leu	Ala	Arg	Gly	Arg	Arg	Val	Gly
			85					90						95	
Glu	Leu	Thr	Glu	Trp	Ala	Ala	Gly	His	Gly	Pro					
			100					105							

<210> 3243

<211> 944

<212> DNA

<213> Homo sapiens

<400> 3243

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 120
 tttagagcaa aggtaaccca gaatctccca atgaaagaag gctgcacaga ggtctctctc
 180
 cttcgagttg ggtggtctgt tgatttttcc cgtccacagc ttggtgaaga tgaattctct
 240
 tacggtttcg atggacgagg actcaaggca gaaaatggac aatttgagga atttggccag
 300

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acttttgggg agaagatgtg tattggctgc ttgctaatt ttgagactga agaagtagaa
360
ctttccttct ccaagaatgg agaagaccta ggtgtggcat tctggatcag caaggattcc
420
ctggcagacc gggcccttct accccatgtc ctctgcaaaa attgtgttgt agaattaaac
480
ttcgggtcaga aggaggagccc cttcttccca ccaccagaag agtttgtgtt cattcatgct
540
gtgcctgttg aggagcgtgt acgcactgca gtccctccca agaccataga ggaatgtgag
600
gtgattctga tgggtgggact acccggtatct ggaaagaccc agtgggcact gaaatatgca
660
aaagaaaacc ctgagaaaag atacaatgtc ctgggagctg agactgtgct caatcaaatg
720
aggatgaagg gtctcgagga gccagagatg gaccccaaaa gcgcagacct tttagttcag
780
caagcctccc agtgccttag taagctggtc cagattgctt cccggacaaa gaggaacttt
840
attcttgatc agtghtaatgt gtacaattct ggccaacggc ggaagctatt gctgttcaag
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944

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<210> 3244

<211> 314

<212> PRT

<213> Homo sapiens

<400> 3244

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Asp Leu His Phe Gln Val Ser Lys Asp Arg Tyr Gly Gly Gln Pro Leu
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Phe Ser Glu Lys Phe Pro Thr Leu Trp Ser Gly Ala Arg Ser Thr Tyr
      20      25      30
Gly Val Thr Lys Gly Lys Val Cys Phe Glu Ala Lys Val Thr Gln Asn
      35      40      45
Leu Pro Met Lys Glu Gly Cys Thr Glu Val Ser Leu Leu Arg Val Gly
      50      55      60
Trp Ser Val Asp Phe Ser Arg Pro Gln Leu Gly Glu Asp Glu Phe Ser
65      70      75      80
Tyr Gly Phe Asp Gly Arg Gly Leu Lys Ala Glu Asn Gly Gln Phe Glu
      85      90      95
Glu Phe Gly Gln Thr Phe Gly Glu Asn Asp Val Ile Gly Cys Phe Ala
      100      105      110
Asn Phe Glu Thr Glu Glu Val Glu Leu Ser Phe Ser Lys Asn Gly Glu
      115      120      125
Asp Leu Gly Val Ala Phe Trp Ile Ser Lys Asp Ser Leu Ala Asp Arg
130      135      140
Ala Leu Leu Pro His Val Leu Cys Lys Asn Cys Val Val Glu Leu Asn
145      150      155      160
Phe Gly Gln Lys Glu Glu Pro Phe Phe Pro Pro Pro Glu Glu Phe Val
      165      170      175
Phe Ile His Ala Val Pro Val Glu Glu Arg Val Arg Thr Ala Val Pro
      180      185      190
Pro Lys Thr Ile Glu Glu Cys Glu Val Ile Leu Met Val Gly Leu Pro

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	195		200		205	
Gly Ser Gly Lys Thr Gln Trp Ala Leu Lys Tyr Ala Lys Glu Asn Pro						
210		215		220		
Glu Lys Arg Tyr Asn Val Leu Gly Ala Glu Thr Val Leu Asn Gln Met						
225	230		235		240	
Arg Met Lys Gly Leu Glu Glu Pro Glu Met Asp Pro Lys Ser Arg Asp						
	245		250		255	
Leu Leu Val Gln Gln Ala Ser Gln Cys Leu Ser Lys Leu Val Gln Ile						
	260		265		270	
Ala Ser Arg Thr Lys Arg Asn Phe Ile Leu Asp Gln Cys Asn Val Tyr						
	275		280		285	
Asn Ser Gly Gln Arg Arg Lys Leu Leu Leu Phe Lys Thr Phe Ser Arg						
	290		295		300	
Lys Val Val Val Val Val Pro Asn Glu Glu						
305		310				

<210> 3245

<211> 980

<212> DNA

<213> Homo sapiens

<400> 3245

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 120
 ccaaccacag agggcctctg agagacaagg tacatcccat gattctagca caggaagaag
 180
 acgacgtcct gggagaggaa gcacaaggca gcccgcacga tatcatcaga atagggtgtg
 240
 cggggcgccc tgctcctggc agactacatc ctgttcggac aggacctctt ccgaggatgt
 300
 acagcgctgg agctcggggc cggcacgggg ctgcgtagca tcatcgcagc caccatggca
 360
 cggaccgttt attgtacaga tgctgggtgca gatcttttgt ccatgtgccca gogaacatt
 420
 gccctcaaca gccacctggc tgccactgga ggtggtatag ttaggggtcaa agaactggac
 480
 tggctgaagg acgacctctg cacagatccc aaggctccct tcagttggtc acaagaggaa
 540
 atttctgacc tgtacgatca caccaccatc ctgtttgcag ccgaagtgtt ttacgacgac
 600
 gacttgactg atgctgtgtt taaaacgctc tcccgaactc cccacagatt gaaaaatgcc
 660
 tgcacagcca tactgtcggt ggagaagagg ctcaacttca cactgagaca cttggacgtc
 720
 acatgtgaag cctacgatca ctccgctcc tgccctgcag cgctggagca gctcacagat
 780
 ggcaagctgc gcttcgtggt ggagcccggt gaggcctcct tcccacagct cctggtttac
 840
 gagcgctctc agcagctgga gctctggaag atcatcgag aaccagtaac atgaccatc
 900
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 960

ctcaccaaag caaaaaaaaaa
980

<210> 3246

<211> 219

<212> PRT

<213> Homo sapiens

<400> 3246

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Val Trp Arg Gly Ala Leu Leu Leu Ala Asp Tyr Ile Leu Phe Arg Gln
 1           5           10           15
Asp Leu Phe Arg Gly Cys Thr Ala Leu Glu Leu Gly Ala Gly Thr Gly
 20           25           30
Leu Ala Ser Ile Ile Ala Ala Thr Met Ala Arg Thr Val Tyr Cys Thr
 35           40           45
Asp Val Gly Ala Asp Leu Leu Ser Met Cys Gln Arg Asn Ile Ala Leu
 50           55           60
Asn Ser His Leu Ala Ala Thr Gly Gly Gly Ile Val Arg Val Lys Glu
 65           70           75           80
Leu Asp Trp Leu Lys Asp Asp Leu Cys Thr Asp Pro Lys Val Pro Phe
 85           90           95
Ser Trp Ser Gln Glu Glu Ile Ser Asp Leu Tyr Asp His Thr Thr Ile
100           105           110
Leu Phe Ala Ala Glu Val Phe Tyr Asp Asp Leu Thr Asp Ala Val
115           120           125
Phe Lys Thr Leu Ser Arg Leu Ala His Arg Leu Lys Asn Ala Cys Thr
130           135           140
Ala Ile Leu Ser Val Glu Lys Arg Leu Asn Phe Thr Leu Arg His Leu
145           150           155           160
Asp Val Thr Cys Glu Ala Tyr Asp His Phe Arg Ser Cys Leu His Ala
165           170           175
Leu Glu Gln Leu Thr Asp Gly Lys Leu Arg Phe Val Val Glu Pro Val
180           185           190
Glu Ala Ser Phe Pro Gln Leu Leu Val Tyr Glu Arg Leu Gln Gln Leu
195           200           205
Glu Leu Trp Lys Ile Ile Ala Glu Pro Val Thr
210           215

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<210> 3247

<211> 977

<212> DNA

<213> Homo sapiens

<400> 3247

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120
agggttcaaca gcggcacgta taacaaccag tggatgatcg tggactacaa ggcgttcac
180
ccgggtgggc ccagccccgg gagccgggtg cttaccatcc tggagcagat ccccggcacg
240
gtggtggtgg ctgacaagac ctccgagctc taccagaaga cctactgggc cagctacaac
300

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ataccgtcct tcgagactgt gttcaatgcc agtgggctgc aggccctagt ggcccagtat
 360
 ggggactggt ttcttatga cgggagcccc cgggcccaga tcttccggcg gaaccagtca
 420
 ctgggtacaag acatggactc catggtcagg ctgatgaggt acaatgactt cctccatgac
 480
 cctctgtcac tgtgcaaagc ctgcaacccc cagcccaatg gggagaatgc tatctccgcc
 540
 cgctccgacc tcaacccggc caatggctcc taccctctcc aggcctacg tcagcgctcc
 600
 catgggggta tcgatgtgaa ggtgaccagc atgtcactgg ccagatctct gagcctgctg
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 720
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 840
 acccccgctc caagccacc ggacttctaa ctccagcccc tctctggggc ttcgtctctc
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 977

<210> 3248

<211> 260

<212> PRT

<213> Homo sapiens

<400> 3248

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Trp	Val	Arg	Asn	Ile	Val	Ala	Asn	Arg	Leu	Ala	Ser	Asp	Gly	Ala	Thr
			20					25					30		
Trp	Ala	Asp	Ile	Phe	Lys	Arg	Phe	Asn	Ser	Gly	Thr	Tyr	Asn	Asn	Gln
		35				40					45				
Trp	Met	Ile	Val	Asp	Tyr	Lys	Ala	Phe	Ile	Pro	Gly	Gly	Pro	Ser	Pro
	50					55				60					
Gly	Ser	Arg	Val	Leu	Thr	Ile	Leu	Glu	Gln	Ile	Pro	Gly	Met	Val	Val
	65				70				75					80	
Val	Ala	Asp	Lys	Thr	Ser	Glu	Leu	Tyr	Gln	Lys	Thr	Tyr	Trp	Ala	Ser
			85					90						95	
Tyr	Asn	Ile	Pro	Ser	Phe	Glu	Thr	Val	Phe	Asn	Ala	Ser	Gly	Leu	Gln
			100					105					110		
Ala	Leu	Val	Ala	Gln	Tyr	Gly	Asp	Trp	Phe	Ser	Tyr	Asp	Gly	Ser	Pro
		115					120					125			
Arg	Ala	Gln	Ile	Phe	Arg	Arg	Asn	Gln	Ser	Leu	Val	Gln	Asp	Met	Asp
	130					135				140					
Ser	Met	Val	Arg	Leu	Met	Arg	Tyr	Asn	Asp	Phe	Leu	His	Asp	Pro	Leu
	145				150				155					160	
Ser	Leu	Cys	Lys	Ala	Cys	Asn	Pro	Gln	Pro	Asn	Gly	Glu	Asn	Ala	Ile
			165					170					175		
Ser	Ala	Arg	Ser	Asp	Leu	Asn	Pro	Ala	Asn	Gly	Ser	Tyr	Pro	Phe	Gln

	180		185		190										
Ala	Leu	Arg	Gln	Arg	Ser	His	Gly	Ile	Asp	Val	Lys	Val	Thr	Ser	
	195		200		205										
Met	Ser	Leu	Ala	Arg	Ile	Leu	Ser	Leu	Leu	Ala	Ala	Ser	Gly	Pro	Thr
	210		215		220										
Trp	Asp	Gln	Val	Pro	Pro	Phe	Gln	Trp	Ser	Thr	Ser	Pro	Phe	Ser	Gly
	225		230		235									240	
Leu	Leu	His	Met	Gly	Gln	Pro	Asp	Leu	Trp	Lys	Phe	Ala	Pro	Val	Lys
			245					250						255	
Val	Ser	Trp	Asp												
			260												

<210> 3249

<211> 4487

<212> DNA

<213> Homo sapiens

<400> 3249

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 120
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 180
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 360
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 1080

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1920
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2220
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2280
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2340
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2400
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2460
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2520
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2580
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2820
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<210> 3250

<211> 849

<212> PRT

<213> Homo sapiens

<400> 3250

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His	Glu	Thr	Thr	Thr	Ala	Val	Thr	Asp	Pro	Arg	Tyr	Arg	Ala	Arg	Gly
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Pro Ala Ala His Ala Lys His Gly Ser Arg Asp Gly Ser Thr Gln Thr		
785	790	800
Asp Gly Pro Pro Asp Ser Thr Ser Thr Cys Leu Pro Pro Glu Pro Asp		
805	810	815
Ser Leu Leu Gly Cys Ser Ser Ser Gln Arg Ala Ala Ser Leu Asp Ser		
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<210> 3251

<211> 2595

<212> DNA

<213> Homo sapiens

<400> 3251

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<210> 3252

<211> 254

<212> PRT

<213> Homo sapiens

<400> 3252

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Val Val Asp Leu Ile Phe Leu Asn Thr Glu Val Ser Leu Ser Gln Ala
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Leu Glu Asp Val Ser Arg Gly Gly Ser Pro Phe Ala Ile Val Ile Thr
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Gln Gln His Gln Ile His Arg Ser Cys Thr Val Asn Ile Met Phe Gly
           65           70           75           80
Thr Pro Gln Glu His Arg Asn Met Pro Gln Ala Asp Ala Met Val Leu
           85           90           95
Val Ala Arg Asn Tyr Glu Arg Tyr Lys Asn Glu Cys Arg Glu Lys Glu
           100          105          110
Arg Glu Glu Ile Ala Arg Gln Ala Ala Lys Met Ala Asp Glu Ala Ile
           115          120          125
Leu Gln Glu Arg Glu Arg Gly Gly Pro Glu Glu Gly Val Arg Gly Gly
           130          135          140
His Pro Pro Ala Ile Gln Ser Leu Ile Asn Leu Leu Ala Asp Asn Arg
           145          150          155          160
Tyr Leu Thr Ala Glu Glu Thr Asp Lys Ile Ile Asn Tyr Leu Arg Glu
           165          170          175
Arg Lys Glu Arg Leu Met Arg Ser Ser Thr Asp Ser Leu Pro Gly Glu
           180          185          190
Leu Arg Gly Arg Pro Arg Pro Asp Phe Pro Pro Thr Thr Arg Gly Asp
           195          200          205
Leu Gly Cys Leu Ala Glu Asp Thr Ala Lys Leu Pro Thr Ala Pro Glu
           210          215          220
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<211> 686

<212> DNA

<213> Homo sapiens

<400> 3253

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<210> 3254

<211> 180

<212> PRT

<213> Homo sapiens

<400> 3254

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 35 40 45
 Arg Asp Lys Glu Phe Tyr Arg Pro Ile Pro Asn Pro Asn Pro Lys Leu
 50 55 60
 Thr Asp Gly Tyr Pro Ala Phe Lys Arg Pro His Met Thr Ala Lys Asp
 65 70 75 80
 Leu Gly Leu Pro Gly Phe Phe Pro Ser Gln Glu His Glu Ala Thr Arg
 85 90 95
 Glu Asp Glu Arg Lys Phe Thr Ser Thr Cys His Phe Thr Tyr Pro Ala
 100 105 110
 Ser His Asp Leu His Leu Ala Gln Gly Asp Pro Asn Gln Val Leu Gln
 115 120 125
 Ser Ala Asp Phe Pro Cys Leu Val Asp Pro Lys His Gln Pro Ala Ala
 130 135 140
 Glu Met Ala Lys Gly Tyr Leu Leu Leu Pro Gly Cys Pro Cys Leu His
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 Pro Phe Tyr Gln
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<210> 3255

<211> 724

<212> DNA

<213> Homo sapiens

<400> 3255

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 420
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<210> 3256

<211> 169

<212> PRT

<213> Homo sapiens

<400> 3256

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		20					25					30			
Gly	Arg	Asn	Glu	Ala	Gly	Glu	Arg	His	Gly	Arg	Gly	Arg	Ala	Arg	Leu
		35					40				45				
Pro	Asn	Gly	Asp	Thr	Tyr	Glu	Gly	Ser	Tyr	Glu	Phe	Gly	Lys	Arg	His
	50					55				60					
Gly	Gln	Gly	Ile	Tyr	Lys	Phe	Lys	Asn	Gly	Ala	Arg	Tyr	Ile	Gly	Glu
65					70				75					80	
Tyr	Val	Arg	Asn	Lys	Lys	His	Gly	Gln	Gly	Thr	Phe	Ile	Tyr	Pro	Asp
			85						90					95	
Gly	Ser	Arg	Tyr	Glu	Gly	Glu	Trp	Ala	Asn	Asp	Leu	Arg	His	Gly	His
		100						105					110		
Gly	Val	Tyr	Tyr	Tyr	Ile	Asn	Asn	Asp	Thr	Tyr	Thr	Gly	Glu	Trp	Phe
		115				120						125			
Ala	His	Gln	Arg	His	Gly	Gln	Gly	Thr	Tyr	Leu	Tyr	Ala	Glu	Thr	Gly
	130					135					140				
Ser	Lys	Tyr	Val	Gly	Thr	Trp	Val	Asn	Gly	Gln	Gln	Glu	Gly	Thr	Ala
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<210> 3257
 <211> 368
 <212> DNA
 <213> Homo sapiens

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<210> 3258
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 3258
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 35 40 45
 Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr Tyr Ala Ser Glu Ser
 50 55 60
 Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val Pro Arg Ala Arg Arg
 65 70 75 80
 Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp Arg Ser Met His Lys
 85 90 95
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<210> 3259
 <211> 747
 <212> DNA
 <213> Homo sapiens

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<210> 3260

<211> 197

<212> PRT

<213> Homo sapiens

<400> 3260

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			20					25					30		
Gly	Ser	Glu	Val	Asp	Arg	Val	Ile	Leu	Lys	Ala	Asn	Glu	Thr	Phe	Ala
		35					40					45			
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65					70					75				80	
Arg	Trp	Leu	Gln	Gln	Tyr	Val	Ala	Glu	Leu	Arg	Leu	His	Pro	Glu	Ala
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			100					105					110		
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<210> 3261
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 <212> DNA
 <213> Homo sapiens

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 tgctgtgccca attgtgtttt ttgtctctgt gtacattttg gttttatttg ggggtgctgt
 180
 tgatgatTtc cttgttccg gtgtctctgc tcccctcgct ggctgtgtgg gggctgcctg
 240
 gcccgctgct tgccgcctcc atagatcccc gttgcgcagc catctgtcat ggacgacatt
 300
 gaggtgtggc tcaggaccga cctgaagggt gatgatctgg aggaggggtgt cacaagtga
 360
 gagtttgata aattccttga agaaagagcc aaagctgctg aaatggttcc cgacctcccc
 420
 tcgcccccca tggaggctcc tgccccagcc tcaaaccctt ctggccggaa gaagccagag
 480
 cggtcagagg atgccctctt cgccctgtga gcagctctgt ggtttgcctc ccagatggc
 540
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 600
 cagggcctgc acacctgtgt ttccatggaa atgccaccgt gtctgtctcc aggcctccca
 660
 ctagtccaga ccagcttcag ccacttcttt tctctgagtg gtgggacaac tgcagccaga
 720
 gactctctcc cctccaccac tgggcccctc tgcccatgtt tctccaccag aagagcgggc
 780
 agagtggccc agccccaggc agtgcttctt gagcagacca cccggaactgt ctttctccca
 840
 cccgcccctg gagaaagagc acgcccggcc ccgcccctgtg ctccactctg cctggctcag
 900
 tgacctcttc aggcattctg cctcctctgg cccctctctc cctgaagggg ctttgtggga
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 1020
 ccttgtgaca ttgtgcttac cagcatttga gaaggctctg ctgggtctcc atggtggggg
 1080
 tctctacact tcttgacct ctctccatca ttcagctgcc agcccaggct tcacacccaa
 1140
 gctggctcag cagccgagcc tggcaccgag ggtccctgca ggctccctgg gcagggagag
 1200
 ggccaaggac aattgggagg gcagcaggca gcccgagat ggtggccatg tggcacgctg
 1260
 ctgagacgac actaccaata aaccaaactg ccacgcacaa aaaaaaaaaa aaaaaaaaaa
 1320

aaa
1323

<210> 3262
<211> 81
<212> PRT
<213> Homo sapiens

<400> 3262
Ile Pro Val Ala Gln Pro Ser Val Met Asp Asp Ile Glu Val Trp Leu
1 5 10 15
Arg Thr Asp Leu Lys Gly Asp Asp Leu Glu Glu Gly Val Thr Ser Glu
20 25 30
Glu Phe Asp Lys Phe Leu Glu Glu Arg Ala Lys Ala Ala Glu Met Val
35 40 45
Pro Asp Leu Pro Ser Pro Pro Met Glu Ala Pro Ala Pro Ala Ser Asn
50 55 60
Pro Ser Gly Arg Lys Lys Pro Glu Arg Ser Glu Asp Ala Leu Phe Ala
65 70 75 80
Leu

<210> 3263
<211> 1128
<212> DNA
<213> Homo sapiens

<400> 3263
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cggggacgca agggccgggg ccgggggtccc ccgtcctcct ctgactccga gcccgaggcc
120
gagctggaga gagaggccaa gaaatcagcg aagaagccgc agtcctcaag cacagagccc
180
gccaggaaac ctggccagaa ggagaagaga gtgcggcccg aggagaagca acaagccaag
240
cccgtagaag tggagcggac ccggaagcgg tccgagggct tctcgatgga caggagggtg
300
gagaagaaga aagagccctc cgtggaggag aagctgcaga agctgcacag tgagatcaag
360
tttgccctaa aggtcgacag cccggacgtg aaggggtgcc tgaatgccct agaggagctg
420
ggaaccctgc aggtgacctc tcagatcctc cagaagaaca cagcgtggt ggccacctg
480
aagaagattc gccgttaca agcgaacaag gacgtaatgg agaaggcagc agaagtctat
540
accgggtcga agtcgcgggt cctcggccca aagatcgagg cggcgcagaa agtgaacaag
600
gctgggatgg agaaggagaa ggccgaggag aagctggccg gggaggagct ggccggggag
660
gaggccccc aggagaaggc ggaggacaag ccagcaccg atctctcagc ccagtgtaat
720
ggcaggacca catcacagaa gggggagagc gcagaggaca aggagcacga ggagggtcgg
780

gactcggagg agggggccaag gtgtggctcc tctgaagacc tgcacgacag cgtacgggag
 840
 gggtcccagacc tggacaggcc tgggagcgac cggcaggagc gcgagagggc acggggggac
 900
 tcggaggccc tggacagga gagctgagcc gcgggcagcc agggccagcc cccgcccag
 960
 ctcaggctgc ccctctcctt ccccgctcg caggagagca gacgagagaa ctgtggggaa
 1020
 cgctgtgctg tttgtatttg ttcccttggg ttttttttc ctgcctaatt tctgtgattt
 1080
 ccaaccaaca tgaaatgact ataaatgggt tttttaatga aaaaaaaaa
 1128

<210> 3264

<211> 308

<212> PRT

<213> Homo sapiens

<400> 3264

Ser	Arg	Tyr	Arg	Ser	Ser	Gly	Asp	Leu	Arg	Glu	Asp	Asp	Glu
1			5				10				15		
Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly	Arg	Pro	Pro
		20					25				30		Ser
Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu	Glu	Arg	Glu	Ala
		35				40					45	Lys	Lys
Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser	Thr	Glu	Pro	Ala	Arg
	50				55					60		Lys	Pro
Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg	Pro	Glu	Glu	Lys	Gln	Gln
	65			70					75			80	Lys
Pro	Val	Lys	Val	Glu	Arg	Thr	Arg	Lys	Arg	Ser	Glu	Gly	Phe
		85						90				95	Ser
Asp	Arg	Lys	Val	Glu	Lys	Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu
		100					105					110	Leu
Gln	Lys	Leu	His	Ser	Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp
	115				120						125		Ser
Asp	Val	Lys	Gly	Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr
	130				135					140			Leu
Val	Thr	Ser	Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala
	145			150					155				Thr
Lys	Lys	Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu
		165						170				175	Lys
Ala	Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro
	180				185						190		Lys
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu
	195				200					205			Ala
Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala
	210				215					220			Pro
Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	Pro
	225			230					235				Val
Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	Asp	Lys
		245						250				255	Glu
Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	Cys	Gly	Ser
	260						265					270	Ser
Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	Asp	Leu	Asp	Arg
													Pro

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275
Ser Asp Arg Gln Glu Arg      280
290      Glu Arg Ala Arg Gly Asp Ser Ser Glu Ala Leu
300
Asp Glu Glu Ser
305

<210> 3265
<211> 524
<212> DNA
<213> Homo sapiens

<400> 3265
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60
ctttttcgtg gttttcaaaa tgtttccatt gagggcgtat tactttttata atcaacaaaa
120
gagaaaagat aacttcattt tagaaattct cacctaaggc atttgaaaaa taatccaaaa
180
ggtacattat tgttgatttt tcttctcttc agaaaggatc ttgttcgagt agaagccaca
240
gtcattgaaa agacagaatc atggccaaga atcattatga gattcaggaa aaggaaaaac
300
ttcaagaaga aaagaagtaa gttagagaaa gtaccgctgg gccctggtgc acgggtgctgg
360
ttgcccaggc gcatgcggac ggaggggtgtg gggcacgtgg gtctcggggac aggaagccca
420
ggcagggtctc aaactggctg ccactgccca cttgccacc ctcctcctaga gggagcacc
480
agaggggtcca gcctcgctcc ccttctcctc cacgctccac gcgt
524

<210> 3266
<211> 82
<212> PRT
<213> Homo sapiens

<400> 3266
Met Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ser Lys Leu
1 5 10 15
Glu Lys Val Pro Leu Gly Pro Val Ala Arg Cys Trp Leu Pro Arg Arg
20 25 30
Met Arg Thr Glu Gly Val Gly His Val Gly Leu Gly Thr Gly Ser Pro
35 40 45
Gly Arg Ser Gln Pro Gly Cys His Cys Pro Leu Ala Thr Leu Ile Leu
50 55 60
Glu Gly Ala Pro Arg Gly Ser Ser Leu Ala Pro Leu Leu Leu His Ala
65 70 75 80
Pro Arg

<210> 3267
<211> 393
<212> DNA
<213> Homo sapiens

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<400> 3267
gtcgaatatg catgcagagt acagggttta gaacatgaca tggaagagat caatgctcga
60
tggaatacat tgaataaaaa ggtcgacaca agaattgcac agctacagga agctttgttg
120
cattgtggga agtttcaaga tgccttgagg ccattgctca gctggttggc agataccgag
180
gagctcatag ccaatcagaa acctccatct gctgagtata aagtgggtgaa agcacagatc
240
caagaacaga agttgtccca gcggctccta gatgatcgaa aggccacagt agacatgctt
300
caagcagaag gaggcagaat agcccagtc gcagagctgg ctgatagaga gaaaatcact
360
ggacagctgg agagtcttga aagtagatgg act
393

<210> 3268
<211> 131
<212> PRT
<213> Homo sapiens

<400> 3268
Val Glu Tyr Ala Cys Arg Val Gln Gly Leu Glu His Asp Met Glu Glu
1 5 10 15
Ile Asn Ala Arg Trp Asn Thr Leu Asn Lys Lys Val Ala Gln Arg Ile
20 25 30
Ala Gln Leu Gln Glu Ala Leu Leu His Cys Gly Lys Phe Gln Asp Ala
35 40 45
Leu Glu Pro Leu Leu Ser Trp Leu Ala Asp Thr Glu Glu Leu Ile Ala
50 55 60
Asn Gln Lys Pro Pro Ser Ala Glu Tyr Lys Val Val Lys Ala Gln Ile
65 70 75 80
Gln Glu Gln Lys Leu Leu Gln Arg Leu Leu Asp Asp Arg Lys Ala Thr
85 90 95
Val Asp Met Leu Gln Ala Glu Gly Gly Arg Ile Ala Gln Ser Ala Glu
100 105 110
Leu Ala Asp Arg Glu Lys Ile Thr Gly Gln Leu Glu Ser Leu Glu Ser
115 120 125
Arg Trp Thr
130

<210> 3269
<211> 1423
<212> DNA
<213> Homo sapiens

<400> 3269
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tttgaagctg taactttatg agcgattatt tactaccttt gagaatgtg ttttagtata
120
aaatatagga tgtggaagcg aaaaaatcgc tgggtagcaa gtgaggtgta ctcaaaaaata
180

agcaaaagtc acgtgggtct gattttatcac cctcgctgga aagcttggtc tcagacacac
 240
 tgttactgca agtgtgtgtg aggggggaaac tctcacacac tttgcagttg aggacagggc
 300
 tagactttga ggtggaccct ggctcccagg gctgtgtact cccagcccggt gtttctcttt
 360
 tgctcagact gaacaagtgg aacgaaatta cattaaagaa aagaaggcag cagtgaagaa
 420
 atttgaagac aagaagggtg agctgaaaga gaacctgatt gctgagctag aagaaaagaa
 480
 gaaaatgatt gaaaacgaaa tgctgacaat ggaactgaat ggagattcta tggagggtgaa
 540
 acctatcatg accagaaagt tgccggaggcg accaaatgat cccgtcccca tcccagacaa
 600
 gaggaggaaa cctgctccag cccagctaaa ctatttggtta acagatgaac agatcatgga
 660
 ggatctgaga acattaaata agcttaagtc acccaagaga ccagcatctc catctctctc
 720
 tgagcaactg cctgcaacac ccgcggaatc tccagcacag agatttgagg cgcggtatga
 780
 agatggcaaa ctgtattatg acaaaagatg gtaccacaag agccaggcca tctatctgga
 840
 gtcaaaaggac aaccagaaac tgagctgcgt gatcagttct gtaggagcca atgagatctg
 900
 ggtgagggaag acaagtgaca gcaccaagat gaggatctac ctgggtcagc ttcagcggg
 960
 gctcttcgtg atccgccggc gctcagctgc ttgactttct acagtgtctt tctcttgacc
 1020
 ctttttctgg agtgggtttt atttttgttt tgtttcgttt tctcttctaat agaaaaatgt
 1080
 taacttactg ggaatagcta ctcagccttg gaaatggaga gcactgcagt gaattcttta
 1140
 gggcactttt gtggccggat gcttccaact ttgtcagttt tttctgcctc aacttcttcc
 1200
 agacatcagt caccatgaga ctgttttact ttcaggcgta ttgggggggtt tgatttactt
 1260
 tccttttatt tctttatttt ttgcttatac ttgtttttga aaacctcttc tgagtttgaa
 1320
 gggacageta tttttattga ttatctttta gtctctctac catggagaag agcaggaagg
 1380
 gatacaactc ccagtgcatt ttcattgttt gaatcggatt agt
 1423

<210> 3270

<211> 169

<212> PRT

<213> Homo sapiens

<400> 3270

Met	Ile	Glu	Asn	Glu	Met	Leu	Thr	Met	Glu	Leu	Asn	Gly	Asp	Ser	Met
1			5						10					15	
Glu	Val	Lys	Pro	Ile	Met	Thr	Arg	Lys	Leu	Arg	Arg	Arg	Pro	Asn	Asp
			20						25				30		
Pro	Val	Pro	Ile	Pro	Asp	Lys	Arg	Arg	Lys	Pro	Ala	Pro	Ala	Gln	Leu

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          35              40              45
Asn Tyr Leu Leu Thr Asp Glu Gln Ile Met Glu Asp Leu Arg Thr Leu
 50              55              60
Asn Lys Leu Lys Ser Pro Lys Arg Pro Ala Ser Pro Ser Ser Pro Glu
 65              70              75              80
His Leu Pro Ala Thr Pro Ala Glu Ser Pro Ala Gln Arg Phe Glu Ala
          85              90              95
Arg Ile Glu Asp Gly Lys Leu Tyr Tyr Asp Lys Arg Trp Tyr His Lys
          100              105              110
Ser Gln Ala Ile Tyr Leu Glu Ser Lys Asp Asn Gln Lys Leu Ser Cys
          115              120              125
Val Ile Ser Ser Val Gly Ala Asn Glu Ile Trp Val Arg Lys Thr Ser
          130              135              140
Asp Ser Thr Lys Met Arg Ile Tyr Leu Gly Gln Leu Gln Arg Gly Leu
          145              150              155              160
Phe Val Ile Arg Arg Arg Ser Ala Ala
          165

```

<210> 3271
 <211> 464
 <212> DNA
 <213> Homo sapiens

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<400> 3271
tcatgagcag ggccaattc tggcttctct gtggtcgcc tccatgtgct gggcgctcact
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gaaggcactg gggatcacgc cgagcacaag atggacagag atccctggcc cctcggagca
120
ggcagtctgt ggcctctggcc cctccagttc cttgtcacca ggagataggc aatgcacgtg
180
atgagaaggg ccccggcagc aagagatcca atgatggtgg ccgccaggat cccagcgttg
240
gtgggcaggt gtgtactggg cagctcctta ttcttttcag ctacctggac ctcaagtctg
300
gccttcatag tccattcaga gttgatggta atggctactt ggtaggtgcc actgtctgta
360
ggctggggcg gccgcagcag catggaacca ttggggaagc ccacgatgct tcgctgtccc
420
atggcaactgc catccctctg aggccttgt atccccaggg atgt
464

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<210> 3272
 <211> 140
 <212> PRT
 <213> Homo sapiens

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<400> 3272
Met Gly Gln Arg Asp Ile Val Gly Phe Pro Asn Gly Ser Met Leu Leu
 1              5              10              15
Arg Arg Ala Gln Pro Thr Asp Ser Gly Thr Tyr Gln Val Ala Ile Thr
          20              25              30
Ile Asn Ser Glu Trp Thr Met Lys Ala Lys Thr Glu Val Gln Val Ala
          35              40              45
Glu Lys Asn Lys Glu Leu Pro Ser Thr His Leu Pro Thr Asn Ala Gly

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      50              55              60
Ile Leu Ala Ala Thr Ile Ile Gly Ser Leu Ala Ala Gly Ala Leu Leu
65              70              75              80
Ile Ser Cys Ile Ala Tyr Leu Leu Val Thr Arg Asn Trp Arg Gly Gln
      85              90              95
Ser His Arg Leu Pro Ala Pro Arg Gly Gln Gly Ser Leu Ser Ile Leu
      100              105              110
Cys Ser Ala Val Ser Pro Val Pro Ser Val Thr Pro Ser Thr Trp Met
      115              120              125
Ala Thr Thr Glu Lys Pro Glu Leu Gly Pro Ala His
      130              135              140

<210> 3273
<211> 387
<212> DNA
<213> Homo sapiens

<400> 3273
ngcgcgccag ggatggaaaa ctttattctg tatgaggaga tcggaagagg aagcaagact
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gttgtctata aagggcgacg gaaggggaaca atcaattttg tagccattct ttgtactgat
120
aagtgcagaa ggccctgaaat aaccaactgg gtccgtctca cccgtgaaat aaaacacaag
180
aatattgtaa cttttcatga atgggtatgaa acaagcaacc acctctggct agtgggtgaa
240
ctccgcacag gtgggtcctt aaaaacagtt attgctcaag atgaaaacct ccagaagat
300
gttgtgagag aatttggaat tgacctgatt agtggattac atcatcttca taaacttggc
360
attctctttt tgacatttct cctagga
387

<210> 3274
<211> 129
<212> PRT
<213> Homo sapiens

<400> 3274
Xaa Ala Pro Gly Met Glu Asn Phe Ile Leu Tyr Glu Glu Ile Gly Arg
1      5      10      15
Gly Ser Lys Thr Val Val Tyr Lys Gly Arg Arg Lys Gly Thr Ile Asn
      20      25      30
Phe Val Ala Ile Leu Cys Thr Asp Lys Cys Arg Arg Pro Glu Ile Thr
      35      40      45
Asn Trp Val Arg Leu Thr Arg Glu Ile Lys His Lys Asn Ile Val Thr
      50      55      60
Phe His Glu Trp Tyr Glu Thr Ser Asn His Leu Trp Leu Val Val Glu
65      70      75      80
Leu Arg Thr Gly Gly Ser Leu Lys Thr Val Ile Ala Gln Asp Glu Asn
      85      90      95
Leu Pro Glu Asp Val Val Arg Glu Phe Gly Ile Asp Leu Ile Ser Gly
      100      105      110
Leu His His Leu His Lys Leu Gly Ile Leu Phe Val Thr Phe Leu Leu

```

	115	120	125
Gly			
<210>	3275		
<211>	1266		
<212>	DNA		
<213>	Homo sapiens		
<400>	3275		
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	60		
	agaacacatg aaaggaatac atggggaaga aataaagtag aaccaagag ttcttttaag		
	120		
	ttttctttta tagagacatg aataacagat acactgaagt ataaacaaaa attggcctga		
	180		
	agcgtccggg ggccggctta gttaggagct atggcctaacc atcatcctga ttgtatcttt		
	240		
	tgccgcaagc aggcgtggtg tgccatcgga agactgtgtg aaaaatgtga tggcaagtgt		
	300		
	gtgatttggt actcctatgt gcgtccctgc actctggtgc gcatatgtga tgagtgtaac		
	360		
	tatggatctt accaggggag ctgtgtgacg tgtggaggac ctggggctctc tgatgcctat		
	420		
	tattgtaaag agtgcacatc ccaggagaag gacagagatg gctgcccaaa gattgtcaat		
	480		
	ctggggagct ctaagacaga cctcttctat gaacgcaaaa aatacggctt caagaagagg		
	540		
	tgattgggtg gtggcccctt cctccccca acatcagtct gctgcagctg ccagaaaaa		
	600		
	tgccctactac taccagcaga aaggagagcag agcccagagc atcaccagga gtgcctgcta		
	660		
	gtgtactggc agcttgccac cccctcctct cccttcaccc agacacgtgg tagggatgga		
	720		
	aaaggattct tcacagagca ctctggcaca ccatatcgga gaaaaattga tagattagtt		
	780		
	aatgggtttt cttgaattcg agaagcatag atctgttctc catattggta tgttctccct		
	840		
	caaccaagat cttctaaaaa gaaataatat tttagtcttc tgcttgagga actgactgtg		
	900		
	aagcgacgcc cagtgaaaaa catgatcttg cagcagctct ggtggcagct gtccttgagg		
	960		
	aacctttggt gtgtggtggg aagctatcag aacaagaaat gtaggcatct cccgtttttt		
	1020		
	ttgggggggg ggtggggggg cagggtctg ccctcttgaa aggcatttac ttgtttaaca		
	1080		
	ctgtccagc tacagtggg tacagtagct ggctattcac aggcattcac atagcccact		
	1140		
	agtctcatat tattttcctt ttgagaaatt ggaaactctt tctgttgcta ttatattaat		
	1200		
	aaagtgtgtg ttatttttct ggtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa		
	1260		
	aaaaaa		
	1266		

<210> 3276
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 3276
 Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg Lys Gln Ala Gly
 1 5 10 15
 Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly Lys Cys Val Ile
 20 25 30
 Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg Ile Cys Asp Glu
 35 40 45
 Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile Cys Gly Gly Pro
 50 55 60
 Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr Ile Gln Glu Lys
 65 70 75 80
 Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly Ser Ser Lys Thr
 85 90 95
 Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys Lys Arg
 100 105 110

<210> 3277
 <211> 1435
 <212> DNA
 <213> Homo sapiens

<400> 3277
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 ctgcgtggga ggagaaaaga gctaatagcgg ccacgcttgt ccctcggcca ccgtcccacc
 120
 cagaactccg tctccttaaa atgttcacgc gtaagtgcgt ggacagaagcg gctcaagcgc
 180
 actcgtgcgt cattgctgtc agggccgagg gagcggtgca aggcgcgcgc gtgacgtcag
 240
 gacgcgcggg tcaggacgct gaagccaaaag aagaccagag ccagccgggt ggacacagcg
 300
 tgcctgtggc gtgttctga tcgcctgggt ggtgtgtggc gtgtccctgc agcgaaggat
 360
 cctgtgttgg agtgaaaaag cagtctggct cccgaggctc accccttata ccccaaggct
 420
 cagatggcgg ccaacgtggg tgatcaacgt agcacagatt ggtctttctca gtacagcatg
 480
 gtggctgggg caggccgaga gaatggcatg gagacgccga tgacagagaa cccggagtgg
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 600
 aagtcacaga gcaatgggcc tgtggccagt gcaagtacgt gtcccaggca gaagcctcag
 660
 ctttcagcga gcagcagtac taccagtggg accagcagta caactatgcc taccctaca
 720
 gctactacta tcccatgagc atgtaccaga gctatggctc cccttcccag tatgggatgg
 780

cgggtccta tggctagcca caccacagca gccatccgca ccccaacacc aagggaactct
 840
 gaaccagccc ccagtcctccg gcatggatga gagcatgtcc taccaggctc cccctcagca
 900
 gctgccgtcg gctcagcccc ctcagccctc aaatccccca catggggctc acacgctgaa
 960
 cagtggccct cagcctggga cagctccagc cacacagcan ncagccaggc ggggcccgcc
 1020
 acgggcccagg cctatgggcc acacacctac accgaacctg ccaagcccaa gaagggccaa
 1080
 cagctgtgga accgcatgaa acccgccctt gggactggag gttcaagttc aacatccaga
 1140
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<210> 3278

<211> 104

<212> PRT

<213> Homo sapiens

<400> 3278

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Tyr	Ser	Met	Val	Ala	Gly	Ala	Gly	Arg	Glu	Asn	Gly	Met	Glu	Thr	Pro
			20					25					30		
Met	His	Glu	Asn	Pro	Glu	Trp	Glu	Lys	Ala	Arg	Gln	Ala	Leu	Ala	Ser
			35				40					45			
Ile	Ser	Lys	Ser	Gly	Ala	Ala	Gly	Gly	Ser	Ala	Lys	Ser	Ser	Ser	Asn
			50			55				60					
Gly	Pro	Val	Ala	Ser	Ala	Ser	Thr	Cys	Pro	Arg	Gln	Lys	Pro	Gln	Leu
65				70					75				80		
Cys	Ser	Ser	Ser	Ser	Thr	Thr	Ser	Gly	Thr	Ser	Ser	Thr	Thr	Met	Pro
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<210> 3279

<211> 1130

<212> DNA

<213> Homo sapiens

<400> 3279

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<210> 3280

<211> 376

<212> PRT

<213> Homo sapiens

<400> 3280

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Gly	Arg	Ser	Thr	Pro	Ser	Ser	Ser	Pro	Ser	Leu	Arg	Lys	Arg	Leu	Gln
				20				25					30		
Leu	Leu	Pro	Pro	Ser	Arg	Pro	Pro	Glu	Pro	Glu	Pro	Gly	Thr	Met	
				35			40					45			
Val	Glu	Lys	Gly	Ser	Asp	Ser	Ser	Ser	Glu	Lys	Gly	Gly	Val	Pro	Gly
				50			55				60				
Thr	Pro	Ser	Thr	Gln	Ser	Leu	Gly	Ser	Arg	Asn	Phe	Ile	Arg	Asn	Ser
65					70				75				80		
Lys	Lys	Met	Gln	Ser	Trp	Tyr	Ser	Met	Leu	Ser	Pro	Thr	Tyr	Lys	Gln
				85					90				95		
Arg	Asn	Glu	Asp	Phe	Arg	Lys	Leu	Phe	Ser	Lys	Leu	Pro	Glu	Ala	Glu

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Arg Leu Ile Val Asp Tyr Ser Cys Ala Leu Gln Arg Glu Ile Leu Leu
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      130          135          140
Ile Phe Arg Trp Glu Thr Thr Ile Ser Ile Gln Leu Lys Glu Val Thr
      145          150          155          160
Cys Leu Lys Lys Glu Lys Thr Ala Lys Leu Ile Pro Asn Ala Ile Gln
      165          170          175
Ile Cys Thr Glu Ser Glu Lys His Phe Phe Thr Ser Phe Gly Ala Arg
      180          185          190
Asp Arg Cys Phe Leu Leu Ile Phe Arg Leu Trp Gln Asn Ala Leu Leu
      195          200          205
Glu Lys Thr Leu Ser Pro Arg Glu Leu Trp His Leu Val His Gln Cys
      210          215          220
Tyr Gly Ser Glu Leu Gly Leu Thr Ser Glu Asp Glu Asp Tyr Val Ser
      225          230          235          240
Pro Leu Gln Leu Asn Gly Leu Gly Thr Pro Lys Glu Val Gly Asp Val
      245          250          255
Ile Ala Leu Ser Asp Ile Thr Ser Ser Gly Ala Ala Asp Arg Ser Gln
      260          265          270
Glu Pro Ser Pro Val Gly Ser Arg Arg Gly His Val Thr Pro Asn Leu
      275          280          285
Ser Arg Ala Ser Ser Asp Ala Asp His Gly Ala Glu Glu Asp Lys Glu
      290          295          300
Glu Gln Val Asp Ser Gln Pro Asp Ala Ser Ser Ser Gln Thr Val Thr
      305          310          315          320
Pro Val Ala Glu Pro Pro Ser Thr Glu Pro Thr Gln Pro Asp Gly Pro
      325          330          335
Thr Thr Leu Gly Pro Leu Asp Leu Leu Pro Ser Glu Glu Leu Leu Thr
      340          345          350
Asp Thr Ser Asn Ser Ser Ser Ser Thr Gly Glu Glu Ala Asp Leu Ala
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Ala Leu Leu Pro Asp Leu Ser Gly
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<210> 3281

<211> 842

<212> DNA

<213> Homo sapiens

<400> 3281

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360

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<210> 3282

<211> 146

<212> PRT

<213> Homo sapiens

<400> 3282

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 35 40 45
 Thr Ser Phe Ala Arg Gly Lys Glu His His Val Gly His Ile His Glu
 50 55 60
 Gly Thr Gly Asn Ser Val Val Pro Ser Val Thr Pro Cys Gln Asp Thr
 65 70 75 80
 Gln Asp Glu Asn Pro Ala Pro Glu Arg Ala Ala Gly Ile Ser Ser Thr
 85 90 95
 His Thr Gln Ala Leu Cys Pro Gln Ala Pro Pro Ser Val Leu Pro Gly
 100 105 110
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<210> 3283

<211> 3268

<212> DNA

<213> Homo sapiens

<400> 3283

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<210> 3284

<211> 1012

<212> PRT

<213> Homo sapiens

<400> 3284

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Ala Phe Thr Arg Xaa His Val Cys Ala Glu Asn Leu Pro Val Leu
      35           40           45
Met Glu His Lys Ala Thr Thr Ile Gln Lys His Val Arg Gly Trp Met
 50           55           60
Ala Arg Arg His Phe Gln Arg Leu Arg Asp Ala Ala Ile Val Ile Gln
 65           70           75
Cys Ala Phe Arg Met Leu Lys Ala Arg Arg Glu Leu Lys Ala Leu Arg
      85           90           95
Ile Glu Ala Arg Ser Ala Glu His Leu Lys Arg Leu Asn Val Gly Met
      100          105          110
Glu Asn Lys Val Val Gln Leu Gln Arg Lys Ile Asp Glu Gln Asn Lys
      115          120          125
Glu Phe Lys Thr Leu Ser Glu Gln Leu Ser Val Thr Thr Ser Thr Tyr
      130          135          140
Thr Met Glu Val Glu Arg Leu Lys Lys Glu Leu Val His Tyr Gln Gln
      145          150          155          160
Ser Pro Gly Glu Asp Thr Ser Leu Arg Leu Gln Glu Glu Val Glu Ser
      165          170          175
Leu Arg Thr Glu Leu Gln Arg Ala His Ser Glu Arg Lys Ile Leu Glu
      180          185          190
Asp Ala His Ser Arg Glu Lys Asp Glu Leu Arg Lys Arg Val Ala Asp
      195          200          205
Leu Glu Gln Glu Asn Ala Leu Leu Lys Asp Glu Lys Glu Gln Leu Asn
      210          215          220
Asn Gln Ile Leu Cys Gln Ser Lys Asp Glu Phe Ala Gln Asn Ser Val
      225          230          235          240
Lys Glu Asn Leu Leu Met Lys Lys Glu Leu Glu Glu Arg Ser Arg
      245          250          255
Tyr Gln Asn Leu Val Lys Glu Tyr Ser Gln Leu Glu Gln Arg Tyr Asp
      260          265          270
Asn Leu Arg Asp Glu Met Thr Ile Ile Lys Gln Thr Pro Gly His Arg
      275          280          285
Arg Asn Pro Ser Asn Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro
      290          295          300
Ser Ile Ser Thr Ser Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln
      305          310          315          320
Val Glu Glu Ile Gly Leu Glu Lys Ala Ala Met Asp Met Thr Val Phe
      325          330          335
Leu Lys Leu Gln Lys Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys
      340          345          350
Leu Gln Val Gln Leu Glu Lys Arg Glu Gln Gln Asp Ser Lys Lys Val
      355          360          365
Gln Ala Glu Pro Pro Gln Thr Asp Ile Asp Leu Asp Pro Asn Ala Asp

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Ala Thr Gln Asn Asn Ser	Ser His Gly Ser	Pro Asp Ser Tyr Ser Leu			
	420	425		430	
Leu Leu Asn Gln Leu Lys	Leu Ala His Glu Glu Leu Glu Val Arg Lys				
	435	440		445	
Glu Glu Val Leu Ile Leu	Arg Thr Gln Ile Val Ser Ala Asp Gln Arg				
	450	455		460	
Arg Leu Ala Gly Arg Asn	Ala Glu Pro Asn Ile Asn Ala Arg Ser Ser				
465	470	475		480	
Trp Pro Asn Ser Glu Arg	His Val Asp Gln Glu Asp Ala Ile Glu Ala				
	485	490		495	
Tyr His Gly Val Cys Gln	Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln				
	500	505		510	
Ala Gln Ser Leu Glu His	Glu Glu Glu Val Glu His Leu Lys Ala Gln				
	515	520		525	
Leu Glu Ala Leu Lys Glu	Met Asp Lys Gln Gln Thr Phe Cys				
	530	535		540	
Gln Thr Leu Leu Leu Ser	Pro Glu Ala Gln Val Glu Phe Gly Val Gln				
545	550	555		560	
Gln Glu Ile Ser Arg Leu	Thr Asn Glu Asn Leu Asp Leu Lys Glu Leu				
	565	570		575	
Val Glu Lys Leu Glu Lys	Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys				
	580	585		590	
Ile Tyr Met Lys Lys Ala	Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala				
	595	600		605	
Gln Ser Glu Arg Lys Arg	His Glu Leu Asn Arg Gln Val Thr Val Gln				
	610	615		620	
Arg Lys Glu Lys Asp Phe	Gln Gly Met Leu Glu Tyr His Lys Glu Asp				
	625	630		635	
Glu Ala Leu Leu Ile Arg	Asn Leu Val Thr Asp Leu Lys Pro Gln Met				
	645	650		655	
Leu Ser Gly Thr Val Pro	Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys				
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Ile Arg His Ala Asp Tyr	Thr Asn Asp Asp Leu Lys Val His Ser Leu				
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Leu Thr Ser Thr Ile Asn	Gly Ile Lys Lys Val Leu Lys Lys His Asn				
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Asp Asp Phe Glu Met Thr	Ser Phe Trp Leu Ser Asn Thr Cys Arg Leu				
	705	710		715	
Leu His Cys Leu Lys Gln	Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln				
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Asn Thr Ala Lys Gln Asn	Glu His Cys Leu Lys Asn Phe Asp Leu Thr				
	740	745		750	
Glu Tyr Arg Gln Val Leu	Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln				
	755	760		765	
Leu Ile Lys Ile Ala Glu	Gly Val Leu Gln Pro Met Ile Val Ser Ala				
	770	775		780	
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Gly Tyr Arg Lys Arg Ser	Ser Ser Ser Met Ala Asp Gly Asp Asn Ser Tyr				

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Cys Asp Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln
      835              840              845
Leu Phe Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg
      850              855              860
Lys Asp Val Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile
      865              870              880
Ser Gln Leu Glu Glu Trp Leu Arg Gly Arg Asn Leu His Gln Ser Gly
      885              890              895
Ala Val Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln
      900              905              910
Leu Lys Lys Lys Thr Gln Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys
      915              920              925
Thr Ser Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr
      930              935              940
Pro Leu Asn Glu Phe Glu Glu Arg Val Thr Val Ala Phe Ile Arg Thr
      945              950              955              960
Ile Gln Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu
      965              970              975
Asp Ala Lys His Met Phe Pro Val Leu Phe Pro Phe Asn Pro Ser Ser
      980              985              990
Leu Thr Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe
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<210> 3285

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 3285

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 1380
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<210> 3286

<211> 142

<212> PRT

<213> Homo sapiens

<400> 3286

Met	Lys	Ser	His	Pro	Gly	Gln	Lys	Thr	Val	His	Phe	Ser	Lys	Thr	Glu
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Lys	Asn	Leu	Arg	Tyr	Glu	Ala	Ala	Thr	Ser	Asp	Thr	Tyr	Arg	Lys	Gly
			20					25					30		
Lys	Asn	Asn	Asp	Asn	Thr	Arg	Pro	Ala	Pro	Pro	Pro	Lys	Ser	Cys	Cys
		35					40					45			
Cys	Glu	Leu	Arg	Leu	Gln	Lys	Arg	Thr	His	Thr	Val	Ala	Asp	Lys	Thr
	50					55					60				
Gln	Ala	Arg	Arg	Met	Phe	Glu	Ser	Gln	Ser	Ala	Leu	Ser	Leu	Val	Pro
65				70						75				80	
Val	Thr	Ser	Tyr	Val	Gln	Leu	Pro	Gly	Pro	Ile	Pro	Tyr	Ser	Asp	Cys
				85					90				95		
Arg	Leu	Arg	Thr	Glu	Asp	Ala	Pro	Leu	Leu	Ser	Leu	His	Phe	Asp	Leu
			100					105					110		
Leu	Phe	Pro	Leu	Lys	Thr	Arg	Arg	Pro	Ala	Phe	Pro	Lys	Thr	Ala	Trp

115	120	125
Pro Trp Leu Cys Thr Leu Phe Thr Thr Asp Gln Asn Ser Ile		
130	135	140

<210> 3287
 <211> 921
 <212> DNA
 <213> Homo sapiens

<400> 3287
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 gcgtaagccc aatccgggaa actcgttgcc cctctcctgg gaaaggaacg tccctcccca
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 300
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 780
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 921

<210> 3288
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 3288
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 Leu Gly Arg Val Gly Ile Val Ser Pro Ala Pro Phe Pro Ala Pro Gln
 20 25 30
 Ser Cys Ser Phe Ser Phe Gly Leu Ser Lys Tyr Pro Gly Pro Pro Cys


```

          35              40              45
Ile Pro Leu Pro Phe Ser Cys Gly Cys Gly Ala Ser Leu Asn Arg Ser
    50              55              60
Thr Phe Leu Phe Pro Ser Thr Arg Asp Arg Glu Ser Leu Lys Gly Ser
    65              70              75              80
Gly Ala Pro Ser Ala His Leu Asp Gly Ala Gly Asp Ala Gln Arg Arg
          85              90              95
Phe Arg Ala Leu Tyr Phe Gln Leu Gln His Ser Gln Val Phe Thr Ala
          100              105              110
Gln Gly Asp Gly Ala Arg Val Thr Arg Asn Pro Gly Glu Gly Arg Ser
          115              120              125
Phe Pro Arg Arg Gly Ala Thr Ser Phe Pro Asp Trp Ala Tyr Ala Gly
          130              135              140
Gly Arg Gln Leu
145

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<210> 3289

<211> 554

<212> DNA

<213> Homo sapiens

<400> 3289

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    120
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    180
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    240
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    300
gaccaggcat ccagtcggg cagcacatgc taccagctcc acagaagagg aaacagaggc
    360
tcggagagga agggactgtg tcagggccgg gaccagggcc cttctgcact gggtaaatga
    420
gccaaagcaca tcacccagc ccttggggag caggagccgg gccttcgagg gtgaggagct
    480
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ataagctgca attg
    554

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<210> 3290

<211> 129

<212> PRT

<213> Homo sapiens

<400> 3290

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Met Ile Pro Gly Cys Leu Pro Trp Ser Phe Ala Phe Pro Ser Ser Ser
    1              5              10              15
Pro Cys Lys Ala Arg Leu Leu Leu Pro Lys Gly Trp Gly Asp Val Leu
          20              25              30
Gly Ser Leu Thr Gln Cys Arg Arg Ala Trp Val Pro Pro Trp Thr Gln

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      35              40              45
Ser Leu Pro Leu Gly Ala Ser Val Ser Ser Ser Val Asp Trp Val Ala
  50              55              60
Cys Ala Ala Arg Arg Gly Cys Leu Val Ser Gly Arg Trp Ser Thr His
  65              70              75              80
His Arg Val Glu Ser Lys Ala Ser Pro Leu Ser Pro Ser Leu Pro Trp
      85              90              95
Thr Ser Pro Leu Pro Ala Thr Leu Ala Gly Leu Cys Glu Trp Glu Gly
      100              105              110
Arg Pro Ala Leu Ala Gly Ser Ser Pro Val Pro Pro Ala Leu Ile Leu
      115              120              125
Gly

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<210> 3291

<211> 1075

<212> DNA

<213> Homo sapiens

<400> 3291

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  120
tgggccccct ctcgccac gcctgcggtg aggtccccgc ccccgctccc taccatagct
  180
gcctctgtcc ctcgcactg gctgttcacc tggctagctg tgtccgtttc tcaaccggga
  240
agcgagctctn ggctgcgacc gctgcgcgca cccagttac cccctccacc cccgcgctcc
  300
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  480
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  960
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1075

<210> 3292

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3292

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Val	Ala	Ala	Leu	Gly	Trp	Arg	Pro	Pro	Arg	Val	Pro	Ser	Pro	Ala	Pro
		20						25					30		
Trp	Ser	Ala	Thr	Pro	Gly	Pro	Pro	Trp	Ala	Pro	Ser	Pro	Ala	Thr	Pro
		35					40					45			
Ala	Val	Arg	Leu	Pro	Ala	Pro	Ser	Pro	Thr	Ile	Ala	Ala	Ser	Val	Pro
		50				55				60					
Pro	His	Trp	Leu	Phe	Thr	Trp	Leu	Ala	Val	Ser	Val	Ser	Gln	Pro	Gly
65					70				75					80	
Ser	Glu	Ser	Xaa	Arg	Arg	Pro	Leu	Pro	Pro	Gln	Leu	Pro	Pro	Pro	Pro
			85					90					95		
Thr	Pro	Pro	Ser	Leu	Pro										
			100												

<210> 3293

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 3293

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2340

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2362

<210> 3294

<211> 353

<212> PRT

<213> Homo sapiens

<400> 3294

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Xaa Ser Pro Lys Pro Ala Leu Pro Ala Gly Asp Glu Glu Thr Glu Ala
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          20          25          30
Thr Ser Leu Pro Pro Gly Pro Pro Ala Gly Arg Arg His Leu Pro Leu
 35          40          45
Ser Arg Arg Arg Glu Met Ser Ser Asn Lys Glu Gln Arg Ser Ala
 50          55          60
Val Phe Val Ile Leu Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser
 65          70          75          80
Ser Asn Ser Ala Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg
          85          90          95
Ser Arg Arg Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr
          100          105          110
Val Pro Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys
          115          120          125
Val Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
          130          135          140
Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro Thr
          145          150          155          160
Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg Val Val
          165          170          175
Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln Glu Phe Val
          180          185          190
Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly Pro Pro Ser Lys
          195          200          205
Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val Ile Gln Arg Ala Gly
          210          215          220
Leu Val Phe Pro Asn Met Glu Ala Tyr Ala Val Ser Pro Gly Arg Met
          225          230          235          240
Arg Gln Phe Asp Asp Leu Phe Arg Gly Glu Thr Gly Lys Asp Arg Glu
          245          250          255
Lys Ser His Ser Trp Leu Ser Thr Gly Trp Phe Thr Met Val Ile Ala
          260          265          270
Val Glu Leu Cys Asp His Val His Val Tyr Gly Met Val Pro Pro Asn
          275          280          285
Tyr Cys Ser Gln Arg Pro Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr
          290          295          300
Glu Pro Lys Gly Pro Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His
          305          310          315          320
Ser Arg Lys Gly Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe
          325          330          335
Ser Ser Trp Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp
          340          345          350
Thr

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<210> 3295
 <211> 690
 <212> DNA
 <213> Homo sapiens

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<210> 3296
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 3296
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 Leu Trp Glu Arg Pro Gly Cys Cys Ile Arg His Arg Ile Thr Trp Glu
 20 25 30
 Pro Arg His Met Gly Pro Ala Leu Arg Ser Leu Gln Val Lys Lys Gly
 35 40 45
 Thr Glu His Ala Asp Pro Leu Pro Phe Pro Ser Val Ser Leu Ser Gly
 50 55 60
 Phe Thr Val Gly Thr Leu Ser Glu Thr Ser Thr Gly Gly Pro Ala Thr
 65 70 75 80
 Pro Thr Trp Lys Glu Cys Pro Ile Cys Lys Glu Arg Phe Pro Ala Glu
 85 90 95
 Ser Asp Lys Asp Ala Leu Glu Asp His Met Asp Gly His Phe Phe
 100 105 110
 Ser Thr Gln Gly Pro Leu His Leu

115

120

<210> 3297
<211> 3176
<212> DNA
<213> Homo sapiens

<400> 3297
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120
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180
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3000

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<210> 3298
<211> 251
<212> PRT
<213> Homo sapiens
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400> 3298															
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Val	Cys	Leu	Cys	Val	Cys	Ala	Leu	Cys	Leu	Cys	Val	Cys	Leu	Cys	Glu
			20					25					30		
Cys	Leu	Trp	Val	Ser	Phe	Cys	Val	Cys	Val	Cys	Ile	Cys	Val	Cys	Val
		35					40					45			
Xaa	Leu	Cys	Ala	Cys	Met	Cys	Leu	Asp	Val	Cys	Phe	Cys	Met	Cys	Leu
	50					55					60				
Cys	Val	Cys	Leu	Tyr	Val	Cys	Ile	Cys	Val	Tyr	Val	Cys	Val	Cys	His
65					70					75					80
Phe	Val	Cys	Phe	Trp	Val	Cys	Leu	Ser	Ala	Cys	Leu	Cys	Ile	Pro	Val
				85					90					95	
Ser	Pro	Cys	Val	Cys	Leu	Cys	Val	Cys	Ile	Cys	Xaa	Cys	Leu	Cys	Met
			100					105					110		
Cys	Val	Arg	Gly	Cys	Val	Ser	Val	Cys	Val	Cys	Val	Cys	Ile	Glu	Arg
			115				120					125			
Glu	Gly	Glu	Arg	Lys	Gly	Ala	Thr	Asp	Gly	Ser	Ala	Trp	Lys	Val	Tyr
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Pro	His	Ser	Gln	Pro	Trp	Glu	Glu	Ser	Val	Asn	Pro	Pro	Thr	Gly	Gln
145					150					155					160
Asp	Gln	Leu	Trp	Trp	Cys	Leu	Ala	Asp	Ser	Gly	Asn	Val	Thr	Phe	His
				165					170					175	
Leu	Arg	Met	Gly	Leu	His	Phe	Leu	Gly	Lys	Glu	Cys	Arg	Ser	Trp	Ser
			180					185					190		
Leu	Lys	Glu	Cys	Phe	Phe	Phe	Pro	Phe	Val	Ile	Glu	Arg	Ala	Gln	Pro
			195				200					205			
Cys	Val	His	Trp	Leu	Thr	Val	Thr	Asn	Leu	Arg	Val	Gly	Asp	Ser	His
	210				215					220					
Arg	Glu	Glu	Thr	Glu	Gly	Thr	Ala	Asp	Ser	Glu	Gln	Glu	Ser	Gly	Gly
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240
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<210> 3300

<211> 219

<212> PRT

<213> Homo sapiens

<400> 3300

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Ser Ile Gln Gln Phe Thr Glu Met Asn Leu Leu Ser Asp Tyr Arg Phe	50	55	60
Leu Glu Asp Val Ala Arg Thr Ala Asp His Ile Ser Arg Asp Ala Phe	65	70	75
Leu Lys Arg Pro Ile Ser Asn Lys Tyr Met Tyr Phe Met Lys Asn Arg	85	90	95
Ala Arg Ser Lys Gly Ile Asn Leu Lys Leu Leu Pro Asn Gly Phe Thr	100	105	110
Lys Arg Lys Glu Asn Ser Thr Phe Phe Asp Lys Lys Lys Gln Gln Phe	115	120	125
Cys Trp His Val Lys Leu Gln Phe Pro Gln Ser Gln Ala Glu Tyr Ile	130	135	140
Glu Lys Arg Val Pro Asp Asp Lys Thr Ile Asn Glu Ile Leu Lys Pro	145	150	155
Tyr Ile Asp Pro Glu Lys Ser Asp Pro Val Ile Arg Gln Arg Leu Lys	165	170	175
Ala Tyr Ile Arg Ser Gln Thr Gly Val Gln Ile Leu Met Lys Ile Glu	180	185	190
Tyr Met Gln Gln Asn Leu Val Arg Tyr Tyr Glu Leu Asp Pro Tyr Lys	195	200	205
Ser Leu Leu Asp Asn Leu Arg Asn Lys Val Ile	210	215	

<210> 3301

<211> 2109

<212> DNA

<213> Homo sapiens

<400> 3301

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<210> 3302

<211> 323

<212> PRT

<213> Homo sapiens

<400> 3302

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20          25          30
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
35          40          45
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
50          55          60
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
65          70          75          80
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
85          90          95
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
100         105         110
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala
115         120         125
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met
130         135         140
Ala Ser Met Glu Ser Pro Xaa Val Asn Ala Phe Pro Ala Gln Asn Asn
145         150         155         160
Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
165         170         175
Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly His Pro
180         185         190
Gly Ser Thr Gln Leu Met Ala Leu Pro Ile Thr Gly Pro Gly Ser Pro
195         200         205
Pro Gly Trp Ala Thr Leu Gln Ile Gln Pro Gln Thr Thr Ser Val Ser
210         215         220
Ala Val Leu Gln Thr Gln Ala Gly Arg Gln Gly Ser Cys Lys Gln Pro
225         230         235
Gly Gly Asp Lys Glu Lys Ser Leu Leu Gly Ser Leu Ser Phe Pro Gly
245         250         255
His Val Ala Asn Ser Ala Ile Pro Ser Ser Arg Ala Ser Ala Ser Gly
260         265         270
Lys Asn Phe Pro Phe Pro Val Ser His Pro Ser Val Ala Gly Ala Ser
275         280         285
His Gln Gly Arg Arg Gly Leu Ser Leu Leu Cys Phe Gly Glu Gly Ala
290         295         300
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<210> 3303

<211> 699

<212> DNA

<213> Homo sapiens

<400> 3303

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 240
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<210> 3304

<211> 233

<212> PRT

<213> Homo sapiens

<400> 3304

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Asp	Ala	Ser	Ala	Ser	Pro	Leu	Ser	Pro	His	Arg	Arg	Ala	Lys	Ser	Leu
			20					25					30		
Asp	Arg	Arg	Ser	Thr	Glu	Pro	Ser	Val	Thr	Pro	Asp	Leu	Leu	Asn	Phe
			35				40				45				
Lys	Lys	Gly	Trp	Leu	Thr	Lys	Gln	Tyr	Glu	Asp	Gly	Gln	Trp	Lys	Lys
	50				55					60					
His	Trp	Phe	Val	Leu	Ala	Asp	Gln	Ser	Leu	Arg	Tyr	Tyr	Arg	Asp	Ser
	65				70					75				80	
Val	Ala	Glu	Glu	Ala	Ala	Asp	Leu	Asp	Gly	Glu	Ile	Asp	Leu	Ser	Ala
			85						90					95	
Cys	Tyr	Asp	Val	Thr	Glu	Tyr	Pro	Val	Gln	Arg	Asn	Tyr	Gly	Phe	Gln
			100				105						110		
Ile	His	Thr	Lys	Glu	Gly	Glu	Phe	Thr	Leu	Ser	Ala	Met	Thr	Ser	Gly
			115				120					125			
Ile	Arg	Arg	Asn	Trp	Ile	Gln	Thr	Ile	Met	Lys	His	Val	His	Pro	Thr
	130				135					140					
Thr	Ala	Pro	Asp	Val	Thr	Ser	Ser	Leu	Pro	Glu	Glu	Lys	Asn	Lys	Ser
	145				150				155					160	
Ser	Cys	Ser	Phe	Glu	Thr	Cys	Pro	Arg	Ser	Thr	Glu	Lys	Gln	Glu	Ala
			165					170						175	
Glu	Leu	Gly	Glu	Pro	Asp	Pro	Glu	Gln	Lys	Arg	Ser	Arg	Ala	Arg	Glu

	180		185		190
Arg	Arg	Arg	Glu	Gly	Arg
	195		200		205
Pro	Ile	Gln	Gln	Ala	Leu
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	225		230		

<210> 3305

<211> 2717

<212> DNA

<213> Homo sapiens

<400> 3305

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<210> 3306

<211> 319

<212> PRT

<213> Homo sapiens

<400> 3306

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Ile Ser Leu Val Met Lys Thr Pro Arg Val Ala Lys Asn Glu Ala Leu
 35           40           45
Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln Gly Thr Val Arg
 50           55           60
Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln Ser Leu Ser Phe
 65           70           75           80
Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe Ser Met Ala Pro
 85           90           95
Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln His Lys Gly Arg
100           105           110
Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly Gln Ala Val Arg
115           120           125
Lys Gly Ala Thr Leu Xaa Ala Cys Thr Thr Gly His Gly Xaa Arg Asp
130           135           140
Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu Gly Thr Tyr
145           150           155           160
Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln Ile Ile Gln
165           170           175
Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu Ala Asn Glu
180           185           190
Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr Tyr Pro Leu
195           200           205
Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly Ser Pro Ala
210           215           220
Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Val Ala Gly
225           230           235           240
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245           250           255
Cys His Leu His Leu Pro Gly His Thr His Leu Ser Gly Gly Ala Pro
260           265           270
Trp Gly Gln His Pro Gly Cys Pro Thr Arg Ala Glu Asn Ser Leu Gly
275           280           285
Ser His Leu Cys Gln Gln Ser Leu Pro Ser Cys Thr Asp Val Pro Gly
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<210> 3307

<211> 352

<212> DNA

<213> Homo sapiens

<400> 3307

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<210> 3308

<211> 110

<212> PRT

<213> Homo sapiens

<400> 3308

Met	Gly	Leu	Pro	Arg	Ala	Leu	Ala	Leu	Pro	Ser	Gly	Gly	Arg	Ser	Gly
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Ser	Leu	His	Pro	Asp	Pro	Gly	Ala	Ser	Leu	Pro	Cys	Pro	Val	Leu	Ile
			20					25				30			
Pro	Arg	Trp	Glu	Pro	Cys	Leu	Gly	Gln	Gly	Gly	Arg	Val	Asp	Gly	Ser
		35					40					45			
Trp	Asp	Cys	Asp	Ile	Gly	Arg	Arg	Gly	Arg	Ser	Pro	Ala	Leu	Ser	Ser
	50					55				60					
Ala	Gly	Trp	Ala	Gly	Ile	His	Leu	Ala	Ala	Ser	Gln	Gly	Leu	Cys	Pro
65					70					75				80	
Ala	Gly	Trp	Ser	Leu	Cys	Cys	Pro	Asn	Gln	Val	Ser	Thr	Phe	Pro	Ala
			85					90						95	
Pro	Met	Arg	Arg	Glu	Gly	Gly	Arg	Trp	Trp	Leu	Gly	Trp	Arg		
			100					105					110		

<210> 3309

<211> 737

<212> DNA

<213> Homo sapiens

<400> 3309

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 120
 cccaggacc ccaagtacca gggctctcgg gcactggcc gggagatccg gaaggagctt
 180
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 240
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 300
 cacatggtgc gagacaagcc agttttctcc ttccaacctc ggggccacct ggaaattggc
 360
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 420
 tacctgcgcg gggctggagc cctcctgcag caccgcttgc tcaacttcac attcaacaag
 480

cttctccgcc ggggcttcac ccccatgacg gtgccagacc ttctccgcgg agcagtgttt
 540
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 600
 cgcttcaaaag atctcaacct tgctggaaca gcggagggtgg ggcttgaggg ctacttcatg
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 720
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 737

<210> 3310

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3310

Ala	His	Leu	Cys	Cys	Pro	Gln	Asp	Pro	Lys	Tyr	Gln	Gly	Leu	Arg	Ala
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Arg	Gly	Arg	Glu	Ile	Arg	Lys	Glu	Leu	Val	His	Leu	Tyr	Pro	Arg	Glu
			20				25						30		
Ala	Gln	Leu	Glu	Glu	Gln	Phe	Tyr	Leu	Gln	Ala	Leu	Lys	Leu	Pro	Asn
		35					40					45			
Gln	Thr	His	Pro	Asp	Val	Pro	Val	Gly	Asp	Glu	Ser	Gln	Ala	Arg	Val
	50				55					60					
Leu	His	Met	Val	Gly	Asp	Lys	Pro	Val	Phe	Ser	Phe	Gln	Pro	Arg	Gly
65					70				75					80	
His	Leu	Glu	Ile	Gly	Glu	Lys	Leu	Asp	Ile	Ile	Arg	Gln	Lys	Arg	Leu
				85				90						95	
Ser	His	Val	Ser	Gly	His	Arg	Ser	Tyr	Tyr	Leu	Arg	Gly	Ala	Gly	Ala
			100					105					110		
Leu	Leu	Gln	His	Gly	Leu	Val	Asn	Phe	Thr	Phe	Asn	Lys	Leu	Leu	Arg
		115					120				125				
Arg	Gly	Phe	Thr	Pro	Met	Thr	Val	Pro	Asp	Leu	Leu	Arg	Gly	Ala	Val
	130					135					140				
Phe	Glu	Gly	Cys	Gly	Met	Thr	Pro	Asn	Ala	Asn	Pro	Ser	Gln	Ile	Tyr
145					150					155				160	
Asn	Ile	Asp	Pro	Ala	Arg	Phe	Lys	Asp	Leu	Asn	Leu	Ala	Gly	Thr	Ala
				165					170					175	
Glu	Val	Gly	Leu	Ala	Gly	Tyr	Phe	Met	Asp	His	Thr	Val	Ala	Phe	Arg
			180					185					190		
Asp	Leu	Pro	Val	Arg	Met	Val	Cys	Ser	Ser	Thr	Cys	Tyr	Arg	Ala	Glu
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Thr	Asn														
	210														

<210> 3311

<211> 486

<212> DNA

<213> Homo sapiens

<400> 3311

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 120
 aggaagatc aaggagtaaa ccagaagaag aagaaaaaga ggacttcaaa gctgggaagg
 180
 atgagttctt gcagcaacgt ctgtgggtcc aggcaggcac aggtgcagc tgaggggtgt
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 360
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 420
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 486

<210> 3312

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3312

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Ala	Glu	Gly	Gly	Tyr	Gln	Arg	Tyr	Gly	Val	Arg	Ser	Tyr	Leu	His	Gln
			20					25					30		
Phe	Tyr	Glu	Asp	Cys	Thr	Ala	Ser	Ile	Trp	Glu	Tyr	Glu	Asp	Asp	Phe
			35				40					45			
Gln	Ile	Gln	Arg	Ser	Pro	Asn	Arg	Trp	Ser	Ser	Val	Phe	Trp	Lys	Val
			50			55					60				
Gly	Leu	Ile	Ser	Gly	Thr	Val	Phe	Val	Ile	Leu	Gly	Leu	Thr	Val	Leu
						70				75				80	
Ala	Val	Gly	Phe	Leu	Val	Pro	Pro	Lys	Ile	Glu	Ala	Phe	Gly	Glu	Ala
				85					90					95	
Asp	Phe	Val	Val	Val	Asp										
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<210> 3313

<211> 1791

<212> DNA

<213> Homo sapiens

<400> 3313

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 120
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 180
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 240
 tctgtggtgg aagcagacct cgtggaagcg ctggaaaaat ttgggacaaat atgctatgtg
 300

atgatgatgc catttaaacg acaggctcta gtggaatttg aaaacataga tagtgccaaa
360
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420
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480
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540
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720
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1791

<210> 3314

<211> 537

<212> PRT

<213> Homo sapiens

<400> 3314

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 Ala Arg Thr Ala Val Lys Arg Arg Pro Gly Ala Gly Arg Val Gly Gly
 35 40 45
 Gly Gly Gly Arg Xaa Arg Ser Arg Gln Pro Glu Gly Leu Arg Ser His
 50 55 60
 His Lys Val Ser Val Ser Pro Val Val His Val Arg Gly Leu Cys Glu
 65 70 75 80
 Ser Val Val Glu Ala Asp Leu Val Glu Ala Leu Glu Lys Phe Gly Thr
 85 90 95
 Ile Cys Tyr Val Met Met Met Pro Phe Lys Arg Gln Ala Leu Val Glu
 100 105 110
 Phe Glu Asn Ile Asp Ser Ala Lys Glu Cys Val Thr Phe Ala Ala Asp
 115 120 125
 Glu Pro Val Tyr Ile Ala Gly Gln Gln Ala Phe Phe Asn Tyr Ser Thr
 130 135 140
 Ser Lys Arg Ile Thr Arg Pro Gly Asn Thr Asp Asp Pro Ser Gly Gly
 145 150 155 160
 Asn Lys Val Leu Leu Leu Ser Ile Gln Asn Pro Leu Tyr Pro Ile Thr
 165 170 175
 Val Asp Val Leu Tyr Thr Val Cys Asn Pro Val Gly Lys Val Gln Arg
 180 185 190
 Ile Val Ile Phe Lys Arg Asn Gly Ile Gln Ala Met Val Glu Phe Glu
 195 200 205
 Ser Val Leu Cys Ala Gln Lys Ala Lys Ala Ala Leu Asn Gly Ala Asp
 210 215 220
 Ile Tyr Ala Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Arg Pro Thr
 225 230 235 240
 Arg Leu Asn Val Ile Arg Asn Asp Asn Asp Ser Trp Asp Tyr Thr Lys
 245 250 255
 Pro Tyr Leu Gly Arg Arg Asp Arg Gly Lys Gly Arg Gln Arg Gln Ala
 260 265 270
 Ile Leu Gly Glu His Pro Ser Ser Phe Arg His Asp Gly Tyr Gly Ser
 275 280 285
 His Gly Pro Leu Leu Pro Leu Pro Ser Arg Tyr Arg Met Gly Ser Arg
 290 295 300
 Asp Thr Pro Glu Leu Val Ala Tyr Pro Leu Pro Gln Ala Ser Ser Ser
 305 310 315 320
 Tyr Met His Gly Gly Asn Pro Ser Gly Ser Val Val Met Val Ser Gly
 325 330 335
 Leu His Gln Leu Lys Met Asn Cys Ser Arg Val Phe Asn Leu Phe Cys
 340 345 350
 Leu Tyr Gly Asn Ile Glu Lys Val Lys Phe Met Lys Thr Ile Pro Gly
 355 360 365
 Thr Ala Leu Val Glu Met Gly Asp Glu Tyr Ala Val Glu Arg Ala Val
 370 375 380
 Thr His Leu Asn Asn Val Lys Leu Phe Gly Lys Arg Leu Asn Val Cys
 385 390 395 400
 Val Ser Lys Gln His Ser Val Val Pro Ser Gln Ile Phe Glu Leu Glu

			405				410				415				
Asp	Gly	Thr	Ser	Ser	Tyr	Lys	Asp	Phe	Ala	Met	Ser	Lys	Asn	Asn	Arg
			420					425					430		
Phe	Thr	Ser	Ala	Gly	Gln	Ala	Ser	Lys	Asn	Ile	Ile	Gln	Pro	Pro	Ser
			435				440					445			
Cys	Val	Leu	His	Tyr	Tyr	Asn	Val	Pro	Leu	Cys	Val	Thr	Glu	Glu	Thr
	450					455					460				
Phe	Thr	Lys	Leu	Cys	Asn	Asp	His	Glu	Val	Leu	Thr	Phe	Ile	Lys	Tyr
	465				470				475					480	
Lys	Val	Phe	Asp	Ala	Lys	Pro	Ser	Ala	Lys	Thr	Leu	Ser	Gly	Leu	Leu
			485					490					495		
Glu	Trp	Glu	Cys	Lys	Thr	Asp	Ala	Val	Glu	Ala	Leu	Thr	Ala	Leu	Asn
			500				505					510			
His	Tyr	Gln	Ile	Arg	Val	Pro	Asn	Gly	Ser	Asn	Pro	Tyr	Thr	Leu	Lys
		515				520						525			
Leu	Cys	Phe	Ser	Thr	Ser	Ser	His	Leu							
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<210> 3315

<211> 934

<212> DNA

<213> Homo sapiens

<400> 3315

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480
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780
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900

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934

<210> 3316
<211> 187
<212> PRT
<213> Homo sapiens

<400> 3316
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Val Pro Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Glu Val Val Leu
35 40 45
Pro Asp Pro Val Glu Glu Thr Arg His His Ala Glu Val Val Lys Lys
50 55 60
Val Asn Glu Met Ile Val Thr Gly Gln Tyr Gly Arg Leu Phe Ala Val
65 70 75 80
Val His Phe Ala Ser Arg Gln Trp Lys Val Thr Ser Glu Asp Leu Ile
85 90 95
Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly Glu Arg Ile Arg Leu
100 105 110
Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe Thr Leu Leu Gly Lys
115 120 125
Pro Leu Leu Gly Lys Asp Leu Val Arg Val Glu Ala Thr Val Ile Glu
130 135 140
Lys Thr Glu Ser Trp Pro Arg Ile Ile Met Arg Phe Arg Lys Arg Lys
145 150 155 160
Asn Phe Lys Lys Lys Arg Ile Val Thr Thr Pro Gln Thr Val Leu Arg
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Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu Leu
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<210> 3317
<211> 1665
<212> DNA
<213> Homo sapiens

<400> 3317
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180
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420

gaatatatta aaaatagaaa attagaaaag cagagaattc gagaagagaa gcgagaagaa
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<210> 3318

<211> 253

<212> PRT

<213> Homo sapiens

<400> 3318

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 20 25 30
 Glu Lys Arg Glu Glu Arg Arg Arg Arg Glu Leu Glu Lys Lys Arg Leu

35	40	45
Arg Glu Glu Glu Lys Arg	Arg Arg Arg Glu Glu Glu	Arg Cys Lys Lys
50	55	60
Lys Glu Thr Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile		
65	70	75
Lys Leu Leu Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys		80
	85	90
Pro Lys Glu Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu		95
	100	105
Ser Cys Ala Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser		110
	115	120
Leu Glu Glu Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His		125
	130	135
Arg Asp Val Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr		140
	145	150
His Val Asp Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg		155
	165	170
Leu Ser Arg Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly		175
	180	185
Gln Asp Arg Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu		190
	195	200
Ala Met Glu Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala		205
	210	215
Pro Arg Lys Glu Arg Leu Ala Asn Lys Val Phe Ile Lys Pro Lys Lys		220
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Lys Asn Val Ser Gly Cys Leu Lys Val Gln Ala Ala Cys		235
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<210> 3319

<211> 1541

<212> DNA

<213> Homo sapiens

<400> 3319

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600

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<210> 3320

<211> 256

<212> PRT

<213> Homo sapiens

<400> 3320

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Lys	Gly	Ala	Ser	Leu	Leu	Tyr	Arg	Lys	Phe	Val	His	Pro	Ser	Leu	Ser
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Arg	His	Glu	Lys	Glu	Ile	Asp	Ala	Tyr	Ile	Val	Gln	Ala	Lys	Glu	Arg
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Ala Pro Ala Arg Pro Arg	Glu Lys Pro Leu Ile	Arg Ser Gln Ser Leu
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<211> 1536

<212> DNA

<213> Homo sapiens

<400> 3321

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<211> 454

<212> PRT

<213> Homo sapiens

<400> 3322

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Cys	Ala	Glu	Gly	Lys	Ile	Pro	Glu	Glu	Ser	Lys	Ala	Leu	Ser	Leu	Leu
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Val Lys Pro Pro Glu Met Thr Pro Gln Ala Ala Lys Glu Leu Glu
      245              250              255
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 275              280              285
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Arg Arg Lys Arg Ser Gln Ser Lys His Arg Ser Arg Ser His Asn Arg
 305              310              315              320
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Lys Arg Ser Lys Ser Arg Glu Arg Arg Lys Ser Arg Ser Arg Ser His
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Arg Glu Lys Asp Arg Glu Lys Asp Lys Glu Lys Asp Arg Glu Arg Glu
      405              410              415
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<213> Homo sapiens

<400> 3323

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<211> 122

<212> PRT

<213> Homo sapiens

<400> 3324

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			20					25					30		
Thr	Thr	Val	Ile	Pro	Arg	Val	Tyr	Thr	Tyr	Tyr	Val	Ser	Thr	Val	Leu
			35				40					45			
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	65				70					75				80	
Lys	Lys	Asp	Glu	Glu	Val	Ser	His	Gly	Thr	Val	Asp	Leu	Asp	Gln	Lys
			85					90						95	
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<211> 5055

<212> DNA

<213> Homo sapiens

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<211> 254

<212> PRT

<213> Homo sapiens

<400> 3326

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<212> DNA

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<400> 3327

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<212> PRT

<213> Homo sapiens

<400> 3328

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 Gly Tyr Val Ser Asp Thr Glu Thr Ser Val Val Trp Asn Asn Glu His
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 Val Lys Thr Asp Trp Asp Arg Ala Lys Ser Gln Lys Met Arg Glu Gln
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<211> 705

<212> DNA

<213> Homo sapiens

<400> 3329

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<212> DNA

<213> Homo sapiens

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Asp Lys Val Trp Val Lys Leu Ile Gly Arg Glu Met Lys Asn Asp Arg
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<212> PRT

<213> Homo sapiens

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Gln	Thr	Glu	Ala	Leu	Glu	Phe	Asn	Pro	Ser	Ala	Asn	Pro	Glu	Ala
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Thr	Ile	Phe	Gln	Arg	Asn	Ser	Gln	Thr	Asp	Val	Val	Glu	Ile	Arg
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Ser	Asn	Cys	Thr	Asn	His	Val	Ser	Ala	Val	Arg	Phe	Ser	Gln	Gln
			115			120					125			
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<211> 477

<212> DNA

<213> Homo sapiens

<400> 3335

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cccagactgc ttgttgaagg ggttgagggtg ggcctgccgg aaacggggcca gcttctcattc
180
atattccata gcatccacc tgcctcgctt gccagggccc aggggctcgc agggacagga
240
tggccattcc tctagggctg ctggccacgg aagcctggcc gtgggttcgg cacctgctga
300
ccgcccgcctc gcatttgccc tgagacaggg ctggacagcc aggattaccg ctgtgccgag
360
tgccggggcgc ccattctctct gcgggggtgtg cccagttagg ccaggcagtg cgaactacac
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477

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<210> 3336

<211> 59

<212> PRT

<213> Homo sapiens

<400> 3336

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          20           25           30
Glu Ala Arg Gln Cys Asp Tyr Thr Gly Gln Tyr Tyr Cys Ser Pro Cys
          35           40           45
His Trp Asn Ala Leu Ala Val Ile Pro Ala Arg
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<210> 3337

<211> 679

<212> DNA

<213> Homo sapiens

<400> 3337

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120
agcttagcct ccaaagacac agatagagtg agagagagag acagagagag acacagagac
180
agacagagac caaaacagaa gcggcaaacg gcaaaaaacga agcagaatca atgcaagtta
240
gagaaaaaaa taaaactaaa catcagagca gggaaaagtc atctactccg tatcacacct
300
gtgtattagc ttaaccagaa ataagctgga agaggagtgc agtagctctc cagcccctta
360
aagatgttgg tcataccccc tctttcacgc tctgagtcga gaggacacca agccaaacaa
420
actgtgcccc aaactgggtc atctagtcct cccaggctct tccttgctaa ctcgaggaaa
480
caaggaaaac caactttgga tggcaacttc aacaaggtaa cctctcttcc ttcaatggcc
540
agactgatgc cactgacaa tggctttgag atgcttggac agcagactgt catgtcaaga
600

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ctgccagac cccaccaca ctgtggaaaa gggcagcacc agaccactg gagatgaggc
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 679

<210> 3338
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 3338
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 20 25 30
 Lys Glu Val Arg Trp Gly Ser Leu Ser Leu Ala Ser Lys Asp Thr Asp
 35 40 45
 Arg Val Arg Glu Arg Asp Arg Glu Arg His Arg Asp Arg Gln Arg Pro
 50 55 60
 Lys Gln Lys Arg Gln Thr Ala Lys Thr Lys Gln Asn Gln Cys Lys Leu
 65 70 75 80
 Glu Lys Lys Ile Lys Leu Asn Ile Arg Ala Gly Lys Ser His Leu Leu
 85 90 95
 Arg Ile Thr Pro Val Tyr
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<210> 3339
 <211> 1341
 <212> DNA
 <213> Homo sapiens

<400> 3339
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 120
 agaagccagt tccatccagg atccactatc tacacaccta tgttacaaca ttatatcaaa
 180
 tctgggtatct gaagaaaaga tacacattta atatgttcat ttaagttagc tttttgcag
 240
 aaagattaaa aattcattca cacaaaactc aaaaactgta ttaaaagtgt gaatataaaa
 300
 ctgagatcca cctggaatga cttaaagaatg gaagtcttgt atccacctgt gttaaaactg
 360
 gtaaatgtaa tgatatctgt taccaataaa acgcattcgt ttattcaatg taagtaagtt
 420
 atctaatttt aacaatatgg caccctaaaa accaactgta tttttatgat gaggcacttt
 480
 tgttagtgat gaaacaaaaa gaacaaattt gctgcacact gatgccagcg attttcttca
 540
 gtgattttgg gtatatgcta tgtagtaagt tgcaacaaat accttgctca tttgtataca
 600
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 720
 acaattctga tacaagaaaa tattgacaga gttactggaa cgtgtaacag tagttttttt
 780
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 840
 tggggtttca gacagtttat gaggttgggc attcgctgca gaactagcat ttttgctcac
 900
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 960
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 1020
 tgtgtcggtc gtggctatct ctcgtgtgct tgggttctct gtctggggat ctccgatttc
 1080
 tcctctgcta aggtcagagg tactgggtgcg taggcgttcc ctggccagcc agtctgagat
 1140
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 1200
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 1320
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<210> 3340

<211> 86

<212> PRT

<213> Homo sapiens

<400> 3340

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Ser	Val	Asn	Ile	Phe	Leu	Tyr	Gln	Asn	Cys	Tyr	Tyr	Ala	Ala	Phe	Ile
		20						25					30		
Trp	Ala	Gly	Phe	Ile	Ile	Leu	His	Cys	Glu	Ile	Ala	Leu	Gln	Cys	Ile
		35					40					45			
Thr	Thr	Ala	Arg	Arg	Thr	Tyr	Ile	Tyr	Ile	Tyr	Ile	Lys	Asn	Ile	Ser
	50					55					60				
Asp	Ser	Cys	Ile	Gln	Met	Ser	Lys	Val	Phe	Val	Ala	Thr	Tyr	Tyr	Ile
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Ala	Tyr	Thr	Gln	Asn	His										
				85											

<210> 3341

<211> 1132

<212> DNA

<213> Homo sapiens

<400> 3341

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 agctggaggc accagggtctg aattccagac tctctcccac caccacact tcacctccaa
 120

ctggagcatg accacagacc cattcagga ggctggcgga ctcttcaccc tggacagtcc
 180
 ctactgtat gtcaagtaaa gctgagaatg aagcggagag catcagacag aggagctggg
 240
 gaaacgtcgg ccagggccaa ggctctagga agtgggattt ctggaaataa tgcaaaagaga
 300
 gctggacat tcatccttgg tccccgtctg ggcaactcac cggtgccaag catagtgcag
 360
 tgtttggcga ggaaagatgg cagggatgac ttctatcagc tgaagatcct gacctggag
 420
 gagagggggg accaagcag agagagccag gaagagcggc agggcaagat gctgctgcac
 480
 accgagtact cactgctgtc tctcctgcac acgcaggatg gcgtgggtga ccaccacggc
 540
 ctcttcagg accgcacctg tgaatcgtt gaggacacag aatccagccg gatgggttaag
 600
 aagatgaaga agcgcactct cctcgtcctg gactgcctct gtgctcatga cttcagcgat
 660
 aagaccgctg acctcatcaa cctgcagcac tacgtcatca aggagaagag gctcagcgag
 720
 agggagactg tggtaatctt ctacgacgtg gtccgcgtgg tggaggccct gcaccagaaa
 780
 aatatcgtgc acagagacct gaagctgggg aacatggtgc tcaacaagag gacacatcgg
 840
 ataaccatca ccaacttctg cctcgggaag catctggtga gcgaggggga cctgctgaag
 900
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 960
 ggcaagccca gtgacatgtg ggcctgggc gtggtgctct tcaccatgct gtatggccag
 1020
 ttccccctct acgacagcat cccgcaggag ctcttcgcga agatcaaggc tgccgagtat
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 1132

<210> 3342

<211> 308

<212> PRT

<213> Homo sapiens

<400> 3342

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Ala	Lys	Ala	Leu	Gly	Ser	Gly	Ile	Ser	Gly	Asn	Asn	Ala	Lys	Arg	Ala
			20					25					30		
Gly	Pro	Phe	Ile	Leu	Gly	Pro	Arg	Leu	Gly	Asn	Ser	Pro	Val	Pro	Ser
			35				40					45			
Ile	Val	Gln	Cys	Leu	Ala	Arg	Lys	Asp	Gly	Thr	Asp	Asp	Phe	Tyr	Gln
			50				55					60			
Leu	Lys	Ile	Leu	Thr	Leu	Glu	Glu	Arg	Gly	Asp	Gln	Gly	Ile	Glu	Ser
			65			70				75				80	
Gln	Glu	Glu	Arg	Gln	Gly	Lys	Met	Leu	Leu	His	Thr	Glu	Tyr	Ser	Leu
				85					90					95	
Leu	Ser	Leu	Leu	His	Thr	Gln	Asp	Gly	Val	Val	His	His	His	Gly	Leu


```

                100                105                110
Phe Gln Asp Arg Thr Cys Glu Ile Val Glu Asp Thr Glu Ser Ser Arg
                115                120                125
Met Val Lys Lys Met Lys Lys Arg Ile Cys Leu Val Leu Asp Cys Leu
                130                135                140
Cys Ala His Asp Phe Ser Asp Lys Thr Ala Asp Leu Ile Asn Leu Gln
145                150                155                160
His Tyr Val Ile Lys Glu Lys Arg Leu Ser Glu Arg Glu Thr Val Val
                165                170                175
Ile Phe Tyr Asp Val Val Arg Val Val Glu Ala Leu His Gln Lys Asn
180                185                190
Ile Val His Arg Asp Leu Lys Leu Gly Asn Met Val Leu Asn Lys Arg
195                200                205
Thr His Arg Ile Thr Ile Thr Asn Phe Cys Leu Gly Lys His Leu Val
210                215                220
Ser Glu Gly Asp Leu Leu Lys Asp Gln Arg Gly Ser Pro Ala Tyr Ile
225                230                235                240
Ser Pro Asp Val Leu Ser Gly Arg Pro Tyr Arg Gly Lys Pro Ser Asp
                245                250                255
Met Trp Ala Leu Gly Val Val Leu Phe Thr Met Leu Tyr Gly Gln Phe
260                265                270
Pro Phe Tyr Asp Ser Ile Pro Gln Glu Leu Phe Arg Lys Ile Lys Ala
275                280                285
Ala Glu Tyr Thr Ile Pro Glu Asp Gly Arg Val Ser Glu Asn Thr Val
290                295                300
Cys Leu Ile Arg
305

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<210> 3343

<211> 594

<212> DNA

<213> Homo sapiens

<400> 3343

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120
ttcagcatga actgggtcgt gggcagcgcg gacctggaga ttatcaacgc caccattggg
180
cggaggagct gtggggggccc atcccggctc tgcaagcacg tgctgtctgc acggtgggag
240
cggctgtatg gcaggctgag cacacggaca cccagccctg gagacacgcc ctccatgtac
300
tgtgaggcca agctgggggc gcacacctac cagtctgtga aacagcagct gttcaaggcc
360
ttcagaagg ctggcctggg cactggggtg aggaaccac cggagcagca gcagtttcta
420
ctgactctct aggctgcggg ctctgggctg ctggagctga gcgggacgct ggaggggatgg
480
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540
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594

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<210> 3344
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 3344
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 Arg Gln Pro Gly Lys Ser Pro Pro Phe Ser Met Asn Trp Val Val Gly
 35 40 45
 Ser Ala Asp Leu Glu Ile Ile Asn Ala Thr Thr Gly Arg Arg Ser Cys
 50 55 60
 Gly Gly Pro Ser Arg Leu Cys Lys His Val Leu Ser Ala Arg Trp Ala
 65 70 75
 Arg Leu Tyr Gly Arg Leu Ser Thr Arg Thr Pro Ser Pro Gly Asp Thr
 85 90 95
 Pro Ser Met Tyr Cys Glu Ala Lys Leu Gly Ala His Thr Tyr Gln Ser
 100 105 110
 Val Lys Gln Gln Leu Phe Lys Ala Phe Gln Lys Ala Gly Leu Gly Thr
 115 120 125
 Trp Val Arg Lys Pro Pro Glu Gln Gln Gln Phe Leu Leu Thr Leu
 130 135 140

<210> 3345
 <211> 1149
 <212> DNA
 <213> Homo sapiens

<400> 3345
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 tcaccgtgag ctctttccaa ggggacgcca ccagtggggg cctgggcagg aggcagctga
 180
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 240
 agtgaaagag gccagcctca cccagacac cccagtgtgg ttgggggaaa ggggtggtcc
 300
 gtggtgagcc tggtagcttg ggactcatcc tggccctgcc tggccctcag gtgggatgct
 360
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 420
 cagtctgggc cgagacagca ttagcagggc cctggggagg aggtcccga cgtcactcct
 480
 gaagaggccc tgcttgagct gcccctggg gagcgggaat tccgctgccc tgaacgcgtg
 540
 atggatctcg gctgtctga ggaccacttc tcccgcctg tgggtctggt cctggcctct
 600
 gacgtccagc agctgcggca ggcgatcgag gactgcaagc aggtgattct ggagctgccc
 660

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 720
 caggagctga aggaccccaa tgaggatgag ccaaacatcc gagtgcctct tgagcaccgc
 780
 tttacaagg agaagagcaa gagcgtcaag cagacctgtg acaagtgtaa caccatcatc
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 900
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 gaactgaaca tctgccctga gacagggctg gacagccagg attaccgctg tgccgagtg
 1020
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<210> 3346

<211> 263

<212> PRT

<213> Homo sapiens

<400> 3346

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Pro	Phe	Asn	Lys	Gln	Ser	Gly	Pro	Arg	Gln	His	Glu	Gln	Gly	Pro	Gly
			20					25					30		
Glu	Glu	Val	Pro	Asp	Val	Thr	Pro	Glu	Glu	Ala	Leu	Pro	Glu	Leu	Pro
		35				40					45				
Pro	Gly	Glu	Pro	Glu	Phe	Arg	Cys	Pro	Glu	Arg	Val	Met	Asp	Leu	Gly
50					55					60					
Leu	Ser	Glu	Asp	His	Phe	Ser	Arg	Pro	Val	Gly	Leu	Phe	Leu	Ala	Ser
65				70				75						80	
Asp	Val	Gln	Gln	Leu	Arg	Gln	Ala	Ile	Glu	Glu	Cys	Lys	Gln	Val	Ile
			85					90						95	
Leu	Glu	Leu	Pro	Glu	Gln	Ser	Glu	Lys	Gln	Lys	Asp	Ala	Val	Val	Arg
		100					105						110		
Leu	Ile	His	Leu	Arg	Leu	Lys	Leu	Gln	Glu	Leu	Lys	Asp	Pro	Asn	Glu
		115				120					125				
Asp	Glu	Pro	Asn	Ile	Arg	Val	Leu	Leu	Glu	His	Arg	Phe	Tyr	Lys	Glu
		130			135					140					
Lys	Ser	Lys	Ser	Val	Lys	Gln	Thr	Cys	Asp	Lys	Cys	Asn	Thr	Ile	Ile
145				150					155					160	
Trp	Gly	Leu	Ile	Gln	Thr	Trp	Tyr	Thr	Cys	Thr	Gly	Cys	Tyr	Tyr	Arg
			165					170						175	
Cys	His	Ser	Lys	Cys	Leu	Asn	Leu	Ile	Ser	Lys	Pro	Cys	Val	Ser	Ser
		180					185						190		
Lys	Val	Ser	His	Gln	Ala	Glu	Tyr	Glu	Leu	Asn	Ile	Cys	Pro	Glu	Thr
		195				200					205				
Gly	Leu	Asp	Ser	Gln	Asp	Tyr	Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile
		210			215					220					
Ser	Leu	Arg	Gly	Val	Pro	Ser	Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly

225		230		235		240
Gln Tyr Tyr Cys Ser His Cys His Trp Asn Asp Leu Ala Val Ile Pro						
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Glu Ala Gly Val Cys Ser Arg						
	260					

<210> 3347

<211> 2267

<212> DNA

<213> Homo sapiens

<400> 3347

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120
ttgcctccag ctttccacct accgctgcca ggacctacc tggccttctt ggtactcagc
180
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240
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300
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420
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480
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660
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720
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780
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1200
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1260

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 1740
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 1800
 ccagccttgt cttcctcttt cctctgtcag ttcaaaaaga acagaaacct ccagctcttt
 1860
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 1920
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 1980
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 2040
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 2100
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 2160
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 2220
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 2267
 <210> 3348
 <211> 288
 <212> PRT
 <213> Homo sapiens

 <400> 3348
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 Lys Ile Glu Asp Thr Leu Cys Pro Phe Gly Phe Glu Val Tyr Pro Phe
 20 25 30
 Gln Val Ala Trp Tyr Asn Glu Leu Leu Pro Pro Ala Phe His Leu Pro
 35 40 45
 Leu Pro Gly Pro Thr Leu Ala Phe Leu Val Leu Ser Thr Pro Ala Met
 50 55 60
 Phe Asp Arg Ala Leu Lys Pro Phe Leu Gln Ser Cys His Leu Arg Met
 65 70 75 80
 Leu Thr Asp Pro Val Asp Gln Cys Val Ala Tyr His Leu Gly Arg Val
 85 90 95
 Gly Glu Ser Leu Pro Glu Leu Gln Ile Glu Ile Ile Ala Asp Tyr Glu
 100 105 110

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Val His Pro Asn Arg Arg Pro Lys Ile Leu Ala Gln Thr Ala Ala His
      115              120              125
Val Ala Gly Ala Ala Tyr Tyr Tyr Gln Arg Gln Asp Val Glu Ala Asp
      130              135              140
Pro Trp Gly Asn Gln Arg Ile Ser Gly Val Cys Ile His Pro Arg Phe
      145              150              155              160
Gly Gly Trp Phe Ala Ile Arg Gly Val Val Leu Leu Pro Gly Ile Glu
      165              170              175
Val Pro Asp Leu Pro Pro Arg Lys Pro His Asp Cys Val Pro Thr Arg
      180              185              190
Ala Asp Arg Ile Ala Leu Leu Glu Gly Phe Asn Phe His Trp Arg Asp
      195              200              205
Trp Thr Tyr Arg Asp Ala Val Thr Pro Gln Glu Arg Tyr Ser Glu Glu
      210              215              220
Gln Lys Ala Tyr Phe Ser Thr Pro Pro Ala Gln Arg Leu Ala Leu Leu
      225              230              235              240
Gly Leu Ala Gln Pro Ser Glu Lys Pro Ser Ser Pro Ser Pro Asp Leu
      245              250              255
Pro Phe Thr Thr Pro Ala Pro Lys Lys Pro Gly Asn Pro Ser Arg Ala
      260              265              270
Arg Ser Trp Leu Ser Pro Arg Val Ser Pro Pro Ala Ser Pro Gly Pro
      275              280              285

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<210> 3349

<211> 1132

<212> DNA

<213> Homo sapiens

<400> 3349

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540
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660
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720

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 840
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 900
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 960
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 1020
 ccagtacttg cctcattctc atcatccaaa ctgaacattt gtatcccaag cagaaataaa
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<210> 3350

<211> 174

<212> PRT

<213> Homo sapiens

<400> 3350

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Asp	Leu	Val	Ser	Val	Lys	Lys	Ser	Leu	Gly	Arg	Asn	Arg	Leu	Leu	Pro
			20					25					30		
Gln	Gly	Leu	Ala	Val	Tyr	Ala	Ser	Pro	Glu	Asn	Lys	Lys	Leu	Phe	Glu
		35				40						45			
Glu	Glu	Lys	Leu	Leu	Arg	Gln	Glu	Gly	Lys	Leu	Glu	Lys	Ile	Gln	Thr
		50				55					60				
Lys	Ala	Gly	Glu	Ala	Thr	Val	Lys	Phe	Leu	Lys	Ser	Cys	Arg	Leu	Glu
65				70				75						80	
Val	Gly	Met	Lys	Asn	Asn	Val	Lys	Trp	Glu	Leu	Asn	Pro	Glu	Ile	Val
			85					90						95	
Ala	Arg	His	Phe	Phe	Lys	Asn	Leu	Gly	Val	Val	Val	Ala	Pro	His	Thr
			100					105					110		
Leu	Lys	Leu	Pro	Ala	Glu	Pro	Ile	Thr	Arg	Trp	Gly	Glu	Tyr	Trp	Cys
		115				120						125			
Glu	Val	Thr	Val	Asn	Gly	Leu	Asp	Thr	Val	Arg	Val	Pro	Met	Ser	Val
		130				135					140				
Val	Asn	Phe	Glu	Lys	Pro	Lys	Thr	Lys	Arg	Tyr	Lys	Tyr	Trp	Leu	Ala
145				150						155				160	
Gln	Gln	Ala	Ala	Lys	Ala	Met	Ala	Pro	Thr	Ser	Pro	Gln	Ile		
			165					170							

<210> 3351

<211> 1422

<212> DNA

<213> Homo sapiens

<400> 3351

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 120

atgatgctct tagtccaat aattcatggt ggcaagcaca gtgaacgaca tcctgccctc
 180
 gctgctgcgc cgcgatgcgc tgagcgccgc caaggagggt ttgtaccacc tggacateta
 240
 cttcagcagc cagctgcaga gcgcgccgct gcccatcgtg gacaagggcc ccgtggagct
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 360
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 420
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 480
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 780
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 840
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 960
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 1080
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 1200
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 1260
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 1320
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 1422

<210> 3352

<211> 97

<212> PRT

<213> Homo sapiens

<400> 3352

Met Trp Pro Ser Gln Leu Leu Ile Phe Met Met Leu Leu Ala Pro Ile

1

5

10

15

Ile His Gly Gly Lys His Ser Glu Arg His Pro Ala Leu Ala Ala Ala


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                20                25                30
Pro Arg Cys Ala Glu Arg Arg Gln Gly Gly Val Val Pro Gly His
      35                40                45
Leu Leu Gln Gln Pro Ala Ala Glu Arg Ala Ala His Arg Gly Gln
      50                55                60
Gly Pro Arg Gly Ala Ala Gly Gly Val Arg Val Pro Gly Ala Gln Gly
      65                70                75                80
Ala Gln Arg Ala Ala Gln Glu Thr Glu Phe Pro Ser Gly Ala Ser Thr
      85                90                95
Ser

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<210> 3353
 <211> 420
 <212> DNA
 <213> Homo sapiens

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120
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180
cctgaagaga cagcctaccc tagcctgagt gggggcaaca gtacctccaa ttgaccac
240
accatgactc acctgggcat cagcaggggc atgggccttg gccaggcta tgaatcacca
300
gggcgtcccc ctggatacca gtaactgtc cactgaccag cggttacccc cataccata
360
cagttcccca agtttggtnt ctgcttacc agccccacac cccaaagttt taacagcagc
420

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<210> 3354
 <211> 107
 <212> PRT
 <213> Homo sapiens

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<400> 3354
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Gly Ile Asn Ile Phe Pro Ser Pro Asp Gln Pro Ala Asn Val Pro Val
      20      25      30
Leu Pro Pro Ala Met Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn
      35      40      45
Leu His Phe Pro Pro Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Thr
      50      55      60
Ala Tyr Pro Ser Leu Ser Gly Gly Asn Ser Thr Ser Asn Leu Thr His
      65      70      75      80
Thr Met Thr His Leu Gly Ile Ser Arg Gly Met Gly Leu Gly Pro Gly
      85      90      95
Tyr Asp Ala Pro Gly Arg Pro Pro Gly Tyr Gln
      100      105

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<210> 3355
 <211> 474
 <212> DNA
 <213> Homo sapiens

<400> 3355
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 120
 gacaagagtc atgctttttt ccccatcatt ccaaaccacc agagagggtca gctagaagac
 180
 agactgaaca accaggcgcg taccatagct ttccttcttg aacaagcctt cgcgcatcaag
 240
 gaggacatct ctgcttgctt gcaggggacc catggctttc gaaaagagga atcgctcgcc
 300
 aggaagttac tggaagcca catccagacc atcaccagca tcgtcaaaaa actcagccaa
 360
 aatattgaga ttttagaaga ccaataaga gctcgagatc aggcggccac aggaactaac
 420
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 474

<210> 3356
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 3356
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 20 25 30
 Asp Arg Leu Asn Asn Gln Ala Arg Thr Ile Ala Phe Leu Leu Glu Gln
 35 40 45
 Ala Phe Arg Ile Lys Glu Asp Ile Ser Ala Cys Leu Gln Gly Thr His
 50 55 60
 Gly Phe Arg Lys Glu Glu Ser Leu Ala Arg Lys Leu Leu Glu Ser His
 65 70 75 80
 Ile Gln Thr Ile Thr Ser Ile Val Lys Lys Leu Ser Gln Asn Ile Glu
 85 90 95
 Ile Leu Glu Asp Gln Ile Arg Ala Arg Asp Gln Ala Ala Thr Gly Thr
 100 105 110
 Asn Phe Ala Val His Glu Ile Asn Ile Lys His Leu Gln Gly Val Gly
 115 120 125
 Arg Ser Phe
 130

<210> 3357
 <211> 2268
 <212> DNA
 <213> Homo sapiens

<400> 3357

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120
agggccctata aaaataattc cttcttgctt acaaagttca gcaaattcca tgttttctga
180
aagaaaaccg catcctggat ggatagcctg tgcagcagag gtcttgGCCa cttgaatgat
240
tttctccata gataggtagc tctgctggga ggaacgggtt tggcggtgag gacgcagctg
300
cctctgtact ggggagtcac ggagtggcgc ggctccaggg acatggcggc ggcctctgcg
360
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420
ctgccgccga ggacatgggt gtggaggcaa agaaccatga agtacacaac agccacagga
480
agaaacatta ccaaggtcct cattgcaaac agaggagaaa ttgcctgcag ggtgatgcgc
540
acagccaaaa aactgggtgt acagactgtg gcggtttata gtgaggctga cagaaattcc
600
atgcatgtag atatggcaga tgaagcatat tccatcggcc ccgctccctc ccagcagagc
660
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720
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gagaagtttg tagacacacc gaggcagtga gaagtcagg tggttggtga tcaccatggc
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aatgctgtgt acttgtttga aagagactgt agtgtgcaga ggcgacatca gaagatcatt
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1620

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 1680
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 1740
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 2100
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 2160
 tagcatgcag attgaagata aaactttcca agtccttggt aatctttaca gcgagggaga
 2220
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<210> 3358

<211> 493

<212> PRT

<213> Homo sapiens

<400> 3358

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Asp	Met	Ala	Asp	Glu	Ala	Tyr	Ser	Ile	Gly	Pro	Ala	Pro	Ser	Gln	Gln
			20					25					30		
Ser	Tyr	Leu	Ser	Met	Glu	Lys	Ile	Ile	Gln	Val	Ala	Lys	Thr	Ser	Ala
		35				40					45				
Ala	Gln	Ala	Ile	His	Pro	Gly	Cys	Gly	Phe	Leu	Ser	Glu	Asn	Met	Glu
		50				55				60					
Phe	Ala	Glu	Leu	Cys	Lys	Gln	Glu	Gly	Ile	Ile	Phe	Ile	Gly	Pro	Pro
65				70					75					80	
Pro	Ser	Ala	Ile	Arg	Asp	Met	Gly	Ile	Lys	Ser	Thr	Ser	Lys	Ser	Ile
				85					90					95	
Met	Ala	Ala	Ala	Gly	Val	Pro	Val	Val	Glu	Gly	Tyr	His	Gly	Glu	Asp
			100					105					110		
Gln	Ser	Asp	Gln	Cys	Leu	Lys	Glu	His	Ala	Arg	Arg	Ile	Gly	Tyr	Pro
		115				120						125			
Val	Met	Ile	Lys	Ala	Val	Arg	Gly	Gly	Gly	Lys	Gly	Met	Arg	Ile	
		130				135				140					
Val	Arg	Ser	Glu	Gln	Glu	Phe	Gln	Glu	Gln	Leu	Glu	Ser	Ala	Arg	Arg
145				150						155				160	
Glu	Ala	Lys	Lys	Ser	Phe	Asn	Asp	Asp	Ala	Met	Leu	Ile	Glu	Lys	Phe
			165						170					175	
Val	Asp	Thr	Pro	Arg	His	Val	Glu	Val	Gln	Val	Phe	Gly	Asp	His	His
			180					185					190		
Gly	Asn	Ala	Val	Tyr	Leu	Phe	Glu	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg

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      195              200              205
His Gln Lys Ile Ile Glu Glu Ala Pro Ala Pro Gly Ile Lys Ser Glu
      210              215              220
Val Arg Lys Lys Leu Gly Glu Ala Ala Val Arg Ala Ala Lys Ala Val
      225              230              235              240
Asn Tyr Val Gly Ala Gly Thr Val Glu Phe Ile Met Asp Ser Lys His
      245              250              255
Asn Phe Cys Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu His Pro
      260              265              270
Val Thr Glu Met Ile Thr Gly Thr Asp Leu Val Glu Trp Gln Leu Arg
      275              280              285
Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser Gln Glu Ile Thr Leu
      290              295              300
Gln Gly His Ala Phe Glu Ala Arg Ile Tyr Ala Glu Asp Pro Ser Asn
      305              310              315              320
Asn Phe Met Pro Val Ala Gly Pro Leu Val His Leu Ser Thr Pro Arg
      325              330              335
Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly Val Arg Gln Gly Asp Glu
      340              345              350
Val Ser Val His Tyr Asp Pro Met Ile Ala Lys Leu Val Val Trp Ala
      355              360              365
Ala Asp Arg Gln Ala Ala Leu Thr Lys Leu Arg Tyr Ser Leu Arg Gln
      370              375              380
Tyr Asn Ile Val Gly Leu His Thr Asn Ile Asp Phe Leu Leu Asn Leu
      385              390              395              400
Ser Gly His Pro Glu Phe Glu Ala Gly Asn Val His Thr Asp Phe Ile
      405              410              415
Pro Gln His His Lys Gln Leu Leu Leu Ser Arg Lys Ala Ala Lys
      420              425              430
Glu Ser Leu Cys Gln Ala Ala Leu Gly Leu Ile Leu Lys Glu Lys Ala
      435              440              445
Met Thr Asp Thr Phe Thr Leu Gln Ala His Asp Gln Phe Ser Pro Phe
      450              455              460
Ser Ser Ser Ser Gly Arg Arg Leu Asn Ile Ser Tyr Thr Arg Asn Met
      465              470              475              480
Thr Leu Lys Asp Gly Lys Asn Ser Phe Arg Leu Leu Gly
      485              490

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<210> 3359

<211> 652

<212> DNA

<213> Homo sapiens

<400> 3359

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120
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180
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240
tccttgtaa caatgtatc attcctgcta ggtgccatat tcattgcttt aagctcaagt
300

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cgcacatcttac tagtgaagta ttctgccaat gaagaaaaca agtatgatta tcttccaact
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 420
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 480
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 540
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 652

<210> 3360

<211> 149

<212> PRT

<213> Homo sapiens

<400> 3360

Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser Thr
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 20 25 30
 Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp
 35 40 45
 Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val
 50 55 60
 Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser
 65 70 75 80
 Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys
 85 90 95
 Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe
 100 105 110
 Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn
 115 120 125
 Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Arg
 130 135 140
 Arg Leu Asn Trp Ile
 145

<210> 3361

<211> 1040

<212> DNA

<213> Homo sapiens

<400> 3361

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 120
 ggagtcgcct gcgcgcgag cggaggccag tgcgccggcg catagcgagc ccgggtctgt
 180
 gatcgccgag cggggagtga agatagtcca agtcctaaga gacagcgct ctctcattca
 240

gtctttgatt atacatcagc atcaccagct ccctcaccac caatgcgacc atgggagatg
 300
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 420
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 480
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 720
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 780
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 900
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 1040

<210> 3362

<211> 252

<212> PRT

<213> Homo sapiens

<400> 3362

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Pro	Ser	Gln	His	His	Phe	Ser	Gly	Glu	Arg	Cys	Asn	Thr	Pro	Ala	Arg
			20					25				30			
Asn	Arg	Arg	Ser	Pro	Pro	Val	Arg	Arg	Gln	Arg	Gly	Arg	Arg	Asp	Arg
			35				40					45			
Leu	Ser	Arg	His	Asn	Ser	Ile	Ser	Gln	Asp	Glu	Asn	Tyr	His	His	Leu
			50			55				60					
Pro	Tyr	Ala	Gln	Gln	Gln	Ala	Ile	Glu	Glu	Pro	Arg	Ala	Phe	His	Pro
					70					75				80	
Pro	Asn	Val	Ser	Pro	Arg	Leu	Leu	His	Pro	Ala	Ala	His	Pro	Pro	Gln
				85				90						95	
Gln	Asn	Ala	Val	Met	Val	Asp	Ile	His	Asp	Gln	Leu	His	Gln	Gly	Thr
			100				105						110		
Val	Pro	Val	Ser	Tyr	Thr	Val	Thr	Thr	Val	Ala	Pro	His	Gly	Ile	Pro
			115				120					125			
Leu	Cys	Thr	Gly	Gln	His	Ile	Pro	Ala	Cys	Ser	Thr	Gln	Gln	Val	Pro
			130			135					140				
Gly	Cys	Ser	Val	Val	Phe	Ser	Gly	Gln	His	Leu	Pro	Val	Cys	Ser	Val

```

145          150          155          160
Pro Pro Pro Met Leu Gln Ala Cys Ser Val Gln His Leu Pro Val Pro
          165          170          175
Tyr Ala Ala Phe Pro Pro Leu Ile Ser Ser Asp Pro Phe Leu Ile His
          180          185          190
Pro Pro His Leu Ser Pro His His Pro Pro His Leu Pro Pro Pro Gly
          195          200          205
Gln Phe Val Pro Phe Gln Thr Gln Gln Ser Arg Ser Pro Leu Gln Arg
          210          215          220
Ile Glu Asn Glu Val Glu Leu Leu Gly Glu His Leu Pro Gly Ala His
225          230          235          240
Pro Gln His Pro His Leu Leu Ile Asn Ile Ser Thr
          245          250

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<210> 3363

<211> 718

<212> DNA

<213> Homo sapiens

<400> 3363

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cagaaggacc ccaggatggc ggtcatcatg cccaggaacg ttggtgatgg ggaatggggt
60
ggccagcatg atcagggacc ccgtcatgcc catgattttt tgggtggcat tggcgaccga
120
gtagctcagg agtgtctccg gagcccactg gagaagcccc ccaacggcct cctcttcccc
180
cagcacgggg actatcagta cggccgcaac aacatctaaa cagaccactt ccaatacagc
240
cggcagagct acccaaaact gtacagtttg aaccgctatg atgtgtagag tccaaaggac
300
aggaccagac tgttggtgac tccttccccg gccccccag cagtatcaga aacttctgac
360
aatcagtga tgtacaaccc agccgagggg acggtgcata actctccatc agaagccctg
420
gggttccctg cccccctga gccgcaggag gatgcgttgc ctgcagtga gacggccgtg
480
agctctgggc aaacctaacc agagaccagt gtcccatgct ctttcttctt ggagcctgtc
540
atctgagggc cgtgtccctg cggagatcct ggccacgttg tacctttcca tgtggaatta
600
ttccccaaag agttagctc agagcacttg tgtctgcatt ccagataaca ttcaggacct
660
gtgtgaaaaa ctgggggtcac tgtggctgta gaccatgaac tggcagtggt ggtgtcca
718

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<210> 3364

<211> 163

<212> PRT

<213> Homo sapiens

<400> 3364

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Met Gly His Trp Ser Leu Phe Arg Phe Ala Gln Ser Ser Arg Pro Ser
1          5          10          15
Ala Leu Gln Ala Thr His Pro Pro Ala Ala His Gly Gly Pro Gly Thr

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	20		25		30										
Pro	Gly	Leu	Leu	Met	Glu	Ser	Tyr	Ala	Pro	Ser	Pro	Arg	Leu	Gly	Cys
	35		40		45										
Thr	Phe	Thr	Asp	Cys	Gln	Lys	Phe	Leu	Ile	Leu	Leu	Trp	Gly	Pro	Gly
	50		55		60										
Lys	Glu	Ser	Pro	Thr	Val	Trp	Ser	Cys	Pro	Leu	Asp	Ser	Thr	His	His
	65		70		75										
Ser	Gly	Ser	Asn	Cys	Thr	Ser	Leu	Gly	Ser	Ser	Ala	Gly	Cys	Ile	Gly
	85		90		95										
Ser	Gly	Leu	Phe	Arg	Cys	Cys	Cys	Gly	Arg	Thr	Asp	Ser	Pro	Arg	Ala
	100		105		110										
Gly	Gly	Arg	Gly	Gly	Arg	Trp	Gly	Ala	Ser	Pro	Val	Gly	Ser	Gly	Asp
	115		120		125										
Thr	Pro	Glu	Leu	Leu	Gly	Arg	Gln	Cys	His	Pro	Lys	Asn	His	Gly	His
	130		135		140										
Asp	Gly	Val	Pro	Asp	His	Ala	Gly	Gln	Pro	Ile	Pro	His	His	Gln	Arg
	145		150		155										
Ser	Trp	Ala													

<210> 3365

<211> 2389

<212> DNA

<213> Homo sapiens

<400> 3365

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120
tcgggtggca gcgccggcg caacgcaggc gtcacggcga cggcggcggc ggctgacggc
180
tggaagggta ggcttccctc accgctcgtc ctcttccctc gctccgctcg gtgtcaggcg
240
cggcggcggc gggcgggcg gacttcgtcc ctctctctgc tccccccac accggagcgg
300
gcactctctg cttcgccatc ccccgacct tcaccccgag gactgggcgc ctctccggc
360
gcagctgagg gagcgggggc cggctctcctg ctcggttgct gagcctccat gtcggataat
420
cagaactgga actcgtcggg ctccgaggag gatccagaga cggagtctgg gcgcctgtg
480
gagcgtctcg gggctctcag taagtggaca aactacattc atgggtggca ggatcgttg
540
gtagttttga aaaataatgc tctgagttac tacaaatctg aagatgaaac agagtattgg
600
tgacaggat ccatctgtct tagcaaggct gtcacacac ctacagattt tgatgaatgt
660
cgatttgata ttagtgtaaa tgatagtgtt tggatatctc gtgctcagga tccagatcat
720
agacagcaat ggatagatgc cattgaacac cacaagactg aatctggata tggatctgaa
780
tcagcttgc gtcgacatgg ctcaatgggt tccttggtgt ctggagcaag tggctactct
840

gcaacatcca cctcttcatt caagaaaggc cacagtttac gtgagaagtt ggctgaaatg
900
gaaacattta gagacatctt atgtagacaa gttgacacgc tacagaagta ctttgatgcc
960
tgtgtctgatg ctgtctctaa ggatgaactt caaagggata aagtggtaga agatgatgaa
1020
gatgactttc ctacaacgcg ttctgatggt gacttcttgc atagtaccaa cggcaataaa
1080
gaaaagtatt ttccacatgt gacacccaaa ggaattaatg gtatagactt taaaggggaa
1140
gcgataactt ttaaagcaac tactgctgga atccttgcaa cactttctca ttgtattgaa
1200
ctaattggta aacgtgagga cagctggcag aagagactgg ataaggaaac tgagaagaaa
1260
agaagaacag aggaagcata taaaaatgca atgacagaaac ttaagaaaaa atcccacttt
1320
ggaggaccag attatgaaga aggccctaac agtctgatta atgaagaaga gttctttgat
1380
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1440
gtgagattac attggcctac atccttgccc tctggagatg cctttctctc tgtggggaca
1500
catagatttg tccaaaagcc ctatagtcgc tcttctccca tgtcttccat tgatctagtc
1560
agtgccctctg atgatgttca cagattcagc tcccagggtg aagagatggt gcagaaccac
1620
atgacttact cattacagga tgtaggcgga gatccaatt ggcagttggt tgtagaagaa
1680
ggagaaatga aggtatacag aagagaagta gaagaaaatg ggattgttct ggatccttta
1740
aaagctaccc atgcagttaa aggcgtcaca ggacatgaag tctgcaatta tttctggaat
1800
gttgacgttc gcaatgactg ggaacaact atagaaaact ttcattgtgtt ggaacatta
1860
gctgataatg caatcatcat ttatcaaaca cacaagaggg tgtggcctgc tctcagcga
1920
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1980
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2040
gtccgtgcca aaataaatgt tgctatgatt tgtcaaacct tggtaaagccc accagagggg
2100
aaccaggaaa tttagcaggga caacatttcta tgcaagatta catatgtagc taatgtgaac
2160
cctggaggat gggcaccagc ctgagtgtta agggcagtg gaaagcgaga gtatcctaaa
2220
tttctaaaac gttttacttc ttacgtccaa gaaaaaactg caggaaagcc tattttgttc
2280
tagtattaac aggtactaga agatatgttt tatctttttt taactttatt tgactaatat
2340
gactgtcaat actaaaattt agttgttgaa agtatttact atgtttttt
2389

<210> 3366

<211> 624

<212> PRT

<213> Homo sapiens

<400> 3366

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Met Ser Asp Asn Gln Asn Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
1      5      10      15
Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
20      25      30
Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35      40      45
Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
50      55      60
Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65      70      75      80
Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
85      90      95
Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100     105     110
Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115     120     125
Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130     135     140
Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145     150     155     160
Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
165     170     175
Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
180     185     190
Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
195     200     205
Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
210     215     220
Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225     230     235     240
Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
245     250     255
Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
260     265     270
Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
275     280     285
Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
290     295     300
Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305     310     315     320
Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
325     330     335
Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
340     345     350
Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
355     360     365
Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
370     375     380
Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met

```

```

385          390          395          400
Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
405          415
Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
420          425          430
Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
435          440          445
Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
450          455          460
Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465          470          475          480
Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Tyr Gln Thr His Lys
485          490          495
Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
500          505          510
Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
515          520          525
Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
530          535          540
Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545          550          555          560
Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
565          570          575
Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
580          585          590
Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
595          600          605
Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
610          615          620

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<210> 3367

<211> 366

<212> DNA

<213> Homo sapiens

<400> 3367

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acgcgtgacg gagaggagag gccaggagat agggagggca gtttgtggat tgaaatgacc
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120
tgccttcccc acttcaggcc tcttagtgtc aaggatgtga gaggcaaggg ctgctgggag
180
agtattttac ggactgaagg aggcgtgccg cctgccctgc cctcctactg gtggaggaa
240
gaggtgctgg gagccccaca actcagggcc ccccgacgcc cagtaaggcc actgtacac
300
cctcctgacc cagaccataa ccagcctccg attgtgcttt tgaccctgtt tccttcaggc
360
accagg
366

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<210> 3368

<211> 104

<212> PRT

<213> Homo sapiens

<400> 3368

```

Met Thr Glu Asn Tyr Ala Thr Glu Val Leu Glu Ala Gly Ile Val Ala
 1           5           10          15
Ser Gln Glu His Gly Gly Cys Leu Pro His Phe Arg Pro Leu Ser Val
          20          25          30
Lys Asp Val Arg Gly Lys Gly Cys Trp Glu Ser Ile Leu Arg Thr Glu
          35          40          45
Gly Gly Val Pro Pro Ala Leu Pro Ser Tyr Trp Trp Arg Lys Glu Val
          50          55          60
Leu Gly Ala Pro Gln Leu Arg Ala Pro Arg Arg Pro Val Arg Pro Leu
65           70           75           80
Tyr Thr Pro Pro Asp Pro Asp His Asn Gln Pro Pro Ile Val Leu Leu
          85           90           95
Thr Leu Phe Pro Ser Gly Thr Arg
100

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<210> 3369

<211> 1405

<212> DNA

<213> Homo sapiens

<400> 3369

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gataaggagc agaaaaatca ggaaaactgt ggtgcaaaga agaataaaaa gaagaggaaa
120
aagggtttat ataatgccaa taaaaatgat gattatgaca acgaggagat cttaacctat
180
gaggaaatgt cactttatca tcagccagca aataggaaga gacctatcat cttgattggt
240
ccacagaact gtggccagaa tgaattgcgt cagaggctca tgaacaaaga aaaggaccgc
300
tttgcatctg cagttcctca tacaaccgg agtaggcgag accaagaagt agccggtaga
360
gattaccact ttgtttcgcg gcaagcattc gaggcagaca tagcagctgg aaagttcatt
420
gagcatgggt aatttgagaa gaatttgat ggaactagca tagattctgt acggcaagtg
480
atcaactctg gcaaaatatg tcttttaagt cttcgtaac agtcattgaa gactctccgg
540
aattcagatt tgaaaccata tattatcttc attgcacccc cttcacaaga aagactctgg
600
gcattattgg ccaaagaagg caagaatcca aagcctgaag agttgagaga aatcattgag
660
aagacaagag agatggagca gaacaatggc cactactttg atacgggcaat tgtgaattcc
720
gatcttgata aagcctatca ggaattgctt aggttaatta acaaacttga tactgaacct
780
cagtgggtac catccacttg gctgaggtga aagaacatc cattctgtgg catgttgagc
840
ttgatctggc aaaaactgcc aataggagga ctgcccgaca ctgcagcaag attgaggata
900

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agatggaagg cagcagtata agctgtagat ctgttcttag atctcttgaa ttagtgagac
 960
 gacagttccc ttaggcagtt tgtgcatggc atccttttatt ctctatacat ggcttttagcg
 1020
 gttcttgccct ctttttgga ttctaaatgg aagctttcaa cagagcattc cttttgtcc
 1080
 tgttaaaacc ttttgttttc acctaaacc tttctgctta gttgtatctc tgtgaaaaac
 1140
 ttgtatacac aagcgtccat gtctcacaca aatattgatg tgattattct taagtgttaa
 1200
 atcattaaca cttaaatgac ttcatggga atattgagca gagggactgt gcttctatgc
 1260
 actgggcaag gcagtatttg cttaggaaac taatttagtc atcagagata ctttccctaaa
 1320
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 1380
 attcatttat atgtcttttg attct
 1405

<210> 3370

<211> 269

<212> PRT

<213> Homo sapiens

<400> 3370

Leu	Val	Pro	Gly	Lys	Ser	Phe	Gln	Gln	Gln	Arg	Glu	Ala	Met	Lys	Gln
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Thr	Ile	Glu	Glu	Asp	Lys	Glu	Gln	Lys	Asn	Gln	Glu	Asn	Cys	Gly	Ala
			20					25					30		
Lys	Lys	Asn	Lys	Lys	Lys	Arg	Lys	Lys	Val	Leu	Tyr	Asn	Ala	Asn	Lys
		35					40					45			
Asn	Asp	Asp	Tyr	Asp	Asn	Glu	Glu	Ile	Leu	Thr	Tyr	Glu	Glu	Met	Ser
		50				55					60				
Leu	Tyr	His	Gln	Pro	Ala	Asn	Arg	Lys	Arg	Pro	Ile	Ile	Leu	Ile	Gly
65					70					75				80	
Pro	Gln	Asn	Cys	Gly	Gln	Asn	Glu	Leu	Arg	Gln	Arg	Leu	Met	Asn	Lys
			85						90					95	
Glu	Lys	Asp	Arg	Phe	Ala	Ser	Ala	Val	Pro	His	Thr	Thr	Arg	Ser	Arg
			100					105						110	
Arg	Asp	Gln	Glu	Val	Ala	Gly	Arg	Asp	Tyr	His	Phe	Val	Ser	Arg	Gln
		115				120						125			
Ala	Phe	Glu	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Phe	Ile	Glu	His	Gly	Glu
		130				135					140				
Phe	Glu	Lys	Asn	Leu	Tyr	Gly	Thr	Ser	Ile	Asp	Ser	Val	Arg	Gln	Val
145				150						155				160	
Ile	Asn	Ser	Gly	Lys	Ile	Cys	Leu	Leu	Ser	Leu	Arg	Thr	Gln	Ser	Leu
			165						170					175	
Lys	Thr	Leu	Arg	Asn	Ser	Asp	Leu	Lys	Pro	Tyr	Ile	Ile	Phe	Ile	Ala
			180					185						190	
Pro	Pro	Ser	Gln	Glu	Arg	Leu	Arg	Ala	Leu	Leu	Ala	Lys	Glu	Gly	Lys
			195					200				205			
Asn	Pro	Lys	Pro	Glu	Glu	Leu	Arg	Glu	Ile	Ile	Glu	Lys	Thr	Arg	Glu
			210			215					220				
Met	Glu	Gln	Asn	Asn	Gly	His	Tyr	Phe	Asp	Thr	Ala	Ile	Val	Asn	Ser

```

225          230          235          240
Asp Leu Asp Lys Ala Tyr Gln Glu Leu Leu Arg Leu Ile Asn Lys Leu
          245          250          255
Asp Thr Glu Pro Gln Trp Val Pro Ser Thr Trp Leu Arg
          260          265

<210> 3371
<211> 790
<212> DNA
<213> Homo sapiens

<400> 3371
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gacagaccag agactccagt caccctcgcc atctgtggaa tcatattctg gctgatcttt
120
ggtttcaaaa gtccggtggc ctggggctgt atggtcccac cccctggggg gggtgaggaa
180
gttgctgtcg tctgaggtac tgccgtacgt gtagtctctg tccccgcttt tgccctggcc
240
aaagaagcac caagggagca tctggaccac caggctgcac accaaccctt ccccgaccg
300
cgattccgac aagagacggg gcacccttca ttgcaaagag atttccccag atcctttctc
360
cttgatctac caaactttcc agatctttcc aaagctgata tcaatgggca gaatccaaat
420
atccagggtc ccatagaggt ggtcgacggt cctgactctg aagcagataa agatcagcat
480
ccggagaata agcccagctg gtcagtcaca tccccgact ggccggcctg gtggcagagg
540
tccctgtcct tgccagggc aaacagcggg gaccaggact acaagtacga cagtacctca
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660
acttttgaaa ccaaagatca gccagaatat gattccacag atggcgaggg tgactggagt
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780
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790

<210> 3372
<211> 198
<212> PRT
<213> Homo sapiens

<400> 3372
Gly Thr Ala Val Arg Val Val Leu Val Pro Ala Phe Ala Leu Ala Lys
1          5          10          15
Glu Ala Pro Arg Glu His Leu Asp His Gln Ala Ala His Gln Pro Phe
20          25          30
Pro Arg Pro Arg Phe Arg Gln Glu Thr Gly His Pro Ser Leu Gln Arg
35          40          45
Asp Phe Pro Arg Ser Phe Leu Leu Asp Leu Pro Asn Phe Pro Asp Leu

```

```

      50              55              60
Ser Lys Ala Asp Ile Asn Gly Gln Asn Pro Asn Ile Gln Val Thr Ile
65              70              75              80
Glu Val Val Asp Gly Pro Asp Ser Glu Ala Asp Lys Asp Gln His Pro
      85              90              95
Glu Asn Lys Pro Ser Trp Ser Val Pro Ser Pro Asp Trp Arg Ala Trp
      100             105             110
Trp Gln Arg Ser Leu Ser Leu Ala Arg Ala Asn Ser Gly Asp Gln Asp
      115             120             125
Tyr Lys Tyr Asp Ser Thr Ser Asp Asp Ser Asn Phe Leu Asn Pro Pro
      130             135             140
Arg Gly Trp Asp His Thr Ala Pro Gly His Arg Thr Phe Glu Thr Lys
145             150             155             160
Asp Gln Pro Glu Tyr Asp Ser Thr Asp Gly Glu Gly Asp Trp Ser Leu
      165             170             175
Trp Ser Val Cys Ser Val Thr Cys Gly Asn Gly Asn Gln Lys Arg Thr
      180             185             190
Arg Ser Cys Gly Tyr Ala
195

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<210> 3373

<211> 726

<212> DNA

<213> Homo sapiens

<400> 3373

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tgtacatggt ttctctgggc tgacaggggc cctgcccttg gggcactgag ccctccctgt
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gggtccctga acagaagcca gggctctgtgc ggcacccacc agctgctggg ccattggcgga
120
gtgttcttgt gcgggccagc gcctgaccgg tgcggggcgc ctcaggagag gagagcttgc
180
tcagtgcgtc acgtagtcag ggctcaggct ggggcccggc tccagagcct ggtcacattc
240
ccaagcttca ttctcttcac ctgtgaattg caggcttccc tgggtgtgcc tgcacatgag
300
ggaagacaca cctgaagcac tgggtccctc catggccttg ggccgcagga accgtggggc
360
cacgagcttg ggaaggacat gtcggaggcc ggcgcctgtg cgggcagaag ctgtgtcttc
420
cagcccttcc accaccagca tgttctcatt tccagggttc tctgtttaaa aaacaaaagt
480
agcgcatcgg tggctcttcc gacgtacacc cagaagcacc cgtccatcga ggacgggctc
540
ccgttttgtg agccgctgct taacttcac tgggttcctg ctgtggctgt ggacgggtgc
600
gtcttgggat cctgcagggg gagggggctg tgaatgtgcg ggttgtgtgt agacgtgggt
660
tggtatagctg tgtgggtgtg tgtgcaagt tagccatggt gtgggtagcc gtgtgggtat
720
atgcat
726

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<210> 3374

<211> 84
 <212> PRT
 <213> Homo sapiens

<400> 3374
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 1 5 10 15
 Phe His His Gln His Val Leu Ile Ser Arg Phe Leu Cys Leu Lys Asn
 20 25 30
 Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro
 35 40 45
 Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile
 50 55 60
 Trp Phe Leu Leu Leu Ala Val Asp Gly Cys Val Leu Gly Ser Cys Arg
 65 70 75 80
 Gly Arg Gly Leu

<210> 3375
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 3375
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 60
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 120
 agccacctgc ctgggctttg ggggcccagc cggcatgggg agccccaggc tccagctggc
 180
 ctgccttggc tctgaaatct aggccaggat gcagagcccg cagtgcggcc agtggagccc
 240
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<211> 970

<212> PRT

<213> Homo sapiens

<400> 3378

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<212> DNA

<213> Homo sapiens

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<211> 1379

<212> DNA

<213> Homo sapiens

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cgtcctactg agcaggaaact gagggcccgt aaagcagcac gggcaggggg acgtgaacgg
720
gctcgcttgg caactgccca ggacaaggcc cgctccaaca aagggtcctt ggccaggatc
780

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tttgagccc cgccaccctc agagagcatg gagggacctt ccttggtcag ggactcctga
840
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900
gaatgatcgt gactaccctg gcagacattt tactgtgttt ctcagaccaa gtgtctactg
960
atggcccaaa catggagttt tgtgggcttc cactgtcccc actccgaact cctgtatgtg
1020
cctggctgag tcacctaatt catactgtca tactagcata attatgacta ttgcatatgc
1080
ttgtttttgt tgactcttgg ctgcctacgt ctgtagggtc ccttgaaaaa cccacttctt
1140
gccccagaa agggccttta tttccaacta ggaggataat gcctagtcca ggcaatcttt
1200
ctctgtttag cagtacacagg tgagggtggt attagcatct tttttatgta gaaaaaattg
1260
agttaatggg gtggactggg ttgggaagaa atacatttcc taatgtattt atagaaaaata
1320
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1379

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<210> 3382

<211> 279

<212> PRT

<213> Homo sapiens

<400> 3382

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Xaa Pro Leu Val Ser Val Asn Met Glu Ala Glu Glu Ser Glu Lys Ala
1      5      10      15
Ala Thr Glu Gln Glu Pro Leu Glu Gly Thr Glu Gln Thr Leu Asp Ala
20     25     30
Glu Glu Glu Gln Glu Glu Ser Glu Glu Ala Ala Cys Gly Ser Lys Lys
35     40     45
Arg Val Val Pro Gly Ile Val Tyr Leu Gly His Ile Pro Pro Arg Phe
50     55     60
Arg Pro Leu His Val Arg Asn Leu Leu Ser Ala Tyr Gly Glu Val Gly
65     70     75     80
Arg Val Phe Phe Gln Ala Glu Asp Arg Phe Val Arg Arg Lys Lys Lys
85     90     95
Ala Ala Ala Ala Ala Gly Gly Lys Lys Arg Ser Tyr Thr Lys Asp Tyr
100    105    110
Thr Glu Gly Trp Val Glu Phe Arg Asp Lys Arg Ile Ala Lys Arg Val
115    120    125
Ala Ala Ser Leu His Asn Thr Pro Met Gly Ala Arg Arg Arg Ser Pro
130    135    140
Phe Arg Tyr Asp Leu Trp Asn Leu Lys Tyr Leu His Arg Phe Thr Trp
145    150    155    160
Ser His Leu Ser Glu His Leu Ala Phe Glu Arg Gln Val Arg Arg Gln
165    170    175
Arg Leu Arg Ala Glu Val Ala Gln Ala Lys Arg Glu Thr Asp Phe Tyr
180    185    190
Leu Gln Ser Val Glu Arg Gly Gln Arg Phe Leu Ala Ala Asp Gly Asp
195    200    205
Pro Ala Arg Pro Asp Gly Ser Trp Thr Phe Ala Gln Arg Pro Thr Glu

```

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      210              215              220
Gln Glu Leu Arg Ala Arg Lys Ala Ala Arg Pro Gly Gly Arg Glu Arg
225              230              235              240
Ala Arg Leu Ala Thr Ala Gln Asp Lys Ala Arg Ser Asn Lys Gly Leu
      245              250              255
Leu Ala Arg Ile Phe Gly Ala Pro Pro Pro Ser Glu Ser Met Glu Gly
      260              265              270
Pro Ser Leu Val Arg Asp Ser
      275

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<210> 3383
<211> 309
<212> DNA
<213> Homo sapiens

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<400> 3383
ttttcttttc ctctgactgt agaacatgct tgctcatcat ggtagcaggg aaaaatgtca
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120
aaatgctcac ttcttaacct cttttgtcct ggagcataga attactgcaa atgctcaccc
180
ctggggagctg tcttgcccc gatctccac acaaacactc cagcatgaaa gagcgagact
240
caatctcaaa aaaaaaaaaagt ttcgggcacc tgaacaggaa ctggtttcca tcataaactc
300
agaaagccc
309

```

```

<210> 3384
<211> 94
<212> PRT
<213> Homo sapiens

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<400> 3384
Met Leu Ala His His Gly Ser Arg Glu Lys Cys Gln Cys Cys Leu His
1      5      10
Thr Asn Phe Val Ala Gly Val Ser Ile Val Val Ile Cys Val Ile Gly
      20      25      30
Asn Ala His Phe Leu Thr Ser Phe Val Leu Glu His Arg Ile Thr Ala
      35      40      45
Asn Ala His Pro Trp Glu Leu Ser Cys Pro Arg Ser Pro Thr Gln Thr
      50      55      60
Leu Gln His Glu Arg Ala Arg Leu Asn Leu Lys Lys Lys Phe Arg
      65      70      75      80
Ala Pro Glu Gln Glu Leu Val Ser Ile Ile Asn Ser Glu Ser
      85      90

```

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<210> 3385
<211> 720
<212> DNA
<213> Homo sapiens

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<400> 3385

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nncctaggag atgaagccgc cagcctgagc aagcctggca gatagacatg gccagacttg
 60
 gttaggggtga gccggccttg ccagagggag gagggctctat gctgaggtct actgatggta
 120
 gtgaaaacac tgacgggtgcg ggggtgggga gcaactgcgtt ccactttctc agccccccac
 180
 tatcctggaa gcttcagggt gggccccagg cagcctccag cttcagcgac caccctgtt
 240
 cctcttgcca ggttctttgt gaacttcccc tcggccaagc agtacttcag ccagttcaag
 300
 cacatggagg atccccgga gatggagcgg agccccagc tcggaagca cgctgcccga
 360
 gtcctggggg ccctcaacac tgcgtggag aacctgcatg accccgaca ggtgtctct
 420
 gtgctgccc ttgtggggaa agccccagc ctcaagcaca aggtggaacc ggtgtacttc
 480
 aagatcctct ctggggctcat tctggagggt gtcgccgagg aatttgcag tgacttccca
 540
 cctgagacgc agagagcctg ggccaagctg cgtggcctca tctacagcca cgtgaccgct
 600
 gcctacaagg aagtgggctg ggtgcagcag gtccccaacy ccaccacccc accggccaca
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 720

<210> 3386

<211> 188

<212> PRT

<213> Homo sapiens

<400> 3386

Met Val Val Lys Thr Val Thr Val Arg Gly Trp Gly Ala Leu Arg Ser
 1 5 10 15
 Thr Ser Ser Ala Pro His Tyr Pro Gly Ser Phe Arg Val Gly Pro Arg
 20 25 30
 Gln Pro Pro Ala Ser Ala Thr Thr Pro Val Pro Leu Ala Arg Phe Phe
 35 40 45
 Val Asn Phe Pro Ser Ala Lys Gln Tyr Phe Ser Gln Phe Lys His Met
 50 55 60
 Glu Asp Pro Leu Glu Met Glu Arg Ser Pro Gln Leu Arg Lys His Ala
 65 70 75 80
 Cys Arg Val Met Gly Ala Leu Asn Thr Val Val Glu Asn Leu His Asp
 85 90 95
 Pro Asp Lys Val Ser Ser Val Leu Ala Leu Val Gly Lys Ala His Ala
 100 105 110
 Leu Lys His Lys Val Glu Pro Val Tyr Phe Lys Ile Leu Ser Gly Val
 115 120 125
 Ile Leu Glu Val Val Ala Glu Glu Phe Ala Ser Asp Phe Pro Pro Glu
 130 135 140
 Thr Gln Arg Ala Trp Ala Lys Leu Arg Gly Leu Ile Tyr Ser His Val
 145 150 155 160
 Thr Ala Ala Tyr Lys Glu Val Gly Trp Val Gln Gln Val Pro Asn Ala
 165 170 175
 Thr Thr Pro Pro Ala Thr Leu Pro Ser Ser Gly Pro

180

185

<210> 3387
<211> 3299
<212> DNA
<213> Homo sapiens

<400> 3387
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atgaggctcg tgatggcgtt ggtaaaggct tcctgggggt ttgccccgcc ggagtaatcc
120
ggaagaggcc tcttattagg gctctggtgg cggcggcgcc ggacccttgg ggtctggacg
180
caacggcgcc gggagcatga acgccccctc agccttcgag tctgtcttgc tcttcgaggg
240
cgagaagaag taagtgcgcg cggctgcggc gggccgagga tcaccattaa caagacaccc
300
aagggtaccac atgcctgttt attcaccatc aacaagaag accacacact gggaaacatc
360
attaaatcac aactcctaaa agaccgcgaa gtgctatttg ctggctacaa agtccccccac
420
cccttggagc acaagatcat catccgagtg cagaccacgc cggactacag ccccagggaa
480
gcctttacca acgcatcac cgacctcgc agtgagctgt ccttgcctga ggagcgcttt
540
cgggtggcca taaaagacaa gcaggaagga attgagtagg ggccagaggg ggcctctgctc
600
ggcctgtgag ccccgctcct acctgtgcct gaccctccgc tccagggtacc acaccgagga
660
gagcggcgccg tccagccatg gggccgcctt gtggccaccc ctcaccctga caccgacgtg
720
ttggccaccc ctaccctga caccgacgtg tcctgtacat agattaggtt ttatatctct
780
aataaagtat agcgaagag acctggatgt ggacttgagc agcggtgact tcgcaagcaa
840
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900
atgaattcat tctggaccaa agatccgggg tccaggggct gctgcggggg ctgtgctgag
960
ccggagagaa gtgtgcaaac ccatgagctc ccaagagtct ctgctctaga agcctcaact
1020
cctgggcctg cctgtcagtc aaagcaggaa cacttcttcc tgacataact gaaacacctt
1080
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1140
accctcatcg gcccaagct gaataagtta gttagctgtg tccctggctc ttgctgagtg
1200
tgtgaggcta catcctcccc cagatggcta cgtgttgga gtccgctcagg gcgggtgaggt
1260
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1320
gggcccaggg ctggggccac ttcaggatct gtgtgggggc ctgcagggct gccggcagca
1380

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1440
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1500
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1560
cccagctctg cctccagctc cacaggcaga tgggtccccc gccgctcccc ttggaggcca
1620
cgatgtcttc attcacaat gccagcccat ccaactctccg tccagatgcc tcggagccct
1680
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1740
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1800
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1980
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2040
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2160
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2220
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2280
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2340
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2460
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2520
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2580
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2640
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2700
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2760
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2820
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2880
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2940
gggtgggacag gcccggttg tccggcagcg tctccaggtg gttgttagac aggtcaagct
3000

cctgcagctg cgctcaggcgg cacaggagtt tgggggtccag gtgctcggaa agcagctcca
 3060
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 3120
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 3180
 gtcgggccac ccggcgtgtg gcgtcgccct gctctcctg gagcccgcca ctggcgctcg
 3240
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 3299

<210> 3388

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3388

Ser	Gly	Arg	Gly	Leu	Leu	Gly	Leu	Trp	Trp	Arg	Arg	Arg	Arg	Thr
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Leu	Gly	Val	Trp	Thr	Gln	Arg	Arg	Arg	Glu	His	Glu	Arg	Pro	Ser
			20					25				30		
Leu	Arg	Val	Val	Leu	Ala	Leu	Arg	Gly	Arg	Glu	Glu	Val	Ser	Asp
		35				40						45		Ala
Gly	Cys	Gly	Gly	Pro	Arg	Ile	Thr	Ile	Asn	Lys	Asp	Thr	Lys	Val
	50				55				60					Pro
Asn	Ala	Cys	Leu	Phe	Thr	Ile	Asn	Lys	Glu	Asp	His	Thr	Leu	Gly
65				70					75					80
Ile	Ile	Lys	Ser	Gln	Leu	Leu	Lys	Asp	Pro	Gln	Val	Leu	Phe	Ala
				85				90					95	Gly
Tyr	Lys	Val	Pro	His	Pro	Leu	Glu	His	Lys	Ile	Ile	Ile	Arg	Val
			100					105					110	Gln
Thr	Thr	Pro	Asp	Tyr	Ser	Pro	Gln	Glu	Ala	Phe	Thr	Asn	Ala	Ile
		115				120						125		Thr
Asp	Leu	Ile	Ser	Glu	Leu	Ser	Leu	Leu	Glu	Glu	Arg	Phe	Arg	Val
	130				135						140			Ala
Ile	Lys	Asp	Lys	Gln	Glu	Gly	Ile	Glu						
145					150									

<210> 3389

<211> 308

<212> DNA

<213> Homo sapiens

<400> 3389

nntgtctcca agcccttcca ccaccagcat gttctcatct ccaggtttct ctgtttaaaa
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 aacaaaagta gcgcacatcggt ggtcttcacg acgtacaccc agaagcaccg gtccatcgag
 120
 gacggggcctc cgtttctgga gccgctgctt aacttcattc gttctcctgct gctggctgtg
 180
 gacgggggaac ctcttgacca gcctcatggg ctctcagag caggaggatg gggaggagag
 240
 cccagcgcag ggcagcccca tcgagctgga ctgaactggc caggccacgt ggagacacca
 300

cggtcgac
308

<210> 3390
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3390
Xaa Val Ser Lys Pro Phe His His Gln His Val Leu Ile Ser Arg Phe
1 5 10 15
Leu Cys Leu Lys Asn Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr
20 25 30
Thr Gln Lys His Pro Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro
35 40 45
Leu Leu Asn Phe Ile Trp Phe Leu Leu Leu Ala Val Asp Gly Glu Pro
50 55 60
Ser Asp Gln Pro His Gly Leu Leu Arg Ala Gly Gly Trp Gly Gly Glu
65 70 75 80
Pro Gln Arg Arg Gln Pro His Arg Ala Gly Leu Asn Trp Pro Gly His
85 90 95
Val Glu Thr Pro Arg Ser
100

<210> 3391
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 3391
atcgtctttt tactttatatt agaaacctgt ttggagggtta tggatgataa acccaatcct
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gaagccctaa gtgacagttc agagcgtctt ttctcctttg gcgtcatcgc agatgttcaa
120
tttgcagact tagaagatgg cttaatttc caaggaacca ggcggcgata ctacagacat
180
agtcttcttc acttacaggg tgccattgaa gactggaata atgaaagcag catgccctgt
240
tgtgtccttc agcttgaggaga tatcatcgat ggatataatg cacagtataa tgcattccaaa
300
aagtccctag aacttggttat ggacatgttc aagaggctta aagtccagat tcatcatata
360
tggggaaacc atgaattcta taacttcagt agagagtatt taacacactc taaacttaac
420
actaagtttc tagaagatca gattgtacat catcctgaga ccatgccttc agaagattat
480
tatgcttacc attttgtacc attccctaaa ttccggttca ttttacttga tgcatatgac
540
ttgagtgtct tgggcgtgga tcagtcttct ccaaaatcac agcagtgatg gaagatattg
600
agggagcaca atccaaatcac ggaactgaat agtcctcaag gactttctga gccccagttt
660
gtccagttta atggaggatt cagccaagaa cagctaaact ggttgaatga agtgctaaca
720

ttctctgaca caaaccaaga aaaggtggtg attgtgagcc atcttcccat ttaccggac
 780
 gcctctgaca atgtgtgcct ggccctggaac tacagagatg ccctggcagt catttggctt
 840
 catgagtgtg tgggtgtgttt ctttgcctggt cacacccatg atgggtggcta ctctgaggat
 900
 ccttttgggt tataccacgt caacctagaa ggagttattg aaacagctcc agacagccaa
 960
 gcctttggga cagttcatgt ctatcctgac aaaatgatgt tgaaagggag aggcagagtt
 1020
 ccagatagaa ttatgaatta caagaaagaa agagccttcc attgttagtc taatttattt
 1080
 taacttgata gaaaatgagc tttgtgtttg tccctcctaa acaaaaaaat aaaaatcctc
 1140
 tgtctcattg tttagtattc agcttgcata acaaaatgta tttatagttt cagttgtgtg
 1200
 tggttgataa aataactcaga aatgttattt tggatcatgt atccattgta agttagaaac
 1260
 aaaccaggga ggaaactgag gcaggggtgt atagt
 1295

<210> 3392

<211> 355

<212> PRT

<213> Homo sapiens

<400> 3392

Ile Val Phe Leu Leu Tyr Leu Glu Thr Cys Leu Glu Val Met Asp Asp
 1 5 10 15
 Lys Pro Asn Pro Glu Ala Leu Ser Asp Ser Ser Glu Arg Leu Phe Ser
 20 25 30
 Phe Gly Val Ile Ala Asp Val Gln Phe Ala Asp Leu Glu Asp Gly Phe
 35 40 45
 Asn Phe Gln Gly Thr Arg Arg Arg Tyr Tyr Arg His Ser Leu Leu His
 50 55 60
 Leu Gln Gly Ala Ile Glu Asp Trp Asn Asn Glu Ser Ser Met Pro Cys
 65 70 75 80
 Cys Val Leu Gln Leu Gly Asp Ile Ile Asp Gly Tyr Asn Ala Gln Tyr
 85 90 95
 Asn Ala Ser Lys Lys Ser Leu Glu Leu Val Met Asp Met Phe Lys Arg
 100 105 110
 Leu Lys Val Pro Val His His Thr Trp Gly Asn His Glu Phe Tyr Asn
 115 120 125
 Phe Ser Arg Glu Tyr Leu Thr His Ser Lys Leu Asn Thr Lys Phe Leu
 130 135 140
 Glu Asp Gln Ile Val His His Pro Glu Thr Met Pro Ser Glu Asp Tyr
 145 150 155 160
 Tyr Ala Tyr His Phe Val Pro Phe Pro Lys Phe Arg Phe Ile Leu Leu
 165 170 175
 Asp Ala Tyr Asp Leu Ser Val Leu Gly Val Asp Gln Ser Ser Pro Lys
 180 185 190
 Tyr Glu Gln Cys Met Lys Ile Leu Arg Glu His Asn Pro Asn Thr Glu
 195 200 205
 Leu Asn Ser Pro Gln Gly Leu Ser Glu Pro Gln Phe Val Gln Phe Asn

```

      210              215              220
Gly Gly Phe Ser Gln Glu Gln Leu Asn Trp Leu Asn Glu Val Leu Thr
225              230              235              240
Phe Ser Asp Thr Asn Gln Glu Lys Val Val Ile Val Ser His Leu Pro
      245              250              255
Ile Tyr Pro Asp Ala Ser Asp Asn Val Cys Leu Ala Trp Asn Tyr Arg
      260              265              270
Asp Ala Leu Ala Val Ile Trp Ser His Glu Cys Val Val Cys Phe Phe
      275              280              285
Ala Gly His Thr His Asp Gly Gly Tyr Ser Glu Asp Pro Phe Gly Val
      290              295              300
Tyr His Val Asn Leu Glu Gly Val Ile Glu Thr Ala Pro Asp Ser Gln
305              310              315              320
Ala Phe Gly Thr Val His Val Tyr Pro Asp Lys Met Met Leu Lys Gly
      325              330              335
Arg Gly Arg Val Pro Asp Arg Ile Met Asn Tyr Lys Lys Glu Arg Ala
      340              345              350
Phe His Cys
      355

```

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<210> 3393
<211> 510
<212> DNA
<213> Homo sapiens

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<400> 3393
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120
agtcggggcg ggtcaaactt cgagtacttg aaacgggagc actcgctgtc gaagccctac
180
caggggtgtg gcacaggcag ttctcactg tggaatctga tgggcaatng catggtgatg
240
accaggtata tccgccttac ccagatatg caaagtaaac aggggtgcctt gtggaaccgg
300
gtgccatggt tcctgagaga ctgggagttg caggtgcact tcaaaatcca tggacaagga
360
aagaagaatc tgcattggga ttgcttgcca atctggtaca caaaggatcg gatgcagcca
420
gggcctgtgt ttggaacat ggacaaattt gtggggcttg gagtatttgt agacacctac
480
ccaatgagg agaagcagcc cttcacgcgt
510

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<210> 3394
<211> 170
<212> PRT
<213> Homo sapiens

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<400> 3394
Xaa Arg Leu Trp Asp Pro Leu Gly Arg Gly Ser Ser Gly Gly Asp Val
1          5          10          15
Cys Arg Leu Gly Met Gly Pro Gly Xaa Val Thr Pro Ser Ser Phe Val

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<210> 3396
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 3396
 Met Glu Ser Lys Pro Ser Arg Ile Pro Arg Arg Ile Ser Val Gln Pro
 1 5 10 15
 Ser Ser Ser Leu Ser Ala Arg Met Met Ser Gly Ser Arg Gly Ser Ser
 20 25 30
 Leu Asn Asp Thr Tyr His Ser Arg Asp Ser Ser Phe Arg Leu Asp Ser
 35 40 45
 Glu Tyr Gln Ser Thr Ser Ala Ser Ala Ser Ala Ser Pro Phe Gln Ser
 50 55 60
 Ala Trp Tyr Ser Glu Ser Glu Ile Thr Gln Gly Ala Arg Ser Arg Ser
 65 70 75 80
 Gln Asn Gln Gln Arg Asp His Asp Ser Lys Arg Pro Lys Leu Ser Cys
 85 90 95
 Thr Asn Cys Thr Thr Ser Ala Gly Arg Asn Val Gly Asn Gly Leu Asn
 100 105 110
 Thr Leu Ser Asp Ser Ser Trp Arg His Ser Gln Val Pro Arg Ser Ser
 115 120 125
 Ser Met Val Leu Gly Ser Phe Gly Thr Asp Leu Met Arg Glu Arg Arg
 130 135 140
 Asp Leu Glu Arg Arg Thr Asp Ser Ser Ile Ser Asn Leu Met Asp Tyr
 145 150 155 160
 Ser His Arg Ser Gly Asp Phe Thr Thr Ser Tyr Val Gln Asp Arg
 165 170 175
 Val Pro Ser Tyr Ser Gln Gly Ala Arg Pro Lys Glu Asn Ser Met Ser
 180 185 190
 Thr Leu Gln Leu Asn Thr Ser Ser Asn His Gln Leu
 195 200 205

<210> 3397
 <211> 492
 <212> DNA
 <213> Homo sapiens

<400> 3397
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 120
 ccacagagag acagtggcac ctacgagcag cccagccccc tgatccatga ccgagactct
 180
 gtgggctccc agccccctct gcctccgggc ctaccccccg gccactatga ctcacccaag
 240
 aacagccaca tccctggaca ttatgacttg cctccagtac ggatccccc atcacctcan
 300
 cttcgacgcc aggatcgttg aggagccagg atggtatggc agaggcagca anacctggct
 360
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 420

cggcaggctg tgaacatgaa caacgcttaa cagagcaagt gatgggagaa taattcatgg
 480
 cttctacat gg
 492

<210> 3398
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 3398
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 Glu Val Met Gly Asp Ala Val Leu Glu Ala Ser His Asn Val Gln Gly
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<210> 3400

<211> 1069

<212> PRT

<213> Homo sapiens

<400> 3400

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Cys	Asp	Val	Leu	Leu	Ile	Val	Gly	Asp	Gln	Lys	Phe	Arg	Ala	His	Lys
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Asn	Val	Leu	Ala	Ala	Ser	Ser	Glu	Tyr	Phe	Gln	Ser	Leu	Phe	Thr	Asn
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Lys	Glu	Asn	Glu	Ser	Gln	Thr	Val	Phe	Gln	Leu	Asp	Phe	Cys	Glu	Pro
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Asp	Ala	Phe	Asp	Asn	Val	Leu	Asn	Tyr	Ile	Tyr	Ser	Ser	Ser	Leu	Phe
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Val	Glu	Lys	Ser	Ser	Leu	Ala	Ala	Val	Gln	Glu	Leu	Gly	Tyr	Ser	Leu
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Gly	Ile	Ser	Phe	Leu	Thr	Asn	Ile	Val	Ser	Lys	Thr	Pro	Gln	Ala	Pro
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Phe	Pro	Thr	Cys	Pro	Asn	Arg	Lys	Lys	Val	Phe	Val	Glu	Asp	Asp	Glu
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Asn	Ser	Ser	Gln	Lys	Arg	Ser	Val	Ile	Val	Cys	Gln	Ser	Arg	Asn	Glu
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Lys	Ser	Trp	Pro	Lys	Asp	Ser	Val	Val	Tyr	Ala	Lys	Ser	Leu	Glu	
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His	Ser	Gly	Ser	Leu	Asp	Asp	Pro	Asn	Arg	Ile	Ser	Leu	Val	Lys	Arg

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260          265          270
Leu Ala Leu Lys Arg Pro Arg Pro Pro Val Leu Ser Val Cys Ser Ser
275          280          285
Ser Glu Thr Pro Tyr Leu Leu Lys Glu Thr Asn Lys Gly Asn Gly Gln
290          295          300
Gly Glu Asp Arg Asn Leu Leu Tyr Tyr Ser Lys Leu Gly Leu Val Ile
305          310          315
Pro Ser Ser Gly Ser Gly Ser Gly Asn Gln Ser Ile Asp Arg Ser Gly
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Pro Leu Val Lys Ser Leu Leu Arg Arg Ser Leu Ser Met Asp Ser Gln
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Val Pro Val Tyr Ser Pro Ser Ile Asp Leu Lys Ser Ser Gln Gly Ser
355          360          365
Ser Ser Val Ser Ser Asp Ala Pro Gly Asn Val Leu Cys Ala Leu Ser
370          375          380
Gln Lys Ser Ser Leu Lys Asp Cys Ser Glu Lys Thr Ala Leu Asp Asp
385          390          395          400
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405          410          415
Gln Ser Thr Asp Arg Glu Gly Ala Ser Pro Val Thr Glu Val Arg Ile
420          425          430
Lys Thr Glu Pro Ser Ser Pro Leu Ser Asp Pro Ser Asp Ile Ile Arg
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Val Thr Val Gly Asp Ala Ala Thr Thr Ala Ala Ser Ser Ser Ser
450          455          460
Val Thr Arg Asp Leu Ser Leu Lys Thr Glu Asp Asp Gln Lys Asp Met
465          470          475          480
Ser Arg Leu Pro Ala Lys Arg Arg Phe Gln Ala Asp Arg Arg Leu Pro
485          490          495
Phe Lys Lys Leu Lys Val Asn Glu His Gly Ser Pro Val Ser Glu Asp
500          505          510
Asn Phe Glu Glu Gly Ser Ser Pro Thr Leu Leu Asp Ala Asp Phe Pro
515          520          525
Asp Ser Asp Leu Asn Lys Asp Glu Phe Gly Glu Leu Glu Gly Thr Arg
530          535          540
Pro Asn Lys Lys Phe Lys Cys Lys His Cys Leu Lys Ile Phe Arg Ser
545          550          555          560
Thr Ala Gly Leu His Arg His Val Asn Met Tyr His Asn Pro Glu Lys
565          570          575
Pro Tyr Ala Cys Asp Ile Cys His Lys Arg Phe His Thr Asn Phe Lys
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595          600          605
Pro Ala Ser Ser Ser His Ala Val Leu Asp Glu Lys Phe Gln Arg Lys
610          615          620
Leu Ile Asp Ile Val Arg Glu Arg Glu Ile Lys Lys Ala Leu Ile Ile
625          630          635          640
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Ala Gln Gln Val Ile Lys Arg Asn Leu Arg Ser Arg Ala Lys Gly Ala

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Lys Val Ala Lys Pro Lys Glu His Ala Pro Leu Ala Ser Pro Val Glu
      705                710                715                720
Asn Lys Glu Val Tyr Gln Cys Arg Leu Cys Asn Ala Lys Leu Ser Ser
      725                730                735
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      740                745                750
Cys Pro Tyr Cys Ser Leu Arg Phe Phe Ser Pro Glu Leu Lys Gln Glu
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His Glu Ser Lys Cys Glu Tyr Lys Lys Leu Thr Cys Leu Glu Cys Met
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      785                790                795                800
His Asn Gln Asn Asn Met Ala Pro Thr Glu Asn Phe Ser Leu Pro Val
      805                810                815
Leu Asp His Asn Gly Asp Val Thr Gly Ser Ser Arg Pro Gln Ser Gln
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Pro Glu Pro Asn Lys Val Asn His Ile Val Thr Thr Lys Asp Asp Asn
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Val Phe Ser Ser Asp Ser Ser Glu Gln Val Asn Phe Asp Ser Glu Asp Ser
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Val Lys Glu Glu Pro Val Glu Glu Ala Glu Glu Ala Pro Glu Ala
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Ser Thr Ala Pro Lys Glu Ala Gly Pro Ser Lys Glu Ala Ser Leu Trp
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Pro Cys Glu Lys Cys Gly Lys Met Phe Thr Val His Lys Gln Leu Glu
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Arg His Gln Glu Leu Leu Cys Ser Val Lys Pro Phe Ile Cys His Val
      930                935                940
Cys Asn Lys Ala Phe Arg Thr Asn Phe Arg Leu Trp Ser His Phe Gln
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Ser His Met Ser Gln Ala Ser Glu Glu Ser Ala His Lys Glu Ser Glu
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Val Cys Pro Val Pro Thr Asn Ser Pro Ser Pro Pro Pro Leu Pro Pro
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Pro Pro Pro Leu Pro Lys Ile Gln Pro Leu Glu Pro Asp Ser Pro Thr
      995                1000                1005
Gly Leu Ser Glu Asn Pro Thr Pro Ala Thr Glu Lys Leu Phe Val Pro
      1010                1015                1020
Gln Glu Ser Asp Thr Leu Phe Tyr His Ala Pro Pro Leu Ser Ala Ile
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Thr Phe Lys Arg Gln Phe Met Cys Lys Leu Cys His Arg Thr Phe Lys
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<211> 579

<212> DNA

<213> Homo sapiens

<400> 3401

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<210> 3402

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3402

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			20					25					30		
Val	Tyr	Thr	Arg	Leu	Gly	Glu	Met	Asn	Asn	Ala	Val	Arg	Asn	Leu	Gln
			35				40					45			
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	50				55				60						
Thr	Val	Gly	Lys	Leu	Cys	Arg	Leu	Ile	Asn	Glu	Asp	Val	Asn	Glu	Gln
	65				70				75				80		
Val	Met	Gln	Val	Leu	Gly	Pro	Glu	Asp	Leu	Gln	Ser	Ile	Ile	Tyr	Lys
			85					90					95		
Leu	Glu	Glu	His	Glu	Glu	Phe	Phe	Pro	Ala	Phe	Gln	Ala	Phe	Thr	Asn
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Asp	Leu	Leu	Glu	Ile	Leu	Glu	Ile	Asp	Asp	Ser	Gly	Cys	His	Cys	Thr
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Cys	Ser	Lys	Glu	Ile	Lys	Ser	Thr	Phe	Ile	Leu	Lys	Thr	Asn	Gln	Ile
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<210> 3403

<211> 1696

<212> DNA

<213> Homo sapiens

<400> 3403

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1500

atgtctacta aaaatacaaa aaaattagct gggcgtagct gcatgcacct gtagtcccag
 1560
 ctgctttggg aggcgtgaggc aggagaatca cttgaacccc cggagggtgga gggtttgagt
 1620
 agcccagatc gtggccattg actccaagcc ttggggacaag tgggaacctc ttccccccaa
 1680
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 1696

<210> 3404

<211> 286

<212> PRT

<213> Homo sapiens

<400> 3404

Met	Ala	Arg	Asn	Ala	Glu	Lys	Ala	Met	Thr	Ala	Leu	Ala	Arg	Phe	Arg
1			5					10						15	
Gln	Ala	Gln	Leu	Glu	Glu	Gly	Lys	Val	Lys	Glu	Arg	Arg	Pro	Phe	Leu
			20					25					30		
Ala	Ser	Glu	Cys	Thr	Glu	Leu	Pro	Lys	Ala	Glu	Lys	Trp	Arg	Arg	Gln
		35					40					45			
Ile	Ile	Gly	Glu	Ile	Ser	Lys	Lys	Val	Ala	Gln	Ile	Gln	Asn	Ala	Gly
		50				55					60				
Leu	Gly	Glu	Phe	Arg	Ile	Arg	Asp	Leu	Asn	Asp	Glu	Ile	Asn	Lys	Leu
				70						75				80	
Leu	Arg	Glu	Lys	Gly	His	Trp	Glu	Val	Arg	Ile	Lys	Glu	Leu	Gly	Gly
				85					90					95	
Pro	Asp	Tyr	Gly	Lys	Val	Gly	Pro	Lys	Met	Leu	Asp	His	Glu	Gly	Lys
			100					105					110		
Glu	Val	Pro	Gly	Asn	Arg	Gly	Tyr	Lys	Tyr	Phe	Gly	Ala	Ala	Lys	Asp
		115				120						125			
Leu	Pro	Gly	Val	Arg	Glu	Leu	Phe	Glu	Lys	Xaa	Thr	Ser	Ser	Ser	Ser
			130			135					140				
Gln	Xaa	Lys	Thr	Arg	Ala	Glu	Leu	Met	Lys	Ala	Ile	Asp	Phe	Glu	Tyr
				150						155				160	
Tyr	Gly	Tyr	Leu	Asp	Glu	Asp	Asp	Gly	Val	Ile	Val	Pro	Leu	Glu	Gln
				165				170						175	
Glu	Tyr	Glu	Lys	Lys	Leu	Arg	Ala	Glu	Leu	Val	Glu	Lys	Trp	Lys	Ala
			180					185					190		
Glu	Arg	Glu	Ala	Arg	Leu	Ala	Arg	Gly	Glu	Lys	Glu	Glu	Glu	Glu	Glu
		195				200					205				
Glu	Glu	Glu	Glu	Ile	Asn	Ile	Tyr	Ala	Val	Thr	Glu	Glu	Glu	Ser	Asp
		210			215						220				
Glu	Glu	Gly	Ser	Gln	Glu	Lys	Gly	Gly	Asp	Asp	Ser	Gln	Gln	Lys	Phe
			225		230				235					240	
Ile	Ala	His	Val	Pro	Val	Pro	Ser	Gln	Gln	Glu	Ile	Glu	Glu	Ala	Leu
				245					250					255	
Val	Arg	Arg	Lys	Lys	Met	Glu	Leu	Leu	Gln	Lys	Tyr	Ala	Ser	Glu	Thr
			260			265						270			
Leu	Gln	Ala	Gln	Ser	Glu	Glu	Ala	Arg	Arg	Leu	Leu	Gly	Tyr		
		275				280						285			

<210> 3405

<211> 402

<212> DNA

<213> Homo sapiens

<400> 3405

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gggtgggagg ccccttgca ggagaggctg gcgttctatc agacagcaat tgaaagcgcc
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agacaagctg gagacagcgc caagatgcgg cgctacgacg gggggcttaa aacctggaa
120
aaactgctgc cctccatccg taagggaat gccattgacg aagcggacat cccgcccca
180
gtggccatag gaaaaggccc ggcgtccacg cctacctaca gccctgcacc caccagccg
240
gccctagaa tcgctcagc cccagagccc agggtcaccc tggagggacc ttctgccacc
300
gccccagcct catctccagg cttgctaag cccagatgc cccagggtcc ctgcagccct
360
ccctctggcc cagttgcaga gccgccagcg cgactacaag ct
402

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<210> 3406

<211> 134

<212> PRT

<213> Homo sapiens

<400> 3406

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Gly Trp Glu Ala Pro Leu Gln Glu Arg Leu Ala Phe Tyr Gln Thr Ala
1      5      10      15
Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser Ala Lys Met Arg Arg Tyr
20     25     30
Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu Leu Ala Ser Ile Arg Lys
35     40     45
Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro Pro Pro Val Ala Ile Gly
50     55     60
Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser Pro Ala Pro Thr Gln Pro
65     70     75     80
Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro Arg Val Thr Leu Glu Gly
85     90     95
Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro Gly Leu Ala Lys Pro Gln
100    105    110
Met Pro Pro Gly Pro Cys Ser Pro Pro Ser Gly Pro Val Ala Glu Pro
115    120    125
Pro Ala Arg Leu Gln Ala
130

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<210> 3407

<211> 535

<212> DNA

<213> Homo sapiens

<400> 3407

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60
tttcccgac accatgcctt ctccggcggtg aggcaggtgg cggcaccgac aggcccgggg
120

```

```

gggacctttc cggacaccc aacctcctcg gtggcgaggg aggtggcggc accgacaggg
180
ccggcgggga cctttcccg ancacctggc ctcttggca agcagggtggc ggcaccaaca
240
ggccccgggg ggacctttcc cggacacctg gcctcctcgg cgaggcaggt ggcagaactg
300
gttccacgtc tgatcttcct tagacaaacc tgccttcaga gaaattgtg ttcaactgga
360
gaaactggaa aatgtactag atattggctg atatgaagga tatatgtttt aagtatgata
420
attcgatttt ggctctgtag ggaaaggctc ttattttaaa aagatgtgca ctagagaaaa
480
aggaaacagc atgtagcaaa tacatccacg gatgtcctcc tggtttaaaa aaaaa
535

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<210> 3408
<211> 131
<212> PRT
<213> Homo sapiens

```

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<400> 3408
Gly Met Arg Gly Asp Gly Glu Glu Pro Pro Arg Thr Ala Pro Ser Arg
1 5 10 15
Ser Ala Gly Thr Phe Pro Gly His His Ala Phe Ser Ala Val Arg Gln
20 25 30
Val Ala Ala Pro Thr Gly Pro Gly Thr Phe Pro Gly His Pro Thr
35 40 45
Ser Ser Val Ala Arg Gln Val Ala Ala Pro Thr Gly Pro Ala Gly Thr
50 55 60
Phe Pro Gly Xaa Pro Gly Leu Leu Gly Lys Gln Val Ala Ala Pro Thr
65 70 75 80
Gly Pro Gly Gly Thr Phe Pro Gly His Leu Ala Ser Ser Ala Arg Gln
85 90 95
Val Ala Glu Leu Val Pro Arg Leu Ile Phe Leu Arg Gln Thr Cys Leu
100 105 110
Gln Arg Lys Leu Cys Ser Thr Gly Glu Thr Gly Lys Cys Thr Arg Tyr
115 120 125
Trp Leu Ile
130

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```

<210> 3409
<211> 959
<212> DNA
<213> Homo sapiens

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<400> 3409
nagatctccg aggcacccg acgggagcgc ttggccatcc tctctccggc agaggagcag
60
acgtttctgt tccaagtgca aaactacaga cacgcgcgcg cacacacgca agcacacgcg
120
gagagagagg aaccttgccg gtccgaggca gctctgcgcg tccctcctcg cgcttagcat
180
ctcgcgccca gcgcggcccg caccgccatg gaggtgctgg agagcgggga gcagggcgtg
240

```


ctgcagtggg accgcaagct gagcgagctg tcagagcccc gggacggcga ggcctcatg
 300
 taccacacgc attctctcaga attctctggat gagttttccc agaagctctt gggtcagctc
 360
 ctgaatgac ctttctctc agagaagagt gtgtcaatgg aggtggaacc ttccccgacg
 420
 tccccggcgc ctctcatcca ggctgagcac agctactccc tgtgcgagga gctcggggc
 480
 cagtcgccct tcacccacat taccaccagt gacagcttca atgacgatga ggtggaaaagt
 540
 nngagaaaat gtacctgtct acagacttcc cttcaacatc catcaagaca gagccagtta
 600
 cagacgaacc acccccagga ctggttcctg ctgtcactct gaccatcaca gccatctcca
 660
 ccncgttgg aaaaggagga acctcctctg gaaatgaaca ctgggggtga ttcctcgtgc
 720
 cagaccatta ttctaaaaat taagctggag cctcatgaag tggatcagtt tctaaacttc
 780
 tctcctaaag aaggtctgtc tngcctccc tgtgtccett tgggttatgg atatggtctc
 840
 tgggtctaca gagagggaaat atggcgagag agctgggatg agtttgtacc acagatgttg
 900
 tagcttgctt tatgaaatag ctctgttctt aaaaaataaa aattttgctt ccaataaa
 959

<210> 3410

<211> 144

<212> PRT

<213> Homo sapiens

<400> 3410

Met	Glu	Val	Leu	Glu	Ser	Gly	Glu	Gln	Gly	Val	Leu	Gln	Trp	Asp	Arg
1				5					10					15	
Lys	Leu	Ser	Glu	Leu	Ser	Glu	Pro	Gly	Asp	Gly	Glu	Ala	Leu	Met	Tyr
			20					25					30		
His	Thr	His	Phe	Ser	Glu	Leu	Leu	Asp	Glu	Phe	Ser	Gln	Asn	Val	Leu
			35				40					45			
Gly	Gln	Leu	Leu	Asn	Asp	Pro	Phe	Leu	Ser	Glu	Lys	Ser	Val	Ser	Met
	50					55				60					
Glu	Val	Glu	Pro	Ser	Pro	Thr	Ser	Pro	Ala	Pro	Leu	Ile	Gln	Ala	Glu
	65				70				75				80		
His	Ser	Tyr	Ser	Leu	Cys	Glu	Glu	Pro	Arg	Ala	Gln	Ser	Pro	Phe	Thr
			85					90					95		
His	Ile	Thr	Thr	Ser	Asp	Ser	Phe	Asn	Asp	Asp	Glu	Val	Glu	Ser	Xaa
			100				105					110			
Arg	Asn	Gly	Thr	Cys	Leu	Gln	Thr	Ser	Leu	Gln	His	Pro	Ser	Arg	Gln
		115				120					125				
Ser	Gln	Leu	Gln	Thr	Asn	His	Pro	Gln	Asp	Ser	Phe	Arg	Leu	Ser	Leu
	130					135					140				

<210> 3411

<211> 958

<212> DNA

<213> Homo sapiens

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<400> 3411
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120
cgacggccct cacagtccgg agcccgcgagg agcccgagc tggcggggag agctgcctcc
180
acggcggggc acccagaccc caccgtcgca gtcgccacca ctcagtcca tccttggtac
240
cggaatggg cttcgatatc tccagtgcac ttgtaactga cttggacacg gaataactaa
300
aactcattc tgtctcatc ccagtgcgc cggcggtgac catctcggt ctttggggt
360
taactgccg tcctctggac tctgtctgac tttgggggca ccatggacca aagtgggatg
420
gagattctg tgacctcat cattaagca cgaatcaga aatacagta ccagactatt
480
agctgtctt tgaactggag cgtggggaaa ctaaaaacgc atctatctaa cgttaccct
540
agcaaacat tgacgaagga tcagagattg gtgtattcgg gcagactgct tcccgatcat
600
ctgcagctga aagacattct cagaaaaaa gatgagatc atattggtca tctagtatgt
660
acttctcga ctctccag ttctccaaa tccagacca atagagaaa tcataagga
720
ttggcatcca gcagaattc tagttcagat cattcaggat caacaactcc atcatctggt
780
caagaaacct tgtctttagc tgtgggttct tcctcagaag gattgaggca gcgtaccctt
840
ccacaagcac aaactgacca agcacagagt caccagtctc catatgtaat gcaaggaaat
900
gtagacaacc aatttctgga gcaagctgct ccacctggat tccagtgtg tcccgcg
958

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<210> 3412

<211> 185

<212> PRT

<213> Homo sapiens

<400> 3412

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Met Asp Gln Ser Gly Met Glu Ile Pro Val Thr Leu Ile Ile Lys Ala
1          5          10          15
Pro Asn Gln Lys Tyr Ser Asp Gln Thr Ile Ser Cys Phe Leu Asn Trp
20         25         30
Thr Val Gly Lys Leu Lys Thr His Leu Ser Asn Val Tyr Pro Ser Lys
35         40         45
Pro Leu Thr Lys Asp Gln Arg Leu Val Tyr Ser Gly Arg Leu Leu Pro
50         55         60
Asp His Leu Gln Leu Lys Asp Ile Leu Arg Lys Gln Asp Glu Tyr His
65         70         75         80
Met Val His Leu Val Cys Thr Ser Arg Thr Pro Pro Ser Ser Pro Lys
85         90         95
Ser Ser Thr Asn Arg Glu Ser His Glu Ala Leu Ala Ser Ser Ser Asn

```


ttttcaaat ttcactctac aaacaacctc accacgaact gttgtgagaa ctgtgggagc
1140
tattgctata gtactctgg tcttgccaa tcccagaagg tttttagttc aacaagtgtc
1200
acggcataca agcagaattc tgcccaaatt cctccatag ccttggggaa gtcattgaga
1260
tcctcagcag aatgattga aaataccaat agcttgggga agacagagct tttctgtctt
1320
attaattgct tatctgtta cagagttaag actgttactt ctgcagggtg ccagggttca
1380
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1440
atatacagct tctgcagctc cagttgtgtg gttgctttcc agaattgtatt tagcaagcca
1500
aaaggacaac actcttcggc ggtgcccttg tctcagggcc aagtgggtgt aagcccgcc
1560
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1620
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1680
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1740
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1800
gaatacaaga agaaaaataa agttgtggca atgtgtgaat attgtaaaa tgagaaaaat
1860
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1920
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1980
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2040
tggtgtgaag attgtatgtc caaatttaca gttctgtttt atcagatggc caagtgtgat
2100
ggttgtaaac gacagggtaa actaagcgag tcataaagt ggcgaggcaa cattaaacat
2160
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2220
ccacaaaata aagtaaatat ttctaaagca aaaactgctg tgacggagct ccttcttgca
2280
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2340
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2460
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2520
gccactttt gcaaacacac tacacagcac aaagaatgtc agacagaatg cctgttctgt
2580
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2640
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2700

gatgctgcaa gagatcagta acttgttctt gattctgctc atgatggggg ctatcttcac
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 3000
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 3060
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 3120
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 3180
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 3240
 ctttaaacag atatatattt tttttaaatg aaaataaaac catatatact attttatttc
 3300
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 3344

<210> 3414

<211> 723

<212> PRT

<213> Homo sapiens

<400> 3414

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Gln	Glu	Leu	Leu	Asp	Lys	Ile	Lys	Glu	Glu	Pro	Asp	Asn	Ala	Gln	Glu
		20						25				30			
Tyr	Gly	Cys	Val	Gln	Gln	Pro	Lys	Thr	Gln	Glu	Ser	Lys	Leu	Lys	Ile
		35				40						45			
Gly	Gly	Val	Ser	Ser	Val	Asn	Glu	Arg	Pro	Ile	Ala	Gln	Gln	Leu	Asn
		50				55					60				
Pro	Gly	Phe	Gln	Leu	Ser	Phe	Ala	Ser	Ser	Gly	Pro	Ser	Val	Leu	Leu
65				70						75				80	
Pro	Ser	Val	Pro	Ala	Val	Ala	Ile	Lys	Val	Phe	Cys	Ser	Gly	Cys	Lys
				85					90					95	
Lys	Met	Leu	Tyr	Lys	Gly	Gln	Thr	Ala	Tyr	His	Lys	Thr	Gly	Ser	Thr
			100					105					110		
Gln	Leu	Phe	Cys	Ser	Thr	Arg	Cys	Ile	Thr	Arg	His	Ser	Ser	Pro	Ala
		115				120						125			
Cys	Leu	Pro	Pro	Pro	Pro	Lys	Lys	Thr	Cys	Thr	Asn	Cys	Ser	Lys	Asp
		130				135					140				
Ile	Leu	Asn	Pro	Lys	Asp	Val	Ile	Thr	Thr	Arg	Phe	Glu	Asn	Ser	Tyr
145				150						155				160	
Pro	Ser	Lys	Asp	Phe	Cys	Ser	Gln	Ser	Cys	Leu	Ser	Ser	Tyr	Glu	Leu
			165						170					175	
Lys	Lys	Lys	Pro	Val	Val	Thr	Ile	Tyr	Thr	Lys	Ser	Ile	Ser	Thr	Lys
			180					185					190		
Cys	Ser	Met	Cys	Gln	Lys	Asn	Ala	Asp	Thr	Arg	Phe	Glu	Val	Lys	Tyr

195				200				205							
Gln	Asn	Val	Val	His	Gly	Leu	Cys	Ser	Asp	Ala	Cys	Phe	Ser	Lys	Phe
210						215					220				
His	Ser	Thr	Asn	Asn	Leu	Thr	Thr	Asn	Cys	Cys	Glu	Asn	Cys	Gly	Ser
225				230						235					240
Tyr	Cys	Tyr	Ser	Ser	Ser	Gly	Pro	Cys	Gln	Ser	Gln	Lys	Val	Phe	Ser
				245						250				255	
Ser	Thr	Ser	Val	Thr	Ala	Tyr	Lys	Gln	Asn	Ser	Ala	Gln	Ile	Pro	Pro
			260					265					270		
Tyr	Ala	Leu	Gly	Lys	Ser	Leu	Arg	Ser	Ser	Ala	Glu	Met	Ile	Glu	Asn
		275					280					285			
Thr	Asn	Ser	Leu	Gly	Lys	Thr	Glu	Leu	Phe	Cys	Ser	Ile	Asn	Cys	Leu
290						295					300				
Ser	Ala	Tyr	Arg	Val	Lys	Thr	Val	Thr	Ser	Ala	Gly	Val	Gln	Val	Ser
305					310					315					320
Cys	His	Ser	Cys	Lys	Thr	Ser	Ala	Ile	Pro	Gln	Tyr	His	Leu	Ala	Met
				325						330				335	
Ser	Asp	Gly	Thr	Ile	Tyr	Ser	Phe	Cys	Ser	Ser	Ser	Cys	Val	Val	Ala
		340						345					350		
Phe	Gln	Asn	Val	Phe	Ser	Lys	Pro	Lys	Gly	Thr	Asn	Ser	Ser	Ala	Val
		355					360					365			
Pro	Leu	Ser	Gln	Gly	Gln	Val	Val	Val	Ser	Pro	Pro	Ser	Ser	Arg	Ser
370					375					380					
Ala	Val	Ser	Ile	Gly	Gly	Gly	Asn	Thr	Ser	Ala	Val	Ser	Pro	Ser	Ser
385					390					395					400
Ile	Arg	Gly	Ser	Ala	Ala	Ala	Ser	Leu	Gln	Pro	Leu	Gly	Glu	Gln	Ser
				405						410				415	
Gln	Gln	Val	Ala	Leu	Thr	His	Thr	Val	Val	Lys	Leu	Lys	Cys	Gln	His
			420					425					430		
Cys	Asn	His	Leu	Phe	Ala	Thr	Lys	Pro	Glu	Leu	Leu	Phe	Tyr	Lys	Gly
		435					440					445			
Lys	Met	Phe	Leu	Phe	Cys	Gly	Lys	Asn	Cys	Ser	Asp	Glu	Tyr	Lys	Lys
450					455						460				
Lys	Asn	Lys	Val	Val	Ala	Met	Cys	Glu	Tyr	Cys	Lys	Ile	Glu	Lys	Ile
465					470					475					480
Val	Lys	Glu	Thr	Val	Arg	Phe	Ser	Gly	Ala	Asp	Lys	Ser	Phe	Cys	Ser
				485						490				495	
Glu	Gly	Cys	Lys	Leu	Leu	Tyr	Lys	His	Asp	Leu	Ala	Lys	Arg	Trp	Gly
			500					505					510		
Asn	His	Cys	Lys	Met	Cys	Ser	Tyr	Cys	Ser	Gln	Thr	Ser	Pro	Asn	Leu
			515				520					525			
Val	Gln	Asn	Arg	Leu	Glu	Gly	Lys	Leu	Glu	Glu	Phe	Cys	Cys	Glu	Asp
530						535					540				
Cys	Met	Ser	Lys	Phe	Thr	Val	Leu	Phe	Tyr	Gln	Met	Ala	Lys	Cys	Asp
545					550					555					560
Gly	Cys	Lys	Arg	Gln	Gly	Lys	Leu	Ser	Glu	Ser	Ile	Lys	Trp	Arg	Gly
				565					570					575	
Asn	Ile	Lys	His	Phe	Cys	Asn	Leu	Phe	Cys	Val	Leu	Glu	Phe	Cys	His
			580					585					590		
Gln	Gln	Ile	Met	Asn	Asp	Cys	Leu	Pro	Gln	Asn	Lys	Val	Asn	Ile	Ser
		595					600						605		
Lys	Ala	Lys	Thr	Ala	Val	Thr	Glu	Leu	Pro	Ser	Ala	Arg	Thr	Asp	Thr
610					615						620				
Thr	Pro	Val	Ile	Thr	Ser	Val	Met	Ser	Leu	Ala	Lys	Ile	Pro	Ala	Thr

625	630	635	640
Leu Ser Thr Gly	Asn Thr Asn Ser Val Leu Lys Gly Ala Val Thr Lys		
	645	650	655
Glu Ala Ala Lys Ile Ile Gln Asp	Glu Ser Thr Gln Glu Asp Ala Met		
	660	665	670
Lys Phe Pro Ser Ser Gln Ser Ser Gln Pro Ser Arg Leu Leu Lys Asn			
	675	680	685
Lys Gly Ile Ser Cys Lys Pro Val Thr Gln Thr Lys Ala Thr Ser Cys			
	690	695	700
Lys Pro His Thr Gln His Lys Glu Cys Gln Thr Glu Cys Pro Val Arg			
705	710	715	720
Ala Val Cys			

<210> 3415

<211> 3501

<212> DNA

<213> Homo sapiens

<400> 3415

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<211> 259

<212> PRT

<213> Homo sapiens

<400> 3416

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<212> DNA

<213> Homo sapiens

<400> 3417

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 3422

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<212> DNA

<213> Homo sapiens

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 caccatctcg ccgaatacgt ccacggctcc caggcctgga ccccgccagc tgacggagag
 420
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 720
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 840
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 960
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 ccctccctct tgtgtgtatg tgacagcgtg tatgtaacgg cttctgattt ctgtgaaagc
 1320
 tgctcagcaa caaacgtact tccaccagat gtgtccccag atccacagca ggcacatatc
 1380
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<210> 3426

<211> 410

<212> PRT

<213> Homo sapiens

<400> 3426

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 Ala Pro Gly Pro Ala Ser Arg Arg Gly Ala Val Gln Ala Gly Gly Asp
 20 25 30
 Ser Leu Gly Arg Asp Pro Gly Arg Glu Glu Val Arg Pro Arg Gly
 35 40 45
 Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp Pro Arg His Ser
 50 55 60
 Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu Glu Leu Pro His

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65          70          75          80
Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala Pro Gly Ala Glu
85
Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg Arg His Ala Glu
100
Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala Glu Tyr Val His
115
Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu Gly Ala Gly Lys
130
Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu Ile Glu Ser Glu
145
Ala Gly Glu Glu Ser Glu Ser Glu Glu Ser Glu Ser Glu Glu Glu
165
Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp Glu Glu Ser Glu
180
Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu Ser Glu Ala Glu
195
Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu Gly Glu Thr Glu
210
Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu Ala Glu Arg Val
225
Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu Ser Thr Tyr Cys
245
Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro Val Ile Gly Ala
260
His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala Phe Glu Glu Leu
275
Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met Ile Glu Leu Val
290
Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val Thr Arg Asp Gln
305
Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val Gln Lys Val Ile
325
Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp Ile Gln Glu Ala
340
Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp Ile Gln Ser His
355
Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys Glu Gln Leu Asp
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Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly Asp Glu Glu Gly
385
Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
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410

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<210> 3427

<211> 580

<212> DNA

<213> Homo sapiens

<400> 3427

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120

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gggcttgat tgagacttgg accttctgag cactggcaga tgtactggct tctcttcagg
 180
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 240
 cagcatggaa gaggccaag ttcccatatt gctcatcttc tcacaatctt ctgtttccat
 300
 ctcttcaaaa ttttgcagag aatacaatga tggccttggc ttgttttctc catccaccga
 360
 agccccctgtg atattggaca atgccaaga atccatcgaa tccgaacac tttgctctgg
 420
 tttcaggctt gacagacact ccagggaatc ttcataccac tgtgtttcat catgattata
 480
 ccctgaagcc ccatgggtcca gttccaattc ctgaagcctt ctactgcttg cagggcctgg
 540
 gtggctgcca taagcagaat cgcccagtc atcttgtgac
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<210> 3428

<211> 132

<212> PRT

<213> Homo sapiens

<400> 3428

Met	Asp	Ser	Leu	Ala	Leu	Ser	Asn	Ile	Thr	Gly	Ala	Ser	Val	Asp	Gly
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Glu	Asn	Lys	Pro	Arg	Pro	Ser	Leu	Tyr	Ser	Leu	Gln	Asn	Phe	Glu	Glu
			20					25					30		
Met	Glu	Thr	Glu	Asp	Cys	Glu	Lys	Met	Ser	Asn	Met	Gly	Thr	Leu	Asn
			35				40					45			
Ser	Ser	Met	Leu	His	Arg	Ser	Ala	Glu	Ser	Leu	Lys	Ser	Leu	Ser	Ser
			50			55				60					
Glu	Leu	Cys	Pro	Glu	Lys	Ile	Leu	Pro	Glu	Glu	Lys	Pro	Val	His	Leu
				70					75					80	
Pro	Val	Leu	Arg	Arg	Ser	Lys	Ser	Gln	Ser	Arg	Pro	Gln	Gln	Val	Lys
			85					90						95	
Phe	Ser	Asp	Asp	Val	Ile	Asp	Asn	Gly	Asn	Tyr	Asp	Ile	Glu	Ile	Arg
			100				105					110			
Gln	Pro	Pro	Met	Ser	Glu	Arg	Thr	Arg	Arg	Arg	Val	Tyr	Asn	Phe	Glu
			115				120					125			
Glu	Arg	Gly	Ser												
			130												

<210> 3429

<211> 634

<212> DNA

<213> Homo sapiens

<400> 3429

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 120
 gtcagcttcc ttttcatact ttccggcggt tctctccaag agcagggtgca ccagggaact
 180

gtccctctgt cctacacggt caccacagt acgacccaag gcttcccctt gcctacaggc
 240
 cagcacatcc ctggctgcag tgcccagcag ctcccagcat gctccgtgat gttcagtggg
 300
 cagcattacc ccctctgctg cctcccgcgc ccgcttatcc aggcggtgcac catgcagcag
 360
 ctgcctgtgt cctatcaggc ctacccccac ctcatctcca gtgaccacta catctgcac
 420
 cccccaccac cgggcacaca cccagcagct ccagggtctg tataaagaac cctgtggaag
 480
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 ttgaaacact ctattaccaa atgtgaacac gcgt
 634

<210> 3430

<211> 122

<212> PRT

<213> Homo sapiens

<400> 3430

Phe	Leu	Leu	Arg	Val	Ala	Leu	Ala	Val	Ser	Phe	Leu	Phe	Ile	Leu	Ser
1				5				10					15		
Arg	Arg	Ser	Leu	His	Glu	Gln	Val	His	Gln	Gly	Pro	Val	Pro	Leu	Ser
			20					25					30		
Tyr	Thr	Val	Thr	Thr	Val	Thr	Thr	Gln	Gly	Phe	Pro	Leu	Pro	Thr	Gly
		35					40					45			
Gln	His	Ile	Pro	Gly	Cys	Ser	Ala	Gln	Gln	Leu	Pro	Ala	Cys	Ser	Val
	50					55				60					
Met	Phe	Ser	Gly	Gln	His	Tyr	Pro	Leu	Cys	Cys	Leu	Pro	Pro	Pro	Leu
65					70				75					80	
Ile	Gln	Ala	Cys	Thr	Met	Gln	Gln	Leu	Pro	Val	Pro	Tyr	Gln	Ala	Tyr
			85					90						95	
Pro	His	Leu	Ile	Ser	Ser	Asp	His	Tyr	Ile	Leu	His	Pro	Pro	Pro	Pro
			100				105							110	
Gly	Thr	His	Pro	Ala	Ala	Pro	Gly	Ser	Val						
		115					120								

<210> 3431

<211> 1396

<212> DNA

<213> Homo sapiens

<400> 3431

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 120
 ctgcgtggga gcagcgtccc aatgccagcg cgtcacgtcg ccagcgtgc cctagcacgc
 180
 agcgccgcca gccgtgtcgc caacagtacc aaatcgctgt gcagcggcctt cgccccgccg
 240

gacttcaacc attgacctca ggattgggac tataatggcc ttctgtgtct caccaccaac
 300
 gccatcgcc agtgggatct ggtgtgtgac ctgggctggc aggtgatctt ggagcagatc
 360
 ctcttcattt tgggctttgc ctccggctac ctgttctctg gttaccccg cagacagattt
 420
 ggccgctcgc ggatttgtgt gctgaccttg gggctggtgg gccctctggt agtaggaggg
 480
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 540
 gccggtgttg acctgggtgt ctacctgatg cgcttgagac tgtgcgacct aaccagagg
 600
 cttcgggttg ccctggcagg ggagttggtg ggggtgggag ggcacttcct gttcctgggc
 660
 ctggcccttg tctctaagga ttggcgattc ctacagcgaa tgatcaccgc tccctgcac
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 960
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 1020
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 1200
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 1260
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 1380
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<210> 3432

<211> 296

<212> PRT

<213> Homo sapiens

<400> 3432

Met Ala Leu Arg Phe Leu Leu Gly Phe Leu Leu Ala Gly Val Asp Leu
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 20 25 30
 Arg Val Ala Leu Ala Gly Glu Leu Val Gly Val Gly Gly His Phe Leu
 35 40 45
 Phe Leu Gly Leu Ala Leu Val Ser Lys Asp Trp Arg Phe Leu Gln Arg

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      50              55              60
Met Ile Thr Ala Pro Cys Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly
65              70              75              80
Leu Phe Leu Glu Ser Ala Arg Trp Leu Ile Val Lys Arg Gln Ile Glu
      85              90              95
Glu Ala Gln Ser Val Leu Arg Ile Leu Ala Glu Arg Asn Arg Pro His
      100              105              110
Gly Gln Met Leu Gly Glu Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu
      115              120              125
Asn Thr Cys Pro Leu Pro Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu
      130              135              140
Leu Asn Tyr Arg Asn Ile Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr
145              150              155              160
Asn Phe Ile Ala His Ala Ile Arg His Cys Tyr Gln Pro Val Gly Gly
      165              170              175
Gly Gly Ser Pro Ser Asp Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly
      180              185              190
Thr Ala Ala Leu Ala Cys Val Phe Leu Gly Val Thr Val Asp Arg Phe
      195              200              205
Gly Arg Arg Gly Ile Leu Leu Leu Ser Met Thr Leu Thr Gly Ile Ala
210              215              220
Ser Leu Val Leu Leu Gly Leu Trp Asp Cys Glu His Pro Ile Phe Pro
225              230              235              240
Thr Val Trp Ala Gln Gln Gly Asn Pro Asn Arg Asp Leu Asn Glu Ala
      245              250              255
Ala Ile Thr Thr Phe Ser Val Leu Gly Leu Phe Ser Ser Gln Ala Ala
260              265              270
Ala Ile Leu Ser Thr Leu Leu Ala Glu Val Ile Pro Thr Thr Val
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Arg Gly Arg Gly Leu Gly Leu Ile
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<210> 3433

<211> 1257

<212> DNA

<213> Homo sapiens

<400> 3433

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120
ccgagccact ccggttccca caccaggtcg aacttgaaaa gggacgtcgc ccacctgtac
180
cgaggagtgc gctcgcgcta catcatgggg tcaggagaat ccttcacgca gctgcagcag
240
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300
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360
tacaccaact gcggtgagca cgcgccagg ggaggggcct tccgcggtct ccgtgtcacc
420
ggtgaggact cgcggggggg agggcagggg gtcctgtctg tctcagtggt gccgtacgac
480

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 720
 ctataccacc accctgtcta cacaatccac ccattctacac catcacctct cctctgtcta
 780
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 840
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 900
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 960
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 1020
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 1080
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 1257

<210> 3434

<211> 311

<212> PRT

<213> Homo sapiens

<400> 3434

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Arg	Pro	Ser	Ser	Val	Pro	Pro	Ser	Pro	Ser	Pro	Arg	Pro	Leu	Pro	Gly
			20				25						30		
Gly	Arg	Gln	Arg	Pro	Gln	Arg	Pro	Ser	His	Ser	Arg	Ser	His	Thr	Arg
		35				40						45			
Ser	Asn	Leu	Lys	Arg	Asp	Val	Ala	His	Leu	Tyr	Arg	Gly	Val	Gly	Ser
	50				55					60					
Arg	Tyr	Ile	Met	Gly	Ser	Gly	Glu	Ser	Phe	Met	Gln	Leu	Gln	Gln	Arg
65					70				75					80	
Leu	Leu	Arg	Glu	Lys	Glu	Ala	Lys	Ile	Arg	Lys	Ala	Leu	Asp	Arg	Leu
				85				90						95	
Arg	Lys	Lys	Arg	His	Leu	Leu	Arg	Arg	Gln	Arg	Thr	Arg	Arg	Glu	Phe
			100				105						110		
Pro	Val	Ile	Ser	Val	Val	Gly	Tyr	Thr	Asn	Cys	Gly	Glu	His	Ala	Pro
		115				120						125			
Arg	Gly	Gly	Ala	Phe	Arg	Gly	Leu	Arg	Val	Thr	Gly	Glu	Asp	Ser	Pro
		130				135						140			
Gly	Gly	Gly	Gln	Gly	Val	Pro	Val	Val	Ser	Val	Val	Pro	Tyr	Asp	Ser
145				150					155					160	
Cys	Gly	Glu	His	Val	Pro	Arg	Arg	Gly	Gly	Ser	His	Gly	Arg	Arg	Val

165										170					175				
Gly	Tyr	Thr	Ser		Cys	Cys	Glu	Ser	Ser	Pro	Arg	Arg	Arg	Val	Ser	Cys			
				180					185					190					
Gly	Leu	Cys	Val		Gly	Tyr	Ser	Ser	Gln	Gly	Glu	Asp	Val	Ile	Tyr	Pro			
				195					200					205					
Ile	Leu	Pro	Ser		Arg	Ala	Leu	Pro	Pro	Cys	Leu	Tyr	His	Asn	Leu	Pro			
				210					215					220					
Ser	Ile	Tyr	Thr		Ile	Leu	Leu	Ser	Arg	Pro	Ser	Pro	Leu	Pro	Tyr	Leu			
				225					230					235					
Tyr	His	His	Pro		Val	Tyr	Thr	Ile	His	Pro	Ser	Thr	Pro	Ser	Pro	Leu			
				245					250					255					
Leu	Cys	Leu	Tyr		His	Pro	Pro	Val	Tyr	Thr	Ser	Thr	Thr	Thr	Pro	Ser			
				260					265					270					
Ile	Pro	Pro	Pro		Arg	Leu	His	Asn	Pro	Pro	Val	Tyr	Thr	Thr	Met	Ser			
				275					280					285					
Pro	Ser	Ser	Ala		Pro	Ser	Ser	Cys	Leu	His	Trp	His	His	Cys	Pro	Ser			
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Tyr	Thr	Thr	Thr		Pro	Ser	Thr												
				305					310										

<210> 3435

<211> 1225

<212> DNA

<213> Homo sapiens

<400> 3435

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180	gacagcaatg	ccgataccta	ctgggagagc	gatgggtccc	agtgccaa	ctgggtacgg
240	cttactatga	agaagggcag	cattgtcaag	aagctgctac	tcgcagtggg	taccacagat
300	gacaaacttta	tgccaaagcg	gggtgggtgtc	tatgggggtg	aaggggacaa	cctgaagaag
360	ctgagtgcg	tgagcattga	cnnagagacc	tcacggggn	atgtctgtgt	cctggaggac
420	atgaccgtcc	acctcccgat	catcgagatc	cgcacgtgg	agtgccgaga	tgatgggatt
480	gatgttcgtc	tccgaggggt	caagatcaag	tcactagac	agcgggaact	agggttgaat
540	gcagacctgt	tccagccaac	tagtctgggtg	cgatatccac	gcctagaagg	caccgacctt
600	gaagtactgt	accgcagagc	tgctcctctg	cagagattca	tcaagatcct	cgatagtgtc
660	ctgcaccacc	tggtacctgc	ctgggaccac	acactgggca	ccttcagtga	gattaagcaa
720	gtgaagcagt	tctactgtct	gtcccgcgag	cggccaggcc	tggtggctca	gtgcctgcgt
780	gactctgaga	gcagcaagcc	cagcttcatg	ccacgcctat	acatcaaccg	ccgtcttgcc
840	atggaacacc	gtgcctgccc	ctctcgagac	cctgcctgca	agaatgcagt	cttaccaccg

gtatatgaag gcctcaagcc ctctgacaaa tatgaaaagc ccttggaacta cagggtggccc
 900
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 1020
 acccccgctg cctcgccctt cttgtacgc acagccaacc agggcaatgg cactggtgag
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 1200
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<210> 3436

<211> 408

<212> PRT

<213> Homo sapiens

<400> 3436

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 20 25 30
 Glu Phe Asn Val Ser Cys Leu Thr Asp Ser Asn Ala Asp Thr Tyr Trp
 35 40 45
 Glu Ser Asp Gly Ser Gln Cys Gln His Trp Val Arg Leu Thr Met Lys
 50 55 60
 Lys Gly Thr Ile Val Lys Lys Leu Leu Leu Ala Val Asp Thr Thr Asp
 65 70 75 80
 Asp Asn Phe Met Pro Lys Arg Val Val Val Tyr Gly Gly Glu Gly Asp
 85 90 95
 Asn Leu Lys Lys Leu Ser Asp Val Ser Ile Asp Xaa Arg Pro Ser Ser
 100 105 110
 Gly Xaa Val Cys Val Leu Glu Asp Met Thr Val His Leu Pro Ile Ile
 115 120 125
 Glu Ile Arg Ile Val Glu Cys Arg Asp Asp Gly Ile Asp Val Arg Leu
 130 135 140
 Arg Gly Val Lys Ile Lys Ser Ser Arg Gln Arg Glu Leu Gly Leu Asn
 145 150 155 160
 Ala Asp Leu Phe Gln Pro Thr Ser Leu Val Arg Tyr Pro Arg Leu Glu
 165 170 175
 Gly Thr Asp Pro Glu Val Leu Tyr Arg Arg Ala Val Leu Leu Gln Arg
 180 185 190
 Phe Ile Lys Ile Leu Asp Ser Val Leu His His Leu Val Pro Ala Trp
 195 200 205
 Asp His Thr Leu Gly Thr Phe Ser Glu Ile Lys Gln Val Lys Gln Phe
 210 215 220
 Leu Leu Leu Ser Arg Gln Arg Pro Gly Leu Val Ala Gln Cys Leu Arg
 225 230 235 240
 Asp Ser Glu Ser Ser Lys Pro Ser Phe Met Pro Arg Leu Tyr Ile Asn
 245 250 255
 Arg Arg Leu Ala Met Glu His Arg Ala Cys Pro Ser Arg Asp Pro Ala

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                260                265                270
Cys Lys Asn Ala Val Phe Thr Gln Val Tyr Glu Gly Leu Lys Pro Ser
275                280                285
Asp Lys Tyr Glu Lys Pro Leu Asp Tyr Arg Trp Pro Met Arg Tyr Asp
290                295                300
Gln Trp Trp Glu Cys Lys Phe Ile Ala Glu Gly Ile Asp Gln Gly
305                310                315                320
Gly Gly Phe Arg Asp Ser Leu Ala Asp Met Ser Glu Glu Leu Cys Pro
325                330                335
Ser Ser Ala Asp Thr Pro Val Pro Leu Pro Phe Phe Val Arg Thr Ala
340                345                350
Asn Gln Gly Asn Gly Thr Gly Glu Ala Arg Asp Met Tyr Val Pro Asn
355                360                365
Pro Ser Cys Arg Asp Phe Ala Lys Tyr Glu Trp Ile Gly Gln Leu Met
370                375                380
Gly Ala Ala Leu Arg Gly Lys Glu Phe Leu Val Leu Ala Leu Pro Gly
385                390                395                400
Phe Val Trp Lys Gln Leu Ser Ala
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<210> 3437

<211> 2081

<212> DNA

<213> Homo sapiens

<400> 3437

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 1980
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<210> 3438

<211> 105

<212> PRT

<213> Homo sapiens

<400> 3438

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 20 25 30
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Arg	Gly	Pro	Arg	Ser	Ala	Gly
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Pro	Leu	Arg	Val	Pro	Cys	Leu
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<210> 3439

<211> 1519

<212> DNA

<213> Homo sapiens

<400> 3439

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 120
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 360
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<210> 3440

<211> 287

<212> PRT

<213> Homo sapiens

<400> 3440

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			20					25					30		
Val	Ala	Ala	Ala	Ala	Arg	Trp	Pro	Arg	Gln	Pro	Arg	His	Pro	Arg	His
			35				40					45			
Thr	Ser	Pro	Met	Pro	Pro	Pro	Ala	Ala	Leu	Arg	Pro	Pro	Ala	Gly	Pro
			50			55				60					
Arg	Arg	Pro	Arg	Xaa	Pro	Gly	Gly	Pro	Gln	His	His	Gln	Pro	Gln	Pro
65				70				75					80		
Pro	Leu	Trp	Thr	Pro	Thr	Pro	Pro	Ser	Pro	Ala	Ser	Asp	Trp	Pro	Pro
			85					90					95		
Leu	Pro	Pro	Asn	Arg	Pro	Pro	Gln	Asn	Pro	Gly	Pro	Thr	Leu	Pro	Trp
			100					105					110		
Arg	Gln	Arg	Asp	Lys	Gly	Gly	Pro	Ser	Pro	Leu	Pro	Glu	Ala	Arg	Thr
			115				120					125			
Pro	Trp	Gly	Gly	Gly	Glu	Asp	Val	Ser	Ala	Gly	Pro	Leu	Xaa	Thr	Pro
			130			135				140					
Phe	Leu	Ser	Ala	Pro	Leu	Val	Pro	Arg	Ser	Pro	Gly	Gly	Glu	Ser	Ala
145				150					155				160		
Asp	Ser	Ser	Gln	Ala	Gly	Thr	Arg	Leu	Val	Pro	Glu	His	Ala	Ala	Ala
			165					170					175		
His	Thr	Gln	Gly	His	Gly	Pro	Ser	Gly	Pro	Gly	Thr	Trp	Ser	Gly	Ser
			180				185						190		
Glu	Arg	Pro	Gly	Cys	Leu	Ala	Asp	Arg	Thr	Ser	Glu	Thr	Thr	Gln	Pro
		195				200					205				
Ser	Phe	Glu	Asp	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Gly	Val	Pro	Trp	Arg
		210				215					220				
Thr	Thr	Leu	Ala	Glu	Thr	Leu	Leu	Ile	Pro	Gly	Leu	Glu	Leu	Leu	Gly
225				230					235				240		
Gly	Arg	Gln	Ala	Ser	Thr	Pro	Thr	Leu	Gly	Asn	Ala	Glu	Pro	Leu	Arg
			245					250					255		
Met	Cys	Ala	Arg	Gly	Arg	Val	Cys	Val	Phe	Leu	Arg	Val	Ser	Leu	Phe

	260		265		270									
Arg	Ser	Asn	Leu	Val	Pro	Gly	Ala	Ala	Gly	Leu	Cys	Met	Leu	Val
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<210> 3441
 <211> 2074
 <212> DNA
 <213> Homo sapiens

<400> 3441
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 1320

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<210> 3442

<211> 374

<212> PRT

<213> Homo sapiens

<400> 3442

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20     25     30
Ala Glu Leu Leu Met Ser Leu His Asp Leu Asp Val Gly Glu Ile Cys
35     40     45
Thr Val Asp Pro Cys His Lys Phe Thr Trp Cys Leu Asp Ala Cys Ile
50     55     60
Arg Glu Arg Phe Val Asp Ser Lys Arg Ala Arg Glu Leu Gln Gly Phe
65     70     75     80
Leu Asp Asp Val Lys Lys Gly Gln Glu Gln Val Leu Gly Asp Leu Ser
85     90     95
Met Ile Leu Cys Asp Pro Phe Ala Ile Asn Thr Leu Ala Leu Ser Thr
100    105    110
Val Arg His Leu Gln Glu Leu Val Gly Gln Glu Thr Leu Pro Arg Asp
115    120    125
Ser Pro Asp Leu Leu Leu Leu Arg Leu Leu Ala Leu Gly Gln Gly
130    135    140
Ala Trp Asp Met Ile Asp Ser Gln Val Phe Lys Glu Pro Lys Met Glu
145    150    155    160
Val Glu Leu Ile Thr Arg Phe Leu Pro Met Leu Met Ser Phe Leu Val

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Asp Asp Tyr Thr Phe Asn Val Asp Gln Lys Leu Pro Ala Glu Glu Lys
      180              185              190
Ala Pro Val Ser Tyr Pro Asn Thr Leu Pro Glu Ser Phe Thr Lys Phe
      195              200              205
Leu Gln Glu Gln Arg Met Ala Cys Glu Val Gly Leu Tyr Tyr Val Leu
      210              215              220
His Ile Thr Lys Gln Arg Asn Lys Asn Ala Leu Leu Arg Leu Leu Pro
      225              230              235              240
Gly Leu Val Glu Thr Phe Gly Asp Leu Ala Phe Gly Asp Ile Phe Leu
      245              250              255
His Leu Leu Thr Gly Asn Leu Ala Leu Leu Ala Asp Glu Phe Ala Leu
      260              265              270
Glu Asp Phe Cys Ser Ser Leu Phe Asp Gly Phe Phe Leu Thr Ala Ser
      275              280              285
Pro Arg Lys Glu Asn Val His Arg His Ala Leu Arg Leu Leu Ile His
      290              295              300
Leu His Pro Arg Val Ala Pro Ser Lys Leu Glu Ala Leu Gln Lys Ala
      305              310              315              320
Leu Glu Pro Thr Gly Gln Ser Gly Glu Ala Val Lys Glu Leu Tyr Ser
      325              330              335
Gln Leu Gly Glu Lys Leu Glu Gln Leu Asp His Arg Lys Pro Ser Pro
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Ala Gln Ala Ala Glu Thr Pro Ala Leu Glu Leu Pro Leu Pro Ser Val
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Pro Ala Pro Ala Pro Leu
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<210> 3443

<211> 2070

<212> DNA

<213> Homo sapiens

<400> 3443

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600

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<210> 3444

<211> 579

<212> PRT

<213> Homo sapiens

<400> 3444

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          20          25          30
Ser Glu Asn Val Glu Lys Ser Lys Ala Tyr Lys Leu Asn Pro Lys Phe
          35          40          45
Cys Ser Leu Ser Phe Gln Ala Thr Lys Cys Lys Leu Ala Gly Leu Glu
          50          55          60
Val Leu Ser Asp Asp Pro Asp Leu Val Lys Val Val Glu Ser Leu Thr
65          70          75          80
Cys Gly Lys Ile Phe Ala Val Glu Ile Leu Asp Lys Ala Asp Ile Pro
          85          90          95
Leu Val Val Leu Tyr Asp Thr Ser Gly Glu Asp Asp Ile Asn Ile Asn
          100          105          110
Ala Thr Cys Leu Lys Ala Ile Cys Asp Lys Ser Leu Glu Val His Leu
          115          120          125
Gln Val Asp Ala Met Tyr Thr Asn Val Lys Ile Thr Asn Ile Cys Ser
          130          135          140
Asp Gly Thr Leu Tyr Cys Gln Val Pro Cys Lys Gly Leu Asn Lys Leu
145          150          155          160
Ser Asp Leu Leu Arg Lys Ile Glu Asp Tyr Phe His Cys Lys His Met
          165          170          175
Thr Ser Glu Cys Phe Val Ser Leu Pro Phe Cys Gly Lys Ile Cys Leu
          180          185          190
Phe His Cys Lys Gly Lys Trp Leu Arg Val Glu Ile Thr Asn Val His
          195          200          205
Ser Ser Arg Ala Leu Asp Val Gln Phe Leu Asp Ser Gly Thr Val Thr
210          215          220
Ser Val Lys Val Ser Glu Leu Arg Glu Ile Pro Pro Arg Phe Leu Gln
225          230          235          240
Glu Met Ile Ala Ile Pro Pro Gln Ala Ile Lys Cys Cys Leu Ala Asp
          245          250          255
Leu Pro Gln Ser Ile Gly Met Trp Thr Pro Asp Ala Val Leu Trp Leu
          260          265          270
Arg Asp Ser Val Leu Asn Cys Ser Asp Cys Ser Ile Lys Val Thr Lys
          275          280          285
Val Asp Glu Thr Arg Gly Ile Ala His Val Tyr Leu Phe Thr Pro Lys
          290          295          300
Asn Phe Pro Asp Pro His Arg Ser Ile Asn Arg Gln Ile Thr Asn Ala
305          310          315          320
Asp Leu Trp Lys His Gln Lys Asp Val Phe Leu Ser Ala Ile Ser Ser
          325          330          335
Gly Ala Asp Ser Pro Asn Ser Lys Asn Gly Asn Met Pro Met Ser Gly
          340          345          350
Asn Thr Gly Glu Asn Phe Arg Lys Asn Leu Thr Asp Val Ile Lys Lys
          355          360          365
Ser Met Val Asp His Thr Ser Ala Phe Ser Thr Glu Glu Leu Pro Pro
          370          375          380
Pro Val His Leu Ser Lys Pro Gly Glu His Met Asp Val Tyr Val Pro
385          390          395          400
Val Ala Cys His Pro Gly Tyr Phe Val Ile Gln Pro Trp Gln Glu Ile

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              420              425              430
Ser Glu Glu Arg His Ile Ala Val Glu Lys Asp Gln Val Tyr Ala Ala
              435              440              445
Lys Val Glu Asn Lys Trp His Arg Val Leu Leu Lys Gly Ile Leu Thr
              450              455              460
Asn Gly Leu Val Ser Val Tyr Glu Leu Asp Tyr Gly Lys His Glu Leu
465              470              475              480
Val Asn Ile Arg Lys Val Gln Pro Leu Val Asp Met Phe Arg Lys Leu
              485              490              495
Pro Phe Gln Ala Val Thr Ala Gln Leu Ala Gly Val Lys Cys Asn Gln
              500              505              510
Trp Ser Glu Glu Ala Ser Met Val Phe Arg Asn His Val Glu Lys Lys
              515              520              525
Pro Leu Val Ala Leu Val Gln Thr Val Ile Glu Asn Ala Asn Pro Trp
              530              535              540
Asp Arg Lys Val Val Val Tyr Leu Val Asp Thr Ser Leu Pro Asp Thr
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Lys Val Asn

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<210> 3445

<211> 2086

<212> DNA

<213> Homo sapiens

<400> 3445

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720

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<210> 3446

<211> 169

<212> PRT

<213> Homo sapiens

<400> 3446

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35
Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro
50
Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln
65
Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr
85
Leu His His Leu Phe Arg Leu Arg His His Lys Asp Glu Val Ala Gly
100
Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys
115
Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp
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<210> 3447

<211> 936

<212> DNA

<213> Homo sapiens

<400> 3447

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780

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 936

<210> 3448

<211> 302

<212> PRT

<213> Homo sapiens

<400> 3448

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Val	Gln	Ala	Ala	Asp	Gly	Gly	Ala	Ala	Gly	Pro	Tyr	Ser	Ser	Ser	Glu
		20						25					30		
Leu	Leu	Glu	Gly	Gln	Glu	Pro	Asp	Gly	Val	Arg	Phe	Asp	Arg	Glu	Arg
		35					40					45			
Ala	Arg	Arg	Leu	Trp	Glu	Ala	Val	Ser	Gly	Ala	Gln	Pro	Val	Gly	Arg
	50					55					60				
Glu	Glu	Val	Glu	His	Met	Ile	Gln	Lys	Asn	Gln	Cys	Leu	Phe	Thr	Asn
	65				70				75					80	
Thr	Gln	Cys	Lys	Val	Cys	Cys	Ala	Leu	Leu	Ile	Ser	Glu	Ser	Gln	Lys
			85						90					95	
Leu	Ala	His	Tyr	Gln	Ser	Lys	Lys	His	Ala	Asn	Lys	Val	Lys	Arg	Tyr
		100					105						110		
Leu	Ala	Ile	His	Gly	Met	Glu	Thr	Leu	Lys	Gly	Glu	Thr	Lys	Lys	Leu
		115					120					125			
Asp	Ser	Asp	Gln	Lys	Ser	Ser	Arg	Ser	Lys	Asp	Lys	Asn	Gln	Cys	Cys
		130				135					140				
Pro	Ile	Cys	Asn	Met	Thr	Phe	Ser	Ser	Pro	Val	Val	Ala	Gln	Ser	His
				150						155				160	
Tyr	Leu	Gly	Lys	Thr	His	Ala	Lys	Asn	Leu	Lys	Leu	Lys	Gln	Gln	Ser
			165					170						175	
Thr	Lys	Val	Glu	Ala	Leu	His	Gln	Asn	Arg	Glu	Met	Ile	Asp	Pro	Asp
			180					185					190		
Lys	Phe	Cys	Ser	Leu	Cys	His	Ala	Thr	Phe	Asn	Asp	Pro	Val	Met	Ala
		195					200					205			
Gln	Gln	His	Tyr	Val	Gly	Lys	Lys	His	Arg	Lys	Gln	Glu	Thr	Lys	Leu
		210				215					220				
Lys	Leu	Met	Ala	Arg	Tyr	Gly	Arg	Leu	Ala	Asp	Pro	Ala	Val	Thr	Asp
				230					235					240	
Phe	Pro	Ala	Gly	Lys	Gly	Tyr	Pro	Cys	Lys	Thr	Cys	Lys	Ile	Val	Leu
			245						250					255	
Asn	Ser	Ile	Glu	Gln	Tyr	Gln	Ala	His	Val	Ser	Gly	Phe	Lys	His	Lys
		260					265						270		
Asn	Gln	Ser	Pro	Lys	Thr	Val	Ala	Ser	Ser	Leu	Gly	Gln	Ile	Pro	Met
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Gln	Arg	Gln	Pro	Ile	Gln	Lys	Asp	Ser	Thr	Thr	Leu	Glu	Asp		
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<210> 3449

<211> 877

<212> DNA

<213> Homo sapiens

<400> 3449

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 180
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 240
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 300
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 360
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 480
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 720
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<210> 3450

<211> 276

<212> PRT

<213> Homo sapiens

<400> 3450

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Ala	Ser	Ser	Asn	Pro	Pro	Gly	Ala	Pro	Ala	Leu	Pro	Leu	His	Asn	Ser
			20					25					30		
Ser	Val	Thr	Ala	Asn	Ser	Gln	Ser	Pro	Ala	Leu	Leu	Ala	Gly	Thr	Asn
			35				40					45			
Pro	Val	Ala	Val	Val	Ala	Asp	Gly	Gly	Ser	Cys	Pro	Ala	His	Tyr	Pro
			50			55					60				
Val	His	Glu	Cys	Val	Phe	Lys	Gly	Asp	Val	Arg	Arg	Leu	Ser	Ser	Leu
					70				75					80	
Ile	Arg	Thr	His	Asn	Ile	Gly	Gln	Lys	Asp	Asn	His	Gly	Asn	Thr	Pro
				85				90					95		
Leu	His	Leu	Ala	Val	Met	Leu	Gly	Asn	Lys	Glu	Cys	Ala	His	Leu	Leu

[illegible]

<210> 3451

<211> 595

<212> DNA

<213> Homo sapiens

<400> 3451

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120					
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180					
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360					
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480					
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540					
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595					

<210> 3452

<211> 192

<212> PRT

<213> Homo sapiens

<400> 3452

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Glu Arg Gln Ser His Pro Ala Thr Gln Gln Leu Gly Lys Thr Leu
 35           40           45
Gln Ser Lys Gln Leu Pro Gln Val Pro Arg Pro Leu Gln Leu Phe Ser
 50           55           60
Ala Lys Glu Leu Arg Asp Ser Ser Ile Asp Thr His Gln Tyr His Glu
 65           70           75           80
Gly Leu Ser Lys Ala Thr Gln Asp Gln Ile Leu Gln Thr Leu Ile Gln
 85           90           95
Arg Val Arg Arg Gln Asn Leu Leu Ser Val Val Pro Pro Ser Gln Phe
100           105           110
Asn Phe Ala His Ser Gly Phe Gln Leu Glu Asp Ile Ser Thr Ser Gln
115           120           125
Arg Phe Met Leu Gly Phe Ala Gly Arg Arg Thr Ser Lys Pro Ala Met
130           135           140
Ala Gly His Tyr Leu Leu Asn Ile Ser Thr Tyr Gly Arg Gly Ser Glu
145           150           155           160
Ser Phe Arg Arg Thr His Ser Val Asn Pro Glu Asp Arg Phe Cys Leu
165           170           175
Ser Ser Pro Thr Glu Ala Leu Lys Met Gly Tyr Thr Asn Cys Lys Asn
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<210> 3453

<211> 477

<212> DNA

<213> Homo sapiens

<400> 3453

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477

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<210> 3454

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3454

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Lys Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly
          20           25           30
Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly
          35           40           45
Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile
          50           55           60
Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu
65          70          75          80
Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val
          85          90          95
Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys
          100         105         110
Phe Arg Pro Pro Glu Thr Thr Glu Arg Ala Lys Ile Val Ile Arg Glu
          115         120         125
Leu Leu Pro Asn Gly Leu Arg Glu Ser Ile Ser Lys Val Arg Ser Ser
          130         135         140
Val Ala Tyr Ala Val Ser Ala Ile Ala His Trp Asp Trp Pro Glu
145          150          155

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<210> 3455

<211> 4886

<212> DNA

<213> Homo sapiens

<400> 3455

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720

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<210> 3456

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3456

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Lys	Lys	Gln	Arg	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln	Asn
			20					25					30		
Pro	Pro	Cys	Pro	Arg	Leu	Asn	Gly	Val	Leu	Met	Glu	Val	Glu	Glu	Pro
		35					40					45			
Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Met
		50				55					60				
Tyr	Phe	Glu	Leu	Pro	Asp	Ser	Phe	Gln	His	Tyr	Arg	Ser	Val	Phe	Tyr
65				70					75					80	
Ser	Phe	Glu	Glu	Glu	His	Ile	Ser	Phe	Ala	Leu	Tyr	Val	Asp	Asn	Arg
				85				90						95	
Phe	Phe	Thr	Leu	Thr	Val	Thr	Ser	Leu	His	Leu	Val	Phe	Gln	Met	Gly
			100				105						110		
Val	Ile	Phe	Pro	Gln											

115

<210> 3457
 <211> 646
 <212> DNA
 <213> Homo sapiens

<400> 3457
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 180
 aagtgaggat gcgtatgtnn ggttggtgtg gtctgtatct gcatttgcac gngtgtattg
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 360
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 420
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 480
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 540
 aacctccag gccttctcct gccacaggct ctgtctctgt cccgtcgctg tgcctctctg
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 646

<210> 3458
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 3458
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 Arg Cys Val Xaa Val Pro Gly Cys Val Cys Ala Cys Val Cys Val Asp
 20 25 30
 Ile Cys Ala Cys Leu Phe Thr His Arg Trp Glu Cys Arg Val Cys Ile
 35 40 45
 Leu Cys Xaa Cys Thr Cys Thr Gln Ala Xaa Ala Gly Lys
 50 55 60

<210> 3459
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 3459
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 120
 gaccctactt cactgcaggg ggctcagccc agtctgcctc aggcagaaca agggctctggg
 180
 ggtggctgtg gggggctgtg gatgggtccc agtgggcttg ctgccactcc caccacatgg
 240
 gacctgcctt cggccctgc caggattcca gtcctgccct gctcacccca gcttcagggc
 300
 ccttccctgt gtgcagctc agtttgctg ctgcagaata agcaccacgc tccctctgtg
 360
 gcagaggcac cggcagactc accacgcgcc ctgcaggcat gtctctgtgt gtgccaggga
 420
 ggccccggcc acgtccctgc ccccgagct ggccttcagc ggggacagtg gtcagcactg
 480
 aagacagtca tacctgcccg gccggcactg cctctgtcag caccgggaca atttgaactt
 540
 aagctttaac ttaattaaaa tgaactaaaa ttaaaaaaaaa aaaaaaaaaa aa
 592

<210> 3460

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3460

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Ser	Gly	Pro	Ala	Arg	Ile	Pro	Val	Leu	Pro	Cys	Ser	Pro	Gln	Leu	Pro
			20					25					30		
Gly	Pro	Ser	Leu	Cys	Ala	Ala	Ser	Val	Cys	Leu	Leu	Gln	Asn	Lys	His
			35				40					45			
His	Ala	Pro	Ser	Trp	Ala	Glu	Ala	Pro	Ala	Asp	Ser	Pro	Arg	Ala	Leu
	50				55					60					
Gln	Ala	Cys	Pro	Val	Leu	Cys	Gln	Ala	Gly	Pro	Gly	His	Val	Pro	Ala
65				70					75					80	
Pro	Gly	Ala	Gly	Leu	Gln	Arg	Gly	Gln	Trp	Ser	Ala	Leu	Lys	Thr	Val
			85					90					95		
Ile	Pro	Ala	Arg	Pro	Ala	Leu	Pro	Cys	Ser	Ala	Arg	Gly	Gln	Phe	Glu
			100					105					110		
Leu	Lys	Leu													
			115												

<210> 3461

<211> 474

<212> DNA

<213> Homo sapiens

<400> 3461

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 120
 agctttgcgt ccgtggcaga tgtcagctcc agtcgcagcc gcaccttcgc gatggccctg
 180

ctggaagcca gcatacggggt ggctgggatg ctggcaagcc tcctcggggg ccactggctc
 240
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 300
 ctctatgcag ctttctgctt tgggtgagacc ttaaaggagc caaagtcac ccggctcttc
 360
 acgttcgcgc accaccgatc cattgtccag ctctatgtgg ctcccccccc agagaagtcc
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 474

<210> 3462

<211> 101

<212> PRT

<213> Homo sapiens

<400> 3462

Met	Ala	Leu	Leu	Glu	Ala	Ser	Ile	Gly	Val	Ala	Gly	Met	Leu	Ala	Ser
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Leu	Leu	Gly	Gly	His	Trp	Leu	Arg	Ala	Gln	Gly	Tyr	Ala	Asn	Pro	Phe
				20				25					30		
Trp	Leu	Ala	Leu	Ala	Leu	Leu	Ile	Ala	Met	Thr	Leu	Tyr	Ala	Ala	Phe
				35				40					45		
Cys	Phe	Gly	Glu	Thr	Leu	Lys	Glu	Pro	Lys	Ser	Thr	Arg	Leu	Phe	Thr
				50				55					60		
Phe	Arg	His	His	Arg	Ser	Ile	Val	Gln	Leu	Tyr	Val	Ala	Pro	Ala	Pro
				65				70					75		80
Glu	Lys	Ser	Arg	Lys	His	Leu	Ala	Leu	Tyr	Ser	Leu	Ala	Ile	Phe	Val
				85				90					95		
Val	Ile	Thr	Val	His											
				100											

<210> 3463

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 3463

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 120
 cagcagcgcc agggcaagca ccataccta tctctcatgg ctaatgaacg catgaacctc
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 420
 cttccaggac ttaagacacc agtaggtaga ggaagagcct ggcttcgctt ggcatatgat
 480

caaaagaaac tttcagaata tatgaaagct ttgatcaata agaaagaact tctcagtga
 540
 ttctacgaac ccaatgccct catgatggaa gaagaaggag ccataattgc tggctgttg
 600
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 660
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 720
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 780
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<210> 3464

<211> 434

<212> PRT

<213> Homo sapiens

<400> 3464

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 20 25 30
 Glu Leu Pro Glu Arg Arg Arg Arg Gln Gln Arg Gln Gly Lys His His

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      35              40              45
Pro Asn Tyr Leu Met Ala Asn Glu Arg Met Asn Leu Met Asn Met Ala
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Lys Leu Ser Ile Lys Gly Leu Ile Glu Ser Ala Leu Asn Leu Gly Arg
  65              70              75              80
Thr Leu Asp Ser Asp Tyr Ala Pro Leu Gln Gln Phe Phe Val Val Met
      85              90              95
Glu His Cys Leu Lys His Gly Leu Lys Ala Lys Lys Thr Phe Leu Gly
  100              105              110
Gln Asn Lys Ser Phe Trp Gly Pro Leu Glu Leu Val Glu Lys Leu Val
  115              120              125
Pro Glu Ala Ala Glu Ile Thr Ala Ser Val Lys Asp Leu Pro Gly Leu
  130              135              140
Lys Thr Pro Val Gly Arg Gly Arg Ala Trp Leu Arg Leu Ala Leu Met
  145              150              155              160
Gln Lys Lys Leu Ser Glu Tyr Met Lys Ala Leu Ile Asn Lys Lys Glu
      165              170              175
Leu Leu Ser Glu Phe Tyr Glu Pro Asn Ala Leu Met Met Glu Glu Glu
  180              185              190
Gly Ala Ile Ile Ala Gly Leu Leu Val Gly Leu Asn Val Ile Asp Ala
  195              200              205
Asn Phe Cys Met Lys Gly Glu Asp Leu Asp Ser Gln Val Gly Val Ile
  210              215              220
Asp Phe Ser Met Tyr Leu Lys Asp Gly Asn Ser Ser Lys Gly Thr Glu
  225              230              235              240
Gly Asp Gly Gln Ile Thr Ala Ile Leu Asp Gln Lys Asn Tyr Val Glu
      245              250              255
Glu Leu Asn Arg His Leu Asn Ala Thr Val Asn Asn Leu Gln Ala Lys
  260              265              270
Val Asp Ala Leu Glu Lys Ser Asn Thr Lys Leu Thr Glu Glu Leu Ala
  275              280              285
Val Ala Asn Asn Arg Ile Ile Thr Leu Gln Glu Glu Met Glu Arg Val
  290              295              300
Lys Glu Glu Ser Ser Tyr Ile Leu Glu Ser Asn Arg Lys Gly Pro Lys
  305              310              315              320
Gln Asp Arg Thr Ala Glu Gly Gln Ala Leu Ser Glu Ala Arg Lys His
      325              330              335
Leu Lys Glu Glu Thr Gln Leu Arg Leu Asp Val Glu Lys Glu Leu Glu
  340              345              350
Met Gln Ile Ser Met Arg Gln Glu Met Glu Leu Ala Met Lys Met Leu
  355              360              365
Glu Lys Asp Val Cys Glu Lys Gln Asp Ala Leu Val Ser Leu Arg Gln
  370              375              380
Gln Leu Asp Asp Leu Arg Ala Leu Lys His Glu Leu Ala Phe Lys Leu
  385              390              395              400
Gln Ser Ser Asp Leu Gly Val Lys Gln Lys Ser Glu Leu Asn Ser Arg
      405              410              415
Leu Glu Glu Lys Thr Asn Gln Met Ala Ala Thr Ile Lys Gln Leu Glu
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Gln Arg

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<210> 3465

<211> 2904

<212> DNA

<213> Homo sapiens

<400> 3465

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120
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180
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240
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300
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360
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720
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1140
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<210> 3466

<211> 315

<212> PRT

<213> Homo sapiens

<400> 3466

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Gly Arg His Arg Lys Leu Pro Glu Asn Trp Thr Asp Thr Arg Glu Thr
          35          40          45
Leu Leu Glu Gly Met Leu Phe Ser Leu Lys Tyr Leu Gly Met Thr Leu
          50          55          60
Val Glu Gln Pro Lys Gly Glu Glu Leu Ser Ala Ala Ile Lys Arg
65          70          75          80
Ile Val Ala Thr Ala Lys Ala Ser Gly Lys Lys Leu Gln Lys Val Thr
          85          90          95
Leu Lys Val Ser Pro Arg Gly Ile Ile Leu Thr Asp Asn Leu Thr Asn
          100          105          110
Gln Leu Ile Glu Asn Val Ser Ile Tyr Arg Ile Ser Tyr Cys Thr Ala
          115          120          125
Asp Lys Met His Asp Lys Val Phe Ala Tyr Ile Ala Gln Ser Gln His
          130          135          140
Asn Gln Ser Leu Glu Cys His Ala Phe Leu Cys Thr Lys Arg Lys Met
          145          150          155          160
Ala Gln Ala Val Thr Leu Thr Val Ala Gln Ala Phe Lys Val Ala Phe
          165          170          175
Glu Phe Trp Gln Val Ser Lys Glu Glu Lys Glu Lys Arg Asp Lys Ala
          180          185          190
Ser Gln Glu Gly Gly Asp Val Leu Gly Ala Arg Gln Asp Cys Thr Pro
          195          200          205
Pro Leu Lys Ser Leu Val Ala Thr Gly Asn Leu Leu Asp Leu Glu Glu
          210          215          220
Thr Ala Lys Ala Pro Leu Ser Thr Val Ser Ala Asn Thr Thr Asn Met
          225          230          235          240
Asp Glu Val Pro Arg Pro Gln Ala Leu Ser Gly Ser Ser Val Val Trp
          245          250          255
Glu Leu Asp Asp Gly Leu Asp Glu Ala Phe Ser Arg Leu Ala Gln Ser
          260          265          270
Arg Thr Asn Pro Gln Val Leu Asp Thr Gly Leu Thr Ala Gln Asp Met
          275          280          285
His Tyr Ala Gln Cys Leu Ser Pro Val Asp Trp Asp Lys Pro Asp Ser
          290          295          300
Ser Gly Thr Glu Gln Asp Asp Leu Phe Ser Phe
          305          310          315

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<210> 3467

<211> 638

<212> DNA

<213> Homo sapiens

<400> 3467

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ggctctgaggt gaaggtccta ggagcatcag ttctctgttg gatatcaagg tgctgggaca
180

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 360
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 420
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 480
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 540
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 638

<210> 3468

<211> 88

<212> PRT

<213> Homo sapiens

<400> 3468

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 20 25 30
 Trp Leu Cys Tyr Thr Ser Cys Tyr Gln Gln Asn Arg Val Ser Leu Gly
 35 40 45
 Gln Ser Cys Gly Tyr Thr Ser Val Ser Gln Asp Phe Leu Cys Gln Arg
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<210> 3469

<211> 1710

<212> DNA

<213> Homo sapiens

<400> 3469

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<210> 3470

<211> 322

<212> PRT

<213> Homo sapiens

<400> 3470

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      35           40           45
Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala
      50           55           60
Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys
      65           70           75           80
Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val
      85           90           95
Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe
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Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu
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Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val
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Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly
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Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr
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Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile
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Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr
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Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met
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Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile
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<210> 3471

<211> 2335

<212> DNA

<213> Homo sapiens

<400> 3471

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<210> 3472

<211> 631

<212> PRT

<213> Homo sapiens

<400> 3472

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Ser	Glu	Gln	Val	Leu	Leu	Cys	Ala	Ser	Ser	Gln	Thr	Ser	Ser	Ile	Val
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Arg	Leu	Leu	Thr	Lys	Leu	Trp	Ile	Cys	Cys	Arg	Asp	Glu	Gly	Pro	Ala
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Gln	Leu	Leu	Ile	Pro	Ser	Leu	Asp	Trp	Leu	Pro	Ala	Ser	Asp	Gly	Leu
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Val	Ser	Arg	Leu	Gln	Pro	Lys	Gln	Pro	Leu	Arg	Leu	Gln	Phe	Gly	Arg
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Ala	Pro	Thr	Leu	Pro	Gly	Ser	Ala	Ala	Thr	Leu	Gln	Leu	Asp	Gly	Leu
			550						555					560	
Ala	Arg	Ala	Pro	Gly	Gln	Pro	Lys	Ile	Asp	His	Leu	Arg	Arg	Leu	His
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<210> 3473

<211> 1660

<212> DNA

<213> Homo sapiens

<400> 3473

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 <211> 474
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Leu Gly Pro Phe Pro Ala Gln Thr Pro Pro Trp Leu Met Ala Ser
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 65 70 75 80
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 Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser Ser Leu
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 Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro Ile Glu
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 Glu Leu Gly Glu Leu Leu Leu Ser Leu Asn Tyr Leu Pro Ser Ala Gly

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Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly Thr Ile
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Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln Glu Glu
          385          390          395          400
Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn Met Lys
          405          410          415
Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr Ser Ser
          420          425          430
Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr His Arg
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<210> 3475

<211> 514

<212> DNA

<213> Homo sapiens

<400> 3475

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<210> 3476

<211> 171

<212> PRT

<213> Homo sapiens

<400> 3476

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      35                40                45
Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu Lys Pro Val
      50                55                60
Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu His Pro Ile
      65                70                75                80
Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys Gly His Glu
      85                90                95
Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe Asn Val Gly
      100                105                110
Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly Tyr Asn Leu
      115                120                125
Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His Leu Pro Gln
      130                135                140
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Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr
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<210> 3477

<211> 356

<212> DNA

<213> Homo sapiens

<400> 3477

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ttgacctctc gcatcgacc cttccatggga cttaatgaag agcagaaga atttcaaaaa
120
gtggcctttg accttgctgc cggagagatg gctccaaata tggcagagtg ggaccagaag
180
gtaggcgctt ttcttgctgc tagacgttct aacaacagat gtctcaggca gacctttatc
240
tttgctctcc gataatgtaa ttgttaaagt tctctccac ttaccaactc ttactgcaag
300
tgagaatacc ggtagtggtat gatttttctc agaaggcatc ctgatcatct tgtaca
356

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<210> 3478

<211> 116

<212> PRT

<213> Homo sapiens

<400> 3478

```

Met Ile Arg Met Pro Ser Arg Lys Asn His Pro Leu Pro Val Phe Ser
1      5      10      15
Leu Ala Val Arg Val Gly Lys Trp Arg Arg His Leu Thr Ile Thr Leu
      20      25      30
Ser Gly Asp Lys Asp Lys Gly Leu Pro Glu Thr Ser Val Val Arg Thr
      35      40      45
Ser Lys His Lys Lys Asn Ala Tyr Leu Leu Val Pro Leu Cys His Ile
      50      55      60
Trp Ser His Leu Ser Gly Ser Lys Val Lys Gly His Phe Leu Lys Phe

```

```

65          70          75          80
Phe Leu Leu Phe Ile Lys Ser His Gly Arg Val Asp Ala Gly Gly Gln
      85          90          95
Ala Pro Val Ala Gly Leu Asp Glu Asp Pro Glu Thr Ala Gly Gln Ala
      100          105          110
Ala Glu Ala Arg
      115

```

```

<210> 3479
<211> 797
<212> DNA
<213> Homo sapiens

```

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<400> 3479
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60
taccocggct ctgacaggat catgctgcag aagtggcaga aaagggacat cagcaatttt
120
gagtatctca tgtacctcaa caccgaggct gggagaacct gcaatgacta catgcagtac
180
ccagtgttcc cctgggttct cgcagactac acctcagaga cattgaactt ggcaaatccg
240
aagattttcc gggatctttc aaagcccatg ggggctcaga ccaaggaaa gaaagtga
300
tttatccaga ggtttaaaga agttgagaaa actgaaggag acatgactgc ccagtgccac
360
tactacacc actactcttc gcccatcctc gtggcctcct acctggtccg gatgccacc
420
ttcaccagg ccttctgcgc tctgcagggt agctgctgcc actctctgta cacacacaca
480
cacacacaca cacacacata cgctgtatc acaagactaa gacctgtgct tgaacaaaga
540
caggatgcct ctgctaaaaa cttagtcatt agccagtgat tccagttga cattggctcc
600
aggattctgg ctccaccgcc aaggcaggct gttcttcttc agttacacct gcacatctgc
660
ccaacaaagt cttgcaaaat gattctaaaa aataagaaat gagacatgaa aaaaatgatt
720
taacataaat aagatttagt ggaaaaagaa aaagcaggaa acttgagac tagaaaggca
780
ggcgggtcaag gattaga
797

```

```

<210> 3480
<211> 192
<212> PRT
<213> Homo sapiens

```

```

<400> 3480
Xaa Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser Glu Asp Thr Leu
1          5          10          15
Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met Leu Gln Lys Trp
      20          25          30
Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met Tyr Leu Asn Thr

```


tggcccaggg agcactaatt ccaagaggca ggccacttgg ttcttgaga aggagaagag
 900
 cagactgctg gctgaggcag cacttgagtt gcgggaggag aacacagggc aggaacggat
 960
 tctggccctg gccaaagcgac tagccatgct gcggggacag gaccccgaga gactgacccct
 1020
 ccaggactat cgctctccag acagtgatga cgacgaggat gaggagacag ccatccaaag
 1080
 agtctctcag cagctcactg aagaagcttc cctggatgag gcaagtggct ttaacatccc
 1140
 tgcagagcag gcttctcgac cctggacgca accccgcggg gcagagcctg agggccaggga
 1200
 tgtggacccc aggcctgagg ctgaggaaga ggagctcccc tgggtgctgca tctgcaatga
 1260
 ggatgccacc ctacgtctcg ctggctgcca tggggacctc ttctgtgccc gctgcttccg
 1320
 agagggccat gatgcctttg agcttaaaga gcaccagaca tctgcctact ctctccacag
 1380
 tgcaggccaa gagcactgaa gacaccttgg tcctcccgga agggcagctc cacaggcagc
 1440
 ggacccatt tctgggcccc gccacaggac gtccgatggg agagcttgct tggctctact
 1500
 gatgatggat agggcccttc ctgagccttg gtgtcccttg aatgaggaag gattctccat
 1560
 tgcagagaat gactggggagg gaagaagtgc gggccctctc attagaagcc cagactggaa
 1620
 gtgagaggca tgatggggag agaccagact gaatctacg gtgagccctg taacctggct
 1680
 ctagggcaca ggccctctcc ctggcactta gtgggtctaa taaagtatgt tgattcattg
 1740
 ggaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa
 1794

<210> 3482

<211> 206

<212> PRT

<213> Homo sapiens

<400> 3482

Met Pro Pro Ser Gly His His Leu Ser Ser Ala Asp Pro Ala Val Leu
 1 5 10 15
 Gly Ala Thr Met Glu Ser Arg Cys Tyr Gly Cys Ala Val Lys Phe Thr
 20 25 30
 Leu Phe Lys Lys Glu Tyr Gly Cys Lys Asn Cys Gly Arg Xaa Phe Cys
 35 40 45
 Ser Gly Cys Leu Ser Phe Ser Ala Ala Val Pro Arg Thr Gly Asn Thr
 50 55 60
 Gln Gln Lys Val Cys Lys Gln Cys His Glu Val Leu Thr Arg Gly Ser
 65 70 75 80
 Ser Ala Asn Ala Ser Lys Trp Ser Pro Pro Gln Asn Tyr Lys Lys Arg
 85 90 95
 Val Ala Ala Leu Glu Ala Lys Gln Lys Pro Ser Thr Ser Gln Ser Gln
 100 105 110
 Gly Leu Thr Arg Gln Asp Gln Met Ile Ala Glu Arg Leu Ala Arg Leu

```

      115              120              125
Arg  Gln Glu Asn Lys Pro Lys Leu Val Pro Ser Gln Ala Glu Ile Glu
    130              135              140
Ala  Arg Leu Ala Ala Leu Lys Asp Glu Arg Gln Gly Ser Ile Pro Ser
    145              150              155              160
Thr  Gln Glu Met Glu Ala Arg Leu Ala Ala Leu Gln Gly Arg Val Leu
      165              170              175
Pro  Ser Gln Thr Pro Gln Pro Gly Thr Ser His Thr Gly His Gln Asp
      180              185              190
Pro  Ser Pro Ala Asp Thr Gly Ser Ala Asn Ala Ala Gly Ser
      195              200              205

```

<210> 3483

<211> 477

<212> DNA

<213> Homo sapiens

<400> 3483

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ncggcgcgcg cgcggaacgg cgcctccgcg ccacccatgg gcaacagcgc gagccgcaac
60
gacttcgagt gggctctacac cgaccagccg cacacgcagc ggcgcaagga gatactggcc
120
aagtaccggg ccatcaaggc cctgatgcgg ccagaccgcg gcctcaagtg ggcggggctg
180
gtgctggtgc tgggtcagat gctggcctgc tggctggtgc gcgggctggc ctggcgctgg
240
ctgctgttct gggcctacgc ctttgggtgc tgcgtgaacc actcgtgtgac gctggccatc
300
cacgacatct cgcacaacgc ggccttcggc acgggcccgtg cggcacgcaa ccgctggctg
360
gccgtgttgc ccaacctgcc cgtgggtgtg ccctacgcgg cctccttcaa gaagtaccac
420
gtggaccacc accgctacct gggcgggcgac ggactggacg tggacgtgcc caccgct
477

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<210> 3484

<211> 147

<212> PRT

<213> Homo sapiens

<400> 3484

```

Met Gly Asn Ser Ala Ser Arg Asn Asp Phe Glu Trp Val Tyr Thr Asp
  1              5              10              15
Gln Pro His Thr Gln Arg Arg Lys Glu Ile Leu Ala Lys Tyr Pro Ala
      20              25              30
Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala Gly Leu
      35              40              45
Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg Gly Leu
      50              55              60
Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly Cys Val
      65              70              75              80
Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn Ala Ala
      85              90              95
Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val Phe Ala

```

```

          100              105              110
Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys Tyr His
          115              120              125
Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val Asp Val
          130              135              140
Pro Thr Arg
145

```

<210> 3485
 <211> 812
 <212> DNA
 <213> Homo sapiens

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<400> 3485
tattttat ttagtcacaaa aactgttcag gaagaaatgt tatgaaaga acatttttac
60
tgcatgctta aacattttaa ttttctatta tacagttaaa catttgcttg aattcagtga
120
gtctaaaaaa tcttattggt ctcagggttag cagttagttg agcagagtcc attgggtgaag
180
caatctagtt attggcaaat tctaacacat ggtaaggtgt gggggaaagg atttaaaaaa
240
acagaaaaat gtaagtacaa acatacataa cagcaaaaata aaactcatt taacaaaaat
300
ttatttaaaa tgttaccccc atatttcctc aatgaccaac ttgtttcagt tttatctccc
360
ctctatccgg ttattttatg tctttttggg aggaagggtg atgagggttt ttgtttttta
420
acaaaaatcac tggcttttta aaaagtgtta ctgcagtcac ttataagatg catgttatgt
480
ggaagtgtata cctgagttgt ttgcatgggc aatggaagag gcagcagctc tgaaaggagt
540
atgagttccag aaaaaaatcc ttcaggaacc ttcaagattg aagaagaac ttcttttaac
600
attaaagacc aagtattatt ggccagagtc tcttctgaga ttgtgagttt ttcattaact
660
ccttgtgttaa aagtcagtaa aatatcaatg atatcattct gaattttctg ttcatcacta
720
tccaaacgac ctgagagggg gatagagcac aggagcatat gtaaagtaac aagcgctgaa
780
ggaacacgca tgtccttaaa ctcaaaggat cc
812

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<210> 3486
 <211> 117
 <212> PRT
 <213> Homo sapiens

```

<400> 3486
Met Arg Val Pro Ser Ala Leu Val Thr Leu His Met Leu Leu Cys Ser
1          5          10          15
Ile Pro Leu Ser Gly Arg Leu Asp Ser Asp Glu Gln Lys Ile Gln Asn
20          25          30
Asp Ile Ile Asp Ile Leu Leu Thr Phe Thr Gln Gly Val Asn Glu Lys

```



```

                20                25                30
Leu Ala Asn Thr Val Lys Pro Arg Leu Ile Leu Ser Phe Leu Thr Pro
                35                40                45
Phe Asn Pro Val Thr Glu Ile Ser Ile Cys Thr
                50                55

```

<210> 3489

<211> 288

<212> DNA

<213> Homo sapiens

<400> 3489

```

tagctaacac tccactatgg gagcccatct cctcccaggg ccaggggagac caggggagacc
60
aggggagacca ggtctggccc ccaactctaa ggctcatctt agaggcgaga ttcaggccca
120
gcccagggtg ccccatgagg cctggtggtt ggaggcagag ggatccctt gcccaaattc
180
gtgccacatt cacagtcact gggaaagcta cggggatggg ccggggcgagg tggtcacac
240
ctgtaatccc agcactttgg agagcccaa gacgacggat cagagtc
288

```

<210> 3490

<211> 90

<212> PRT

<213> Homo sapiens

<400> 3490

```

Met Gly Ala His Leu Leu Pro Gly Pro Gly Arg Pro Gly Arg Pro Gly
1          5          10          15
Arg Pro Gly Leu Ala Pro Asn Ser Lys Ala His Leu Arg Gly Glu Ile
          20          25          30
Gln Ala Gln Pro Arg Val Pro His Glu Ala Trp Trp Leu Glu Ala Glu
          35          40          45
Gly Ile Pro Cys Pro Asn Ser Cys His Ile His Ser His Trp Glu Ser
          50          55          60
Tyr Gly Asp Gly Pro Gly Ala Val Ala His Thr Cys Asn Pro Ser Thr
65          70          75          80
Leu Glu Ser Pro Lys Thr Thr Asp His Glu
          85          90

```

<210> 3491

<211> 568

<212> DNA

<213> Homo sapiens

<400> 3491

```

gggaaccgac gtccctctgt ggtgaaattc cacccttca cgccgtgcat cgccgtagcc
60
gacaaggaca gcatctgctt ttgggactgg gagaaagggg agaagctgga ttatttccac
120
aatgggaacc ctcggtacac gaggtgact gccatggagt atctgaatgg ccaggactgc
180

```

tcgcttctgc tgacggccac agacgatggg gccatcaggg tctggaagaa ttttgctgat
 240
 ttggaaaaga acccagagat ggtgaccgcg tggcaggggc tctcggacat gctgccaacg
 300
 acgcgaggag ctgggatggg ggtggactgg gagcaggaga ccggcctect catgagctca
 360
 ggagacgtgc ggaatgctcg gatctgggac acagaccgtg agatgaaggt gcaggacatc
 420
 cctacggggc cagacagctg tgtgacgagt ctgtcctgtg attccaccgc ctactcatc
 480
 gtggctggcc tcggtgacgg ctccatccgc gtctacgaca gaaggatggc actcagcgaa
 540
 tgccgcgtca tgacgtaccg ggagcaca
 568

<210> 3492

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3492

Gly	Asn	Arg	Arg	Pro	Ser	Val	Val	Lys	Phe	His	Pro	Phe	Thr	Pro	Cys
1				5					10					15	
Ile	Ala	Val	Ala	Asp	Lys	Asp	Ser	Ile	Cys	Phe	Trp	Asp	Trp	Glu	Lys
			20					25					30		
Gly	Glu	Lys	Leu	Asp	Tyr	Phe	His	Asn	Gly	Asn	Pro	Arg	Tyr	Thr	Arg
		35						40				45			
Val	Thr	Ala	Met	Glu	Tyr	Leu	Asn	Gly	Gln	Asp	Cys	Ser	Leu	Leu	Leu
		50					55				60				
Thr	Ala	Thr	Asp	Asp	Gly	Ala	Ile	Arg	Val	Trp	Lys	Asn	Phe	Ala	Asp
65					70					75				80	
Leu	Glu	Lys	Asn	Pro	Glu	Met	Val	Thr	Ala	Trp	Gln	Gly	Leu	Ser	Asp
			85						90					95	
Met	Leu	Pro	Thr	Thr	Arg	Gly	Ala	Gly	Met	Val	Val	Asp	Trp	Glu	Gln
		100						105					110		
Glu	Thr	Gly	Leu	Leu	Met	Ser	Ser	Gly	Asp	Val	Arg	Ile	Val	Arg	Ile
		115						120				125			
Trp	Asp	Thr	Asp	Arg	Glu	Met	Lys	Val	Gln	Asp	Ile	Pro	Thr	Gly	Ala
		130					135				140				
Asp	Ser	Cys	Val	Thr	Ser	Leu	Ser	Cys	Asp	Ser	His	Arg	Ser	Leu	Ile
145					150					155				160	
Val	Ala	Gly	Leu	Gly	Asp	Gly	Ser	Ile	Arg	Val	Tyr	Asp	Arg	Arg	Met
			165						170					175	
Ala	Leu	Ser	Glu	Cys	Arg	Val	Met	Thr	Tyr	Arg	Glu	His			
		180						185							

<210> 3493

<211> 2244

<212> DNA

<213> Homo sapiens

<400> 3493

ngggggggat atccatgcag cgatcaggat gaaagaggtg attcaggaca accaagtaat
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aaggaactgt ttggagatga cagtgaggac gagggagctt cacatcatag tggtagtgat
120
aatcactctg aaagatcaga caatagatca gaagcttctg agcgttctga ccatgaggac
180
aatgacctct cagatgtaga tcagcacagt ggatcagaag cccctaataa tgatgaagac
240
gaaggtcata gatcggatgg agggagccat cattcagaag cagaaggttc tgaaaaagca
300
cattcagatg atgaaaaatg gggcagagaa gataaaagt accagtcaga tgatgaaaaa
360
atacaaaatt ctgatgatga ggagagggca caaggatctg atgaagataa gctgcagaat
420
tctgacgatg atgagaaaat gcagaacaca gatgatgagg agaggcctca gctttccgat
480
gatgagagac aacagctatc tgaggaggaa aaggctaatt ctgatgatga acggcccgta
540
gcttctgata atgatgatga gaaacagaat tctgatgatg aagaacaacc acagctgtct
600
gatgaagaga aaatgcaaaa ttctgatgat gaaaggccac agggcccaga tgaagaacac
660
aggcattcag atgatgaaga ggaacaggat cataaatcag aatccgcaag aggcagtgat
720
agtgaagatg aagttttacg aatgaaacgc aagaatgcga ttgcatctga ttcagaagcg
780
gatagtgaca ctgaggtgcc aaaagataat agtggaaacca tggatttatt tggagggtgca
840
gatgatatac cttcaggagg tgatggagaa gacaaaccac ctactccagg acagcctggt
900
gatgaaaaatg gattgcctca ggatcaacag gaagaggagc caattcctga gaccagaata
960
gaagtagaaa taccctaaagt aaacactgat ttaggaaaag acttatattt tgttaaactg
1020
ccaacttttc tcagtgtaga gccagacct tttgatcttc agtattatga agatgaattt
1080
gaagatgaag aaatgctgga tgaagaaggt agaaccagggt taaaattaaa ggtagaaaaa
1140
actataagat ggaggatagc cggagatgaa gaaggaaatg aaattaaaga aagcaatgct
1200
cggatagtca agtggtcaga ttgaagcatg tccctgcatt taggcaatga agtgtttgat
1260
gtgtacaaag cccactgca gggcgaccac aatcatcttt ttataagaca aggtactggt
1320
ctacagggac aagcagtcctt taaagcgaaa ctacacctca gacctcactc tacggacagt
1380
gccacacata gaaagatgac tctgtcactt gcagataggt gttcagaagc acagaagatt
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1500
gaagaagaac gtttgagggc ttccatacgt agggaaatctc agcagcgccg aatgagagag
1560
aaacagcacc agcgggggct gagcgccagt tacctggaac ctgatcgata cgatgaggag
1620
gagggaaggc aggagtcctc cagcttggtt gccattaaaa accgatataa agggggcatt
1680

cgagaggaac gagccagaat ctattcatca gacagtgatg agggatcaga agaagataaa
 1740
 gctcaaagat tactcaaagc aaagaaactt accagtgatg aggaaggtga accttccgga
 1800
 aagagaaaag cagaagatga tgataaaagca aataaaaagc ataagaagta tgtgatcagc
 1860
 gatgaagagg aagaagatga tgattgaagt atgaaatatg aaaacatttt atatatttta
 1920
 ttgtacagtt ataaatatgt aaacatgagt tattttgatt gaaatgaatc gatttgcttt
 1980
 tgtgtaattt taattgtaat aaaacaattt aaaagcaagt ctctatgttt aagaaatcta
 2040
 cttttccggc caggcgcggt ggctcatgcc tgtaatccca gcacttcggg aggccgaggc
 2100
 aggtggatca caaggtcgtg gtggcgggtg cctgtagtcg cagctactcg ggaggctgag
 2160
 gcgggggaaat tgggtgaacc caggaggcag aggttgacgt tagccgagat cgcgccactg
 2220
 cactccagcc tggcgacaga gcta
 2244

<210> 3494

<211> 628

<212> PRT

<213> Homo sapiens

<400> 3494

Xaa	Gly	Gly	Tyr	Pro	Cys	Ser	Asp	Gln	Asp	Glu	Arg	Gly	Asp	Ser	Gly
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Gln	Pro	Ser	Asn	Lys	Glu	Leu	Phe	Gly	Asp	Asp	Ser	Glu	Asp	Glu	Gly
			20					25				30			
Ala	Ser	His	His	Ser	Gly	Ser	Asp	Asn	His	Ser	Glu	Arg	Ser	Asp	Asn
		35				40						45			
Arg	Ser	Glu	Ala	Ser	Glu	Arg	Ser	Asp	His	Glu	Asp	Asn	Asp	Pro	Ser
		50				55					60				
Asp	Val	Asp	Gln	His	Ser	Gly	Ser	Glu	Ala	Pro	Asn	Asp	Asp	Glu	Asp
65				70						75				80	
Glu	Gly	His	Arg	Ser	Asp	Gly	Gly	Ser	His	His	Ser	Glu	Ala	Glu	Gly
			85					90						95	
Ser	Glu	Lys	Ala	His	Ser	Asp	Asp	Glu	Lys	Trp	Gly	Arg	Glu	Asp	Lys
		100						105				110			
Ser	Asp	Gln	Ser	Asp	Asp	Glu	Lys	Ile	Gln	Asn	Ser	Asp	Asp	Glu	Glu
		115				120						125			
Arg	Ala	Gln	Gly	Ser	Asp	Glu	Asp	Lys	Leu	Gln	Asn	Ser	Asp	Asp	Asp
		130				135						140			
Glu	Lys	Met	Gln	Asn	Thr	Asp	Asp	Glu	Glu	Arg	Pro	Gln	Leu	Ser	Asp
145				150						155				160	
Asp	Glu	Arg	Gln	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Ala	Asn	Ser	Asp	Asp
			165					170						175	
Glu	Arg	Pro	Val	Ala	Ser	Asp	Asn	Asp	Asp	Glu	Lys	Gln	Asn	Ser	Asp
		180						185				190			
Asp	Glu	Glu	Gln	Pro	Gln	Leu	Ser	Asp	Glu	Glu	Lys	Met	Gln	Asn	Ser
		195				200						205			
Asp	Asp	Glu	Arg	Pro	Gln	Ala	Pro	Asp	Glu	Glu	His	Arg	His	Ser	Asp

210 215 220
 Asp Glu Glu Glu Gln Asp His Lys Ser Glu Ser Ala Arg Gly Ser Asp
 225 230 235 240
 Ser Glu Asp Glu Val Leu Arg Met Lys Arg Lys Asn Ala Ile Ala Ser
 245 250 255
 Asp Ser Glu Ala Asp Ser Asp Thr Glu Val Pro Lys Asp Asn Ser Gly
 260 265 270
 Thr Met Asp Leu Phe Gly Gly Ala Asp Asp Ile Ser Ser Gly Ser Asp
 275 280 285
 Gly Glu Asp Lys Pro Pro Thr Pro Gly Gln Pro Val Asp Glu Asn Gly
 290 295 300
 Leu Pro Gln Asp Gln Gln Glu Glu Glu Pro Ile Pro Glu Thr Arg Ile
 305 310 315 320
 Glu Val Glu Ile Pro Lys Val Asn Thr Asp Leu Gly Asn Asp Leu Tyr
 325 330 335
 Phe Val Lys Leu Pro Asn Phe Leu Ser Val Glu Pro Arg Pro Phe Asp
 340 345 350
 Pro Gln Tyr Tyr Glu Asp Glu Phe Glu Asp Glu Glu Met Leu Asp Glu
 355 360 365
 Glu Gly Arg Thr Arg Leu Lys Leu Lys Val Glu Asn Thr Ile Arg Trp
 370 375 380
 Arg Ile Arg Arg Asp Glu Glu Gly Asn Glu Ile Lys Glu Ser Asn Ala
 385 390 395 400
 Arg Ile Val Lys Trp Ser Asp Gly Ser Met Ser Leu His Leu Gly Asn
 405 410 415
 Glu Val Phe Asp Val Tyr Lys Ala Pro Leu Gln Gly Asp His Asn His
 420 425 430
 Leu Phe Ile Arg Gln Gly Thr Gly Leu Gln Gly Gln Ala Val Phe Lys
 435 440 445
 Ala Lys Leu Thr Phe Arg Pro His Ser Thr Asp Ser Ala Thr His Arg
 450 455 460
 Lys Met Thr Leu Ser Leu Ala Asp Arg Cys Ser Lys Thr Gln Lys Ile
 465 470 475 480
 Arg Ile Leu Pro Met Ala Gly Arg Asp Pro Glu Cys Gln Arg Thr Glu
 485 490 495
 Met Ile Lys Lys Glu Glu Glu Arg Leu Arg Ala Ser Ile Arg Arg Glu
 500 505 510
 Ser Gln Gln Arg Arg Met Arg Glu Lys Gln His Gln Arg Gly Leu Ser
 515 520 525
 Ala Ser Tyr Leu Glu Pro Asp Arg Tyr Asp Glu Glu Glu Gly Glu
 530 535 540
 Glu Ser Ile Ser Leu Ala Ala Ile Lys Asn Arg Tyr Lys Gly Gly Ile
 545 550 555 560
 Arg Glu Glu Arg Ala Arg Ile Tyr Ser Ser Asp Ser Asp Glu Gly Ser
 565 570 575
 Glu Glu Asp Lys Ala Gln Arg Leu Leu Lys Ala Lys Lys Leu Thr Ser
 580 585 590
 Asp Glu Glu Gly Glu Pro Ser Gly Lys Arg Lys Ala Glu Asp Asp Asp
 595 600 605
 Lys Ala Asn Lys Lys His Lys Lys Tyr Val Ile Ser Asp Glu Glu Glu
 610 615 620
 Glu Asp Asp Asp
 625

<210> 3495
 <211> 1085
 <212> DNA
 <213> Homo sapiens

<400> 3495
 cgggggccag ggtgccgca ggggcgtccg gggcgctctg accggcctcg cccgcccccc
 60
 cgcagacaca agatgggtgaa ggagacccag tactatgaca tctctgggcgt gaagcccgac
 120
 gcgtccccgg aggagatcaa gaaggcctat cggaagctgg cgctcaagta ccacccggac
 180
 aagaacccgg atgagggcga gaagtttaaa ctcatatccc aggcataatga agtgctttca
 240
 gatccaaaga aaagggatgt ttatgaccaa ggcgagagc aggcataatga agaaggaggc
 300
 tcaggcgacc ccagcttctc ttcacccatg gacatctttg acatgttctt tgggtggtgg
 360
 ggacggatgg ctagagagag aagaggcaag aatgtgttac accagttatc tgtaactctt
 420
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 780
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 900
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 960
 aagcacgggg acctgagatg cgtgcgcgat gaaggaatgc ccatctacaa agcaccctg
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 1085

<210> 3496
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 3496
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<210> 3497
<211> 1638
<212> DNA
<213> Homo sapiens
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120
tttttagtat atccttctaa aaagttttcc tgagaatttt tagtttggcc tctcaagttt
180

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300
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420
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1638

<210> 3498

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3498

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      20              25              30
Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg Asn Glu Glu Arg
      35              40              45
Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys Met Glu Ser Ile
      50              55              60
Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu Glu Val Leu Ser
65              70              75              80
Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro Ala Gly Arg Asn
      85              90              95
Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu Glu Asn Leu Leu
      100              105              110
Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln Asn Lys Lys Val
      115              120              125
Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr Ile Ser Ile Leu
      130              135              140
Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg Glu Val Ile Asn
145              150              155              160
Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu Asp Ala Gln Leu
      165              170              175
Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro Arg Phe Leu Asn
      180              185              190
Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala Gly Ser Ser Ser
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Glu Ser
210

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<210> 3499

<211> 732

<212> DNA

<213> Homo sapiens

<400> 3499

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120
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180
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240
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300
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360
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420
gtcctcagtc ccctccac tcctgctggt cccctgggac atggggcaca cgactcagga
480
ccaggccaga ggcaaaggca aggagcaggc agtaagccag caagagtccc tgtccacggg
540

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 600
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<210> 3500

<211> 168

<212> PRT

<213> Homo sapiens

<400> 3500

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			20					25					30		
Ala	Ser	Thr	Gly	Lys	Gln	Gly	Ala	Pro	Gly	Pro	Asp	Trp	Ala	Cys	Ile
			35				40					45			
Phe	His	Val	Val	Leu	Gln	Pro	Ser	Arg	His	Gly	Pro	Glu	Ala	Thr	Ala
	50					55					60				
Ala	Pro	Gln	Ser	Pro	Pro	Thr	Pro	Ala	Val	Pro	Pro	Gly	His	Gly	Ala
	65				70					75				80	
His	Asp	Ser	Gly	Pro	Gly	Gln	Arg	Gln	Arg	Gln	Gly	Ala	Gly	Ser	Thr
			85						90					95	
Pro	Ala	Arg	Val	Pro	Val	His	Gly	Ser	Pro	Ser	Ser	Cys	Arg	Ala	Leu
			100						105					110	
Arg	Pro	Ala	Gly	Arg	Ser	Ser	Arg	Ala	Ala	Pro	Arg	Ala	Ser	Pro	Ala
			115				120							125	
Gly	Gln	Ala	Ser	Ser	Arg	Pro	Xaa	Ser	Gly	Ala	Met	His	Arg	Leu	Gly
			130				135				140				
Glu	Gly	Asn	Arg	Ala	Gly	Glu	Lys	Val	Phe	Arg	Arg	Thr	Ala	Val	Gln
					150					155					160
Lys	Arg	Arg	Val	Gly	Gly	Gly	Thr								
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<210> 3501

<211> 691

<212> DNA

<213> Homo sapiens

<400> 3501

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 180
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 240
 ttatcttttag gaagaacaaa cataaagaac ttaaatggac tggaggcagt aggggacaca
 300

ttagaagaac tgtggatctc ctacaatttt attgagaagt tgaagggat ccacataatg
 360
 aagaaattga agattctcta catgtctaata aacctggtaa aagactgggc tgagtttgtg
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 480
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 691

<210> 3502

<211> 196

<212> PRT

<213> Homo sapiens

<400> 3502

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 Glu Ile Lys Leu Tyr Ala Gln Ile Pro Pro Ile Glu Lys Met Asp Ala
 35 40 45
 Ser Leu Ser Met Leu Ala Asn Cys Glu Lys Leu Ser Leu Ser Thr Asn
 50 55 60
 Cys Ile Glu Lys Ile Ala Asn Leu Asn Gly Leu Lys Asn Leu Arg Ile
 65 70 75 80
 Leu Ser Leu Gly Arg Asn Asn Ile Lys Asn Leu Asn Gly Leu Glu Ala
 85 90 95
 Val Gly Asp Thr Leu Glu Glu Leu Trp Ile Ser Tyr Asn Phe Ile Glu
 100 105 110
 Lys Leu Lys Gly Ile His Ile Met Lys Lys Leu Lys Ile Leu Tyr Met
 115 120 125
 Ser Asn Asn Leu Val Lys Asp Trp Ala Glu Phe Val Lys Leu Ala Glu
 130 135 140
 Leu Pro Cys Leu Glu Asp Leu Val Phe Val Gly Asn Pro Leu Glu Glu
 145 150 155 160
 Lys His Ser Ala Glu Asn Asn Trp Ile Glu Glu Ala Thr Lys Arg Val
 165 170 175
 Pro Lys Leu Lys Lys Leu Asp Gly Thr Pro Val Ile Lys Gly Asp Glu
 180 185 190
 Glu Glu Asp Asn
 195

<210> 3503

<211> 857

<212> DNA

<213> Homo sapiens

<400> 3503

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 120
 aatgcccaga gattagcgga gaagctccga gcccgaaac gggaacaaga cacaagaaga
 180
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 240
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<210> 3504

<211> 285

<212> PRT

<213> Homo sapiens

<400> 3504

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Gln	Gly	Cys	Gly	Ser	Leu	Phe	Thr	Leu	Val	Ser	Lys	Pro	Phe	Cys	Ala
			20					25					30		
Ala	Ala	Ala	Ala	Ser	Thr	Ala	Ile	Asn	Ala	Gln	Arg	Leu	Ala	Glu	Lys
		35				40						45			
Leu	Arg	Ala	Gln	Lys	Arg	Glu	Gln	Asp	Thr	Lys	Lys	Glu	Pro	Val	Ser
		50				55				60					
Thr	Asn	Ala	Val	Gln	Arg	Arg	Val	Gln	Glu	Ile	Val	Arg	Phe	Thr	Arg
65				70						75				80	
Gln	Leu	Gln	Arg	Val	His	Pro	Asn	Val	Leu	Ala	Lys	Ala	Leu	Thr	Arg
				85				90						95	
Gly	Ile	Leu	His	Gln	Asp	Lys	Asn	Leu	Val	Val	Ile	Asn	Lys	Pro	Tyr
			100					105					110		
Gly	Leu	Pro	Val	His	Gly	Gly	Pro	Gly	Val	Gln	Leu	Cys	Ile	Thr	Asp
		115					120					125			
Val	Leu	Pro	Ile	Leu	Ala	Lys	Met	Leu	His	Gly	His	Lys	Ala	Glu	Pro

130	135	140
Leu His Leu Cys His Arg	Leu Asp Lys Glu Thr	Thr Gly Val Met Val
145	150	155
Leu Ala Trp Asp Lys Asp	Met Ala His Gln Val	Gln Glu Leu Phe Arg
165	170	175
Thr Arg Gln Val Val Lys	Lys Tyr Trp Ala Ile Thr	Val His Val Pro
180	185	190
Met Pro Ser Ala Gly Val	Val Asp Ile Pro Ile Val	Glu Lys Glu Gly
195	200	205
Gln Gly Gln Gln Gln His	Pro Arg Met Thr Leu Ser	Pro Ser Ser Arg
210	215	220
Met Asp Asp Gly Lys Met	Val Lys Val Arg Arg Ser	Arg Asn Ala Gln
225	230	235
Val Ala Val Thr Gln Tyr	Gln Val Leu Ser Ser Thr	Leu Ser Ser Ala
245	250	255
Leu Val Glu Leu Gln Pro	Ile Thr Gly Ile Lys His	Gln Leu Arg Val
260	265	270
His Leu Ser Phe Gly Leu	Asp Cys Pro Ile Leu Gly	Asp
275	280	285

<210> 3505

<211> 1612

<212> DNA

<213> Homo sapiens

<400> 3505

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<210> 3506

<211> 502

<212> PRT

<213> Homo sapiens

<400> 3506

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			20					25					30		
Met	Leu	Leu	Ala	Trp	Pro	Leu	Ala	Leu	Val	Ala	Ser	Leu	Gly	Ser	Ala
		35					40					45			
Glu	Lys	Glu	Pro	Glu	Gln	Pro	Pro	Ala	Leu	Trp	Arg	Lys	Val	Val	Asp
		50				55					60				
Phe	Leu	Leu	Lys	Ala	Ile	Met	Arg	Thr	Met	Trp	Phe	Ala	Gly	Gly	Phe
65					70					75				80	
His	Arg	Val	Ala	Val	Lys	Gly	Arg	Gln	Ala	Leu	Pro	Thr	Glu	Ala	Ala
				85				90						95	
Ile	Leu	Thr	Leu	Ala	Pro	His	Ser	Ser	Tyr	Phe	Asp	Ala	Ile	Pro	Val
			100					105					110		
Thr	Met	Thr	Met	Ser	Ser	Ile	Val	Met	Lys	Thr	Glu	Ser	Arg	Asp	Ile
		115				120					125				
Pro	Ile	Trp	Gly	Thr	Leu	Ile	Gln	Tyr	Ile	Arg	Pro	Val	Phe	Val	Ser
		130				135					140				
Arg	Ser	Asp	Gln	Asp	Ser	Arg	Arg	Lys	Thr	Val	Glu	Glu	Ile	Lys	Arg
145				150						155				160	
Arg	Ala	Gln	Ser	Asn	Gly	Lys	Trp	Pro	Gln	Ile	Met	Ile	Phe	Pro	Glu

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      180              185              190
Phe Ile Pro Gly Ala Pro Val His Pro Gly Val Leu Arg Tyr Pro Asn
      195              200              205
Lys Leu Asp Thr Ile Thr Trp Thr Trp Gln Gly Pro Gly Ala Leu Glu
      210              215              220
Ile Leu Trp Leu Thr Leu Cys Gln Phe His Asn Gln Val Glu Ile Glu
      225              230              235
Phe Leu Pro Val Tyr Ser Pro Ser Glu Glu Lys Arg Asn Pro Ala
      245              250              255
Leu Tyr Ala Ser Asn Val Arg Arg Val Met Ala Glu Ala Leu Gly Val
      260              265              270
Ser Val Thr Asp Tyr Thr Phe Glu Asp Cys Gln Leu Ala Leu Ala Glu
      275              280              285
Gly Gln Leu Arg Leu Pro Ala Asp Thr Cys Leu Leu Glu Phe Ala Arg
      290              295              300
Leu Val Arg Gly Leu Gly Leu Lys Pro Glu Lys Leu Glu Lys Asp Leu
      305              310              315
Asp Arg Tyr Ser Glu Arg Ala Arg Met Lys Gly Gly Glu Lys Ile Gly
      325              330              335
Ile Ala Glu Phe Ala Ala Ser Leu Glu Val Pro Val Ser Asp Leu Leu
      340              345              350
Glu Asp Met Phe Ser Leu Phe Asp Glu Ser Gly Ser Gly Glu Val Asp
      355              360              365
Leu Arg Glu Cys Val Val Ala Leu Ser Val Val Cys Trp Pro Ala Arg
      370              375              380
Thr Leu Asp Thr Ile Gln Leu Ala Phe Lys Met Tyr Gly Ala Gln Glu
      385              390              395
Asp Gly Ser Val Gly Glu Gly Asp Leu Ser Cys Ile Leu Lys Thr Ala
      405              410              415
Leu Gly Val Ala Glu Leu Thr Val Thr Asp Leu Phe Arg Ala Ile Asp
      420              425              430
Gln Glu Glu Lys Gly Lys Ile Thr Phe Ala Asp Phe His Arg Phe Ala
      435              440              445
Glu Met Tyr Pro Ala Phe Ala Glu Glu Tyr Leu Tyr Pro Asp Gln Thr
      450              455              460
His Phe Glu Ser Cys Ala Glu Thr Ser Pro Ala Pro Ile Pro Asn Gly
      465              470              475
Phe Cys Ala Asp Phe Ser Pro Glu Asn Ser Asp Ala Gly Arg Lys Pro
      485              490              495
Val Arg Lys Lys Lys Leu Asp
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<210> 3507

<211> 885

<212> DNA

<213> Homo sapiens

<400> 3507

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120

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 480
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 885

<210> 3508

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3508

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			20					25					30		
Cys	Ile	Ala	Phe	Leu	Ile	Ile	Ile	Gly	Asp	Gln	Gln	Asp	Lys	Ile	Ile
		35					40					45			
Ala	Val	Met	Ala	Lys	Glu	Pro	Glu	Gly	Ala	Ser	Gly	Pro	Trp	Tyr	Thr
		50				55					60				
Asp	Arg	Lys	Phe	Thr	Ile	Ser	Leu	Thr	Ala	Phe	Leu	Phe	Ile	Leu	Pro
65					70				75					80	
Leu	Ser	Ile	Pro	Arg	Glu	Ile	Gly	Phe	Gln	Lys	Tyr	Ala	Ser	Phe	Leu
				85				90						95	
Ser	Val	Val	Gly	Thr	Trp	Tyr	Val	Thr	Ala	Ile	Val	Ile	Ile	Lys	Tyr
			100					105						110	
Ile	Trp	Pro	Asp	Lys	Glu	Met	Thr	Pro	Gly	Asn	Ile	Leu	Thr	Arg	Pro
		115				120					125				
Ala	Ser	Trp	Met	Ala	Val	Phe	Asn	Ala	Met	Pro	Thr	Ile	Cys	Phe	Gly
		130				135				140					
Phe	Gln	Cys	His	Val	Ser	Ser	Val	Pro	Val	Phe	Asn	Ser	Met	Gln	Gln
145				150						155				160	
Pro	Glu	Val	Lys	Thr	Trp	Gly	Gly	Val	Val	Thr	Ala	Ala	Met	Val	Ile

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Gly Ala Ala Val Asp Pro Asp
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<210> 3509

<211> 331

<212> DNA

<213> Homo sapiens

<400> 3509

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240
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<210> 3510

<211> 110

<212> PRT

<213> Homo sapiens

<400> 3510

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Leu Val His Arg Thr Met Ala Gln Pro Pro Val His Asp Tyr Val Pro
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Val Ser Trp Thr Ala Leu Val His Val Lys Ala Glu Tyr Phe Arg Ser
20      25      30
Leu Ala His Tyr His Val Ala Met Ala Leu Cys Asp Gly Ser Pro Thr
35      40      45
Glu Gly Glu Leu Pro Thr His Glu Gln Val Phe Leu Ser Pro Pro Pro
50      55      60
Pro Leu Ser Pro Arg Gly Pro Gly Leu Pro Gln Lys Leu Glu Glu Arg
65      70      75      80
Arg Gln Leu Gly Lys Ala Pro Met Gly Gly Val Pro Trp Gly Ser Asp
85      90      95
Gly His Gln Arg Trp Gln Gly Val Pro His His Pro His Ala
100      105      110

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<210> 3511

<211> 3319

<212> DNA

<213> Homo sapiens

<400> 3511

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120
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180
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240
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300
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360
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420
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1680

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3319

<210> 3512

<211> 462

<212> PRT

<213> Homo sapiens

<400> 3512

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 Ser Arg Met Lys Arg Gly Gly Arg Asp Ser Asp Arg Asn Ser Ser Glu
 35 40 45
 Glu Gly Thr Ala Glu Lys Ser Lys Lys Leu Arg Thr Thr Asn Glu His
 50 55 60
 Ser Gln Thr Cys Asp Trp Gly Asn Leu Leu Gln Asp Ile Ile Leu Gln
 65 70 75 80
 Val Phe Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val
 85 90 95
 Cys Arg Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys
 100 105 110
 Phe Glu Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr
 115 120 125
 His Pro Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu
 130 135 140
 Gln Tyr Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala
 145 150 155 160
 Ala Cys Asp Ile Leu Ser Gln Leu Val Asn Cys Ser Leu Lys Thr Leu
 165 170 175
 Gly Leu Ile Ser Thr Ala Arg Pro Ser Phe Met Asp Leu Pro Lys Ser
 180 185 190
 His Phe Ile Ser Ala Leu Thr Val Val Phe Val Asn Ser Lys Ser Leu
 195 200 205
 Ser Ser Leu Lys Ile Asp Asp Thr Pro Val Asp Asp Pro Ser Leu Lys
 210 215 220
 Val Leu Val Ala Asn Asn Ser Asp Thr Leu Lys Leu Leu Lys Met Ser
 225 230 235 240
 Ser Cys Pro His Val Ser Pro Ala Gly Ile Leu Cys Val Ala Asp Gln
 245 250 255
 Cys His Gly Leu Arg Glu Leu Ala Leu Asn Tyr His Leu Leu Ser Asp
 260 265 270
 Glu Leu Leu Leu Ala Leu Ser Ser Glu Lys His Val Arg Leu Glu His
 275 280 285
 Leu Arg Ile Asp Val Val Ser Glu Asn Pro Gly Gln Thr His Phe His
 290 295 300
 Thr Ile Gln Lys Ser Ser Trp Asp Ala Phe Ile Arg His Ser Pro Lys
 305 310 315 320
 Val Asn Leu Val Met Tyr Phe Phe Leu Tyr Glu Glu Phe Asp Pro
 325 330 335
 Phe Phe Arg Tyr Glu Ile Pro Ala Thr His Leu Tyr Phe Gly Arg Ser
 340 345 350
 Val Ser Lys Asp Val Leu Gly Arg Val Gly Met Thr Cys Pro Arg Leu

355	360	365
Val Glu Leu Val Val Cys	Ala Asn Gly Leu Arg	Pro Leu Asp Glu Glu
370	375	380
Leu Ile Arg Ile Ala Glu Arg Cys Lys Asn Leu Ser	Ala Ile Gly Leu	
385	390	395
Gly Glu Cys Glu Val Ser Cys Ser Ala Phe Val Glu Phe Val Lys Met		400
405	410	415
Cys Gly Gly Arg Leu Ser Gln Leu Ser Ile Met Glu Glu Val Leu Ile		
420	425	430
Pro Asp Gln Lys Tyr Ser Leu Glu Gln Ile His Trp Glu Val Ser Lys		
435	440	445
His Leu Gly Arg Val Trp Phe Pro Asp Met Met Pro Thr Trp		
450	455	460

<210> 3513

<211> 2103

<212> DNA

<213> Homo sapiens

<400> 3513

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 180
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 240
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 300
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 360
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 420
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 480
 aaggccctca gccagagctc agtccttagt aaacacagga gaattcacac aggtgagaa
 540
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 660
 caactctcac atctcattca gcaccagcgg atccacacgg gagaagggcc atatgtgtgt
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 780
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 840
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 1020

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 1920
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 1980
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 2103

<210> 3514

<211> 484

<212> PRT

<213> Homo sapiens

<400> 3514

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 20 25 30
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 35 40 45
 Lys Gly Glu Ser Gln Asn Thr Asp Leu Ser Pro Lys Pro Leu Ile Ser
 50 55 60
 Glu Gln Thr Val Ile Leu Gly Lys Thr Pro Leu Gly Arg Ile Asp Gln

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Glu	Asn	Asn	Glu	Thr	Lys	Gln	Ser	Phe	Cys	Leu	Ser	Pro	Asn	Ser
					85				90				95	Val
Asp	His	Arg	Glu	Val	Gln	Val	Leu	Ser	Gln	Ser	Met	Pro	Leu	Thr
			100					105					110	Pro
His	Gln	Ala	Val	Pro	Ser	Gly	Glu	Arg	Pro	Tyr	Met	Cys	Val	Glu
			115				120					125		Cys
Gly	Lys	Cys	Phe	Gly	Arg	Ser	Ser	His	Leu	Leu	Gln	His	Gln	Arg
			130				135				140			Ile
His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Ser	Val	Cys	Gly	Lys	Ala
					150					155				Phe
145														160
Ser	Gln	Ser	Ser	Val	Leu	Ser	Lys	His	Arg	Arg	Ile	His	Thr	Gly
					165				170					Glu
													175	
Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Arg	Val	Ser
								185					190	Ser
Asp	Leu	Ala	Gln	His	His	Lys	Ile	His	Thr	Gly	Glu	Lys	Pro	His
							200					205		Glu
Cys	Leu	Glu	Cys	Arg	Lys	Ala	Phe	Thr	Gln	Leu	Ser	His	Leu	Ile
							215					220		Gln
210														
His	Gln	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Val	Cys	Pro	Leu
					230					235				Cys
225														240
Gly	Lys	Ala	Phe	Asn	His	Ser	Thr	Val	Leu	Arg	Ser	His	Gln	Arg
				245					250					Val
													255	
His	Thr	Gly	Glu	Lys	Pro	His	Arg	Cys	Asn	Glu	Cys	Gly	Lys	Thr
					260			265					270	Phe
Ser	Val	Lys	Arg	Thr	Leu	Leu	Gln	His	Gln	Arg	Ile	His	Thr	Gly
					275		280				285			Glu
Lys	Pro	Tyr	Thr	Cys	Ser	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Asp	Arg
						295						300		Ser
290														
Val	Leu	Ile	Gln	His	His	Asn	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr
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305														320
Cys	Ser	Glu	Cys	Gly	Lys	Thr	Phe	Ser	His	Arg	Ser	Thr	Leu	Met
					325				330					Asn
													335	
His	Glu	Arg	Ile	His	Thr	Glu	Glu	Lys	Pro	Tyr	Ala	Cys	Tyr	Glu
					340			345					350	Cys
Gly	Lys	Ala	Phe	Val	Gln	His	Ser	His	Leu	Ile	Gln	His	Gln	Arg
					355			360			365			Val
His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Gly	Glu	Cys	Gly	His	Ala
						375				380				Phe
370														
Ser	Ala	Arg	Arg	Ser	Leu	Ile	Gln	His	Glu	Arg	Ile	His	Thr	Gly
					390				395					Glu
385														400
Lys	Pro	Phe	Gln	Cys	Thr	Glu	Cys	Gly	Lys	Ala	Xaa	Ser	Leu	Lys
				405					410					Ala
													415	
Thr	Leu	Ile	Val	His	Leu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr
					420			425					430	Glu
Cys	Asn	Ser	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Tyr	Ser	Val	Leu	Ile
					435			440				445		Gln
His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Gly	Glu
					450			455			460			Cys
Gly	Arg	Ala	Phe	Asn	Gln	His	Gly	His	Leu	Ile	Gln	His	Gln	Lys
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<210> 3515

<211> 5003

<212> DNA

<213> Homo sapiens

<400> 3515

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180
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360
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960
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1440

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<211> 547

<212> PRT

<213> Homo sapiens

<400> 3516

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Tyr Leu Lys Arg Gln Thr Arg Ser Ser Pro Val Leu Gln His Lys Ile
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Ser Glu Thr Leu Glu Ser Arg His His Lys Ile Lys Thr Gly Ser Pro
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Gly Ser Glu Val Val Thr Leu Gln Gln Phe Leu Glu Glu Ser Asn Lys
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Leu Thr Ser Val Gln Ile Lys Ser Ser Ser Gln Glu Asn Leu Leu Asp
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Glu Val Met Lys Ser Leu Ser Val Ser Ser Asp Phe Leu Gly Lys Asp
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Gly Asp Phe Tyr Asp Arg Arg Thr Thr Lys Pro Glu Phe Leu Arg Pro
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Gly Pro Arg Lys Thr Glu Asp Thr Tyr Phe Ile Ser Ser Ala Gly Lys
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Pro Thr Pro Gly Thr Gln Gly Lys Ile Lys Leu Val Lys Glu Ser Ser
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Ile His Asp Phe Leu Thr Lys Asp Ser Arg Leu Pro Ile Ser Val Asp
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<211> 342

<212> DNA

<213> Homo sapiens

<400> 3517

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 Gln Arg Met Pro Asp Arg Pro Thr Ser Arg Pro Leu Leu Val Arg Ala
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<211> 303

<212> PRT

<213> Homo sapiens

<400> 3520

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85      90      95
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225     230     235     240
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245     250     255
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<211> 638

<212> DNA

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<211> 181

<212> PRT

<213> Homo sapiens

<400> 3522

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<210> 3524

<211> 444

<212> PRT

<213> Homo sapiens

<400> 3524

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Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	Ile	Ser	Asp	Phe
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Gln	Asp	Ala	Thr	Asp	Pro	Phe	Val	Ala	Phe	His	Ile	Asn	Lys	Gly	Leu
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Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
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195              200              205
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Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe Phe Phe Ala
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Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
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<210> 3525

<211> 1116

<212> DNA

<213> Homo sapiens

<400> 3525

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<210> 3526

<211> 304

<212> PRT

<213> Homo sapiens

<400> 3526

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			20					25					30		
Arg	Lys	Gly	Ile	Cys	Glu	Tyr	His	Leu	Lys	Asn	Tyr	Ala	Ala	Ala	Leu
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Gln Ala Trp Leu Pro Ala Gly Val Arg Val Pro Leu His Gln Val Pro		
195	200	205
Tyr Ala Val Lys Gly Cys Phe Arg Phe Leu Pro Pro Ala Gln Val Thr		
210	215	220
Val Val Gly Ser Tyr Leu Leu Gly Thr Cys Ile Arg Pro Asp Ile Asn		
225	230	235
Val Asp Val Ala Leu Thr Met Pro Arg Glu Ile Leu Gln Asp Lys Asp		
245	250	255
Gly Leu Asn Gln Arg Tyr Phe Arg Lys Arg Ala Leu Tyr Leu Ala His		
260	265	270
Leu Ala His His Leu Ala Gln Asp Pro Leu Phe Gly Ser Val Cys Phe		
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<210> 3527

<211> 2838

<212> DNA

<213> Homo sapiens

<400> 3527

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<211> 281

<212> PRT

<213> Homo sapiens

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Asp	Pro	Asn	Leu	Gly	Cys	Ser	Ser	Asp	Thr	Ile	Glu	Val	Ser	Cys	Asn
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Phe	Thr	His	Gly	Gly	Gln	Thr	Cys	Leu	Lys	Pro	Ile	Thr	Ala	Ser	Lys
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Val	Glu	Phe	Ala	Ile	Ser	Arg	Val	Gln	Met	Asn	Phe	Leu	His	Leu	Leu
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Ser	Ser	Glu	Val	Thr	Gln	His	Ile	Thr	Ile	His	Cys	Leu	Asn	Met	Thr
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Val	Trp	Gln	Glu	Gly	Thr	Gly	Gln	Thr	Pro	Ala	Lys	Gln	Ala	Val	Arg
	195						200					205			
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Pro	Glu	Val	Ser	Met	Asp	Gly	Cys	Lys	Val	Gln	Asp	Gly	Arg	Trp	His

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	245		250		255	
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<210> 3529

<211> 3026

<212> DNA

<213> Homo sapiens

<400> 3529

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<211> 206

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<210> 3532

<211> 254

<212> PRT

<213> Homo sapiens

<400> 3532

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 35 40 45
 Lys Lys Ala Asp Met Val Asn Glu Asp Leu Leu Ser Asp Gly Thr Ser
 50 55 60
 Glu Asn Glu Ser Gly Phe Trp Asp Ser Phe Lys Trp Gly Phe Thr Gly
 65 70 75 80
 Gln Lys Thr Glu Glu Val Lys Gln Asp Lys Asp Asp Ile Ile Asn Ile
 85 90 95
 Phe Ser Val Ala Ser Gly His Leu Tyr Glu Arg Phe Leu Arg Ile Met
 100 105 110
 Met Leu Ser Val Leu Lys Asn Thr Lys Thr Pro Val Lys Phe Trp Phe
 115 120 125
 Leu Lys Asn Tyr Leu Ser Pro Thr Phe Lys Glu Phe Ile Pro Tyr Met
 130 135 140
 Ala Asn Glu Tyr Asn Phe Gln Tyr Glu Leu Val Gln Tyr Lys Trp Pro
 145 150 155 160
 Arg Trp Leu His Gln Gln Thr Glu Lys Gln Arg Ile Ile Trp Gly Tyr
 165 170 175
 Lys Ile Leu Phe Leu Asp Val Leu Phe Pro Leu Val Val Asp Lys Phe

	180		185		190
Leu	Phe Val Asp Ala Asp Gln Ile Val Arg Thr Asp Leu Lys Glu Leu				
	195		200		205
Arg Asp Phe Asn Leu Asp Gly Ala Pro Tyr Gly Thr Pro Phe Cys					
	210		215		220
Asp Ser Arg Arg Glu Met Asp Gly Tyr Arg Phe Trp Lys Ser Gly Tyr					
	225		230		235
Trp Ala Ser His Leu Ala Gly Arg Lys Tyr His Ile Arg Tyr					
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<210> 3533

<211> 1151

<212> DNA

<213> Homo sapiens

<400> 3533

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 180
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 300
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 360
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 480
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 540
 accatcaaca ccaccatcca ggatgtcaac cgctacctcc tcaagagtgg agggctctcc
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 720
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 1020
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1151

<210> 3534

<211> 313

<212> PRT

<213> Homo sapiens

<400> 3534

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          20          25          30
Met Asp Asn Leu Pro Ser Ala Ala Ser Pro Leu Glu Gln Asn Pro Ser
          35          40          45
Lys His Gly Ala Ile Pro Gly Gly Leu Ser Ile Gly Pro Gly Lys
          50          55          60
Ser Ser Ile Asp Asp Ser Tyr Gly Arg Tyr Asp Leu Ile Gln Asn Ser
65          70          75          80
Glu Ser Pro Ala Ser Pro Pro Val Ala Val Pro His Ser Trp Ser Arg
          85          90          95
Ala Lys Ser Asp Ser Asp Lys Ile Ser Asn Gly Ser Ser Ile Asn Trp
          100          105          110
Pro Pro Glu Phe His Pro Gly Val Pro Trp Lys Gly Leu Gln Asn Ile
          115          120          125
Asp Pro Glu Asn Asp Pro Asp Val Thr Pro Gly Ser Val Pro Thr Gly
130          135          140
Pro Thr Ile Asn Thr Thr Ile Gln Asp Val Asn Arg Tyr Leu Leu Lys
145          150          155          160
Ser Gly Gly Ser Ser Pro Pro Ser Ser Gln Asn Ala Thr Leu Pro Ser
          165          170          175
Ser Ser Ala Trp Pro Leu Ser Ala Ser Gly Tyr Ser Ser Ser Phe Ser
          180          185          190
Ser Ile Ala Ser Ala Pro Ser Val Ala Gly Lys Leu Ser Asp Ile Lys
195          200          205          210
Ser Thr Trp Ser Ser Gly Pro Thr Ser His Thr Gln Ala Ser Leu Ser
210          215          220
His Glu Leu Trp Lys Val Pro Arg Asn Ser Thr Ala Pro Thr Arg Pro
225          230          235          240
Pro Pro Gly Leu Thr Asn Pro Lys Pro Ser Ser Thr Trp Gly Ala Ser
          245          250          255
Pro Leu Gly Trp Thr Ser Ser Tyr Ser Ser Gly Ser Ala Trp Ser Thr
260          265          270
Asp Thr Ser Gly Arg Thr Ser Ser Trp Leu Val Leu Arg Asn Leu Thr
275          280          285
Pro Gln Val Gln Tyr Gly Ala Pro Ala Ser Leu Ser Met Ile Gln Gly
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Gly Phe Pro Leu Gly Pro Gln Cys Arg
305          310

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<210> 3535

<211> 723

<212> DNA

<213> Homo sapiens

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 120
 cggcagacct gctacagggt ctctctgctg gtgaccacc accccacaac cactcaagaa
 180
 gcctcatcaa aacattgttg gagaaaactg ggtgcccacg gaggagaaa ggaatgcaag
 240
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 300
 aagatcagct tagagaagaa gtggtccaga gagtttctct tctccttctc tattacatta
 360
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 480
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 723

<210> 3536
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 3536
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 Arg Val Ser Leu Leu Leu Tyr Tyr Ile Ile His Gln Glu Glu Ile
 35 40 45
 Cys Ser Ser Lys Leu Asn Met Ser Asn Lys Glu Tyr Lys Phe Tyr Leu
 50 55 60
 His Ser Leu Leu Ser Leu Arg Gln Asp Glu Asp Ser Ser Phe Leu Ser
 65 70 75 80
 Gln Asn Glu Thr Glu Asp Ile Leu Ala Phe Thr Arg Gln Tyr Phe Asp
 85 90 95
 Thr Ser Gln Ser Gln Cys Met Glu Thr Lys Thr Leu Gln Lys Lys Ser
 100 105 110
 Gly Ile Val Ser Ser Glu Gly Ala Asn Glu Ser Thr Leu Pro Gln Leu
 115 120 125
 Ala Ala Met Ile Ile Thr Leu Ser Leu Gln Gly Val Cys Leu Gly Gln
 130 135 140
 Gly Asn Leu Pro Ser Pro Asp Tyr Phe Thr Glu Tyr Ile Phe Ser Ser

150

155

160

Leu Asn Arg

<210> 3537

<211> 714

<212> DNA

<213> Homo sapiens

<400> 3537

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120

cataaggcca agagtaagtg cgtgaatgca cttaagacaa agtcaggaca cgagcttcac

180

atgacaggcc ccgctgtggg gaccagccag ccttggggag gggcacgcca cgccacacac

240

acactcacca ctgtacagcc tgggactccc attgcatatt cacaggcccc gccgggcagg

300

gcacctcaag gctggggggag gggcaggggg agggaggagc cgtgggggtg ccttgggtgg

360

gtggagaggg cagcatgtga gaggcaaatg tgcaccaaca ctgggcgtga gacgtgagca

420

gcctcagggt tacggcatga gatgtgtgtg gttggggggg gtctgcgtga cccgggaggg

480

gggtgtgtgt gagatgagca cagaggcatg gcgtggcacg tgctcgtgtg gtggtcgcgt

540

gcctgaatcc agggggctacc cctgtccggt ctgtggccct cggtcctgca ggggtggaag

600

aagggtcctt cagacgtgcc cctaccagc aggcacagaa atgtttgcat aagggtccagc

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<210> 3538

<211> 154

<212> PRT

<213> Homo sapiens

<400> 3538

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20 25 30

Leu Lys Asp Pro Ser Ser Asn Pro Ala Gly Pro Arg Ala Thr Ala Gly

35 40 45

Gln Gly Val Ala Pro Gly Phe Arg His Ala Thr Thr Thr Arg Ala Arg

50 55 60

Ala Thr His Ala Ser Cys Ala His Leu Thr His Thr Pro Leu Pro Gly

65 70 75 80

His Ala Asp Thr Pro Gln Pro His Thr Ser His Ala Val His Leu Arg

85 90 95

Leu Leu Thr Ser His Ala Gln Cys Trp Cys Thr Phe Ala Ser His Met

	100		105		110										
Leu	Pro	Ser	Pro	Pro	Thr	Gln	Gly	His	Pro	Thr	Ala	Pro	Pro	Cys	Pro
	115				120					125					
Cys	Pro	Ser	Pro	Ser	Leu	Glu	Val	Pro	Cys	Pro	Ala	Gly	Pro	Val	Asn
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<210> 3539
 <211> 818
 <212> DNA
 <213> Homo sapiens

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 180
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 300
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<210> 3540
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 3540
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 20 25 30
 Thr Leu Gly Ser Ser Arg Ala Lys Leu Gly Asn Phe Pro Trp Gln Ala

	35		40		45	
Phe Thr Ser Ile His Gly Arg Gly Gly Ala Leu Gly Asp Arg						
50		55		60		
Trp Ile Leu Thr Ala Ala His Thr Val Tyr Pro Lys Asp Ser Val Ser						
65	70		75		80	
Leu Arg Lys Asn Gln Ser Val Asn Val Phe Leu Gly His Thr Ala Ile						
	85		90		95	
Asp Glu Met Leu Lys Leu Gly Asn His Pro Val His Arg Val Val Val						
100		105		110		
His Pro Asp Tyr Arg Gln Asn Glu Ser His Asn Phe Ser Gly Asp Ile						
115		120		125		
Ala Leu Leu Glu Leu Gln His Ser Ile Pro Leu Gly Pro Asn Val Leu						
130		135		140		
Pro Val Cys Leu Pro Asp Asn Glu Thr Leu Tyr Arg Ser Gly Leu Leu						
145	150		155		160	
Gly Tyr Val Ser Gly Phe Gly Met Glu Met Gly Trp Leu Thr Thr Glu						
	165		170		175	
Leu Lys Tyr Ser						
180						

<210> 3541

<211> 722

<212> DNA

<213> Homo sapiens

<400> 3541

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180
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240
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<210> 3542

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3542

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Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
      35           40           45
Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
      50           55           60
His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
      65           70           75           80
Ala Ile Lys Gln Asn Pro Leu Leu Ala Glu Ala Tyr Ser Asn Leu Gly
      85           90           95
Asn Val Tyr Lys Glu Arg Gly Gln Leu Gln Glu Ala Ile Glu His Tyr
      100          105          110
Arg His Ala Leu Arg Leu Lys Pro Asp Phe Ile Asp Gly Tyr Ile Asn
      115          120          125
Ala Ala Ala Ala Leu Val Ala Ala Gly Asp Met Glu Gly Ala Val Gln
      130          135          140
Ala Tyr Val Ser Ala Leu Gln Pro Gly
145          150

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<210> 3543

<211> 1206

<212> DNA

<213> Homo sapiens

<400> 3543

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gtttgggttg tgctcaggat gtgtaaatgt ttctcttcag ccataagcca cgcttggtag
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240
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360
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480
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540
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600
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660

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<210> 3544

<211> 273

<212> PRT

<213> Homo sapiens

<400> 3544

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		20					25					30			
Lys	Ile	Val	Leu	Phe	Pro	His	Tyr	Glu	Glu	Gly	His	Ile	Pro	Gly	Ile
	35					40					45				
Leu	Ile	Ile	Ile	Phe	Tyr	Gly	Ile	Ser	Ile	Phe	Cys	Leu	Val	Ala	Leu
	50				55					60					
Val	Arg	Ala	Ser	Ile	Thr	Asp	Pro	Gly	Arg	Leu	Pro	Glu	Asn	Pro	Lys
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Leu	Met	Arg	Pro	Lys	Arg	Ser	His	His	Cys	Ser	Arg	Cys	Gly	His	Cys
		100						105					110		
Val	Arg	Arg	Met	Asp	His	His	Cys	Pro	Trp	Ile	Asn	Asn	Cys	Val	Gly
	115				120						125				
Glu	Asp	Asn	His	Trp	Leu	Phe	Leu	Gln	Leu	Cys	Phe	Tyr	Thr	Glu	Leu
	130				135						140				
Leu	Thr	Cys	Tyr	Ala	Leu	Met	Phe	Ser	Phe	Cys	His	Tyr	Tyr	Tyr	Phe
145				150					155					160	
Leu	Pro	Leu	Lys	Lys	Arg	Asn	Leu	Asp	Leu	Phe	Val	Phe	Arg	His	Glu
		165					170						175		
Leu	Ala	Ile	Met	Arg	Leu	Ala	Ala	Phe	Met	Gly	Ile	Thr	Met	Leu	Val
	180						185					190			
Gly	Ile	Thr	Gly	Leu	Phe	Tyr	Thr	Gln	Leu	Ile	Gly	Ile	Ile	Thr	Pro
	195					200					205				
Cys	Ser	Leu	Ile	Leu	Leu	Lys	Cys	Gly	Ser	Val	Ser	Asn	Asn	Ser	Leu

210	215	220
Gly Asp Leu Met Lys	Ile Ser Glu Thr Phe Ala Leu Arg Ile Pro Ser	
225	230	235
Phe Val Val Met Cys	Pro Glu Asn Ser Ser Leu Arg Val Phe Asn Ser	240
245	250	255
Val Lys Leu Leu Cys	Leu Asp Ser Pro Leu Ile Gln Trp Ser Thr	260
260	265	270

Lys

<210> 3545

<211> 3657

<212> DNA

<213> Homo sapiens

<400> 3545

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 480
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<211> 792

<212> PRT

<213> Homo sapiens

<400> 3546

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 35 40 45
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 50 55 60
 Val Lys His Leu Arg His Ser Ala Trp Pro Pro Thr Leu Leu Gln Met
 65 70 75 80
 Val His Thr Leu Ala Ser Asn Gly Ala Asn Ser Ile Trp Glu His Ser
 85 90 95
 Leu Leu Asp Pro Ala Gln Val Gln Ser Gly Arg Arg Lys Ala Asn Pro
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 Gln Asp Lys Val His Pro Ile Lys Ser Glu Phe Ile Arg Ala Lys Tyr
 115 120 125
 Gln Met Leu Ala Phe Val His Lys Leu Pro Cys Arg Asp Asp Asp Gly

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Asn	Phe	Phe	His	Pro	Glu	Lys	Gly	Thr	Thr	Pro	Leu	His	Val	Ala	Ala
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Lys	Ala	Gly	Gln	Thr	Leu	Gln	Ala	Glu	Leu	Leu	Val	Val	Tyr	Gly	Ala
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Asp	Pro	Gly	Ser	Pro	Asp	Val	Asn	Gly	Arg	Thr	Pro	Ile	Asp	Tyr	Ala
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Tyr	Glu	Leu	Thr	Asp	Arg	Leu	Ala	Phe	Tyr	Leu	Cys	Gly	Arg	Lys	Pro
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Ala	Val	Pro	Phe	Leu	Pro	Val	Asn	Pro	Glu	Tyr	Ser	Ala	Thr	Arg	Asn
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Leu	Ile	Ile	Asp	Ile	Leu	Ser	Glu	Ala	Lys	Arg	Arg	Gln	Gln	Gly	Lys
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Asp	Thr	Asp	Gln	Glu	Pro	Leu	Arg	Ser	Thr	Gly	Ala	Thr	Arg	Ser	Asn
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Arg	Ala	Arg	Ser	Met	Asp	Ser	Ser	Asp	Leu	Ser	Asp	Gly	Ala	Val	Thr
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Leu	Gln	Glu	Tyr	Leu	Glu	Leu	Lys	Lys	Ala	Leu	Ala	Thr	Ser	Glu	Ala
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Pro Glu Leu Glu Ser Leu Asp Gly Asp Leu Asp Pro Gly Leu Pro Ser
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Thr Glu Asp Val Ile Leu Lys Thr Glu Gln Val Thr Lys Asn Ile Gln
                    675                      680                      685
Glu Leu Leu Arg Ala Ala Gln Glu Phe Lys His Asp Ser Phe Val Pro
690                      695                      700
Cys Ser Glu Lys Ile His Leu Ala Val Thr Glu Met Ala Ser Leu Phe
705                      710                      715                      720
Pro Lys Arg Pro Ala Leu Glu Pro Val Arg Ser Ser Leu Arg Leu Leu
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Asn Ala Ser Ala Tyr Arg Leu Gln Ser Glu Cys Arg Lys Thr Val Pro
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<211> 1039

<212> DNA

<213> Homo sapiens

<400> 3547

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<211> 346

<212> PRT

<213> Homo sapiens

<400> 3548

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Lys	Ser	Pro	Phe	Thr	Val	Lys	Gly	Asn	Trp	Tyr	Pro	Tyr	Asn	Gly	Gln
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Cys	Leu	Pro	Asp	Ile	Asp	Ser	Glu	Glu	Tyr	Phe	Cys	Val	Lys	Arg	Ile
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Phe	Ser	Gly	Gly	Asp	Gln	Ser	Phe	Ser	His	Tyr	Ser	Ser	Pro	Gln	Asn
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Cys	Gly	Pro	Pro	Asp	Asp	Phe	Arg	Cys	Pro	Asn	Pro	Thr	Lys	Gln	Ile
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		180					185					190			
Ser	Ser	Gly	Cys	Leu	Asn	Gly	Ser	Phe	Leu	Ala	Val	Ser	Asn	Asp	Asp
	195					200					205				
His	Tyr	Arg	Thr	Gly	Thr	Arg	Phe	Ser	Gly	Val	Asp	Met	Asn	Ala	Ala
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                260                265                270
Glu Cys Pro Leu Met Ser Asp Ser Asn Asn Phe Ile Thr Ile Ala Ile
                275                280                285
Pro Phe Gly Thr Ala Leu Val Asn Leu Glu Lys Ala Pro Leu Lys Val
                290                295                300
Leu Glu Asn Trp Trp Ser Val Leu Glu Pro Pro Leu Phe Leu Lys Ile
305                310                315                320
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<210> 3549

<211> 2542

<212> DNA

<213> Homo sapiens

<400> 3549

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960

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<210> 3550
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 3550

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Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys Lys Arg Asp Lys Asp
 50          55          60
Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu Gln Arg
 65          70          75          80
Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Arg Arg Ala Met Glu
 85          90          95
Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg Glu Arg Arg Glu Arg Glu
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 115         120         125
Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu Arg Glu Arg
 130         135         140
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 145         150         155         160
Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu Glu Leu Arg
 165         170         175
Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg Asn Ser Leu
 180         185         190
Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro Tyr Trp Ser
 195         200         205
Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp Ala Arg Phe Gly His Gly
 210         215         220
Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe Asn Asp Phe Asp His Arg
 225         230         235         240
Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala Val Gln Ser Ser Ser Phe
 245         250         255
Glu Arg Arg Asp Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Ala Arg
 260         265         270
Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe Glu Arg Tyr Pro Lys Asn
 275         280         285
Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro Arg Asn Glu Leu
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Arg Glu Ser Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu Arg Arg
 305         310         315         320
Thr Val Ile Ile His Asp Arg Pro Asp Ile Thr His Pro Arg His Pro
 325         330         335
Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys Ser Asp
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Gly Ser Met Ser Thr Asp Lys Arg Glu Thr Arg Val Glu Arg Pro Glu
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      405              410              415
Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro Arg Lys
      420              425              430
Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp Thr Arg
      435              440              445
Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln His Ser
      450              455              460
Ser Asn Ala Ser Pro Ile Asn Arg Ile Val Gln Ile Ser Gly Asn Ser
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Met Pro Arg Gly Ser Gly Ser Gly Phe Lys Pro Phe Lys Gly Gly Pro
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<210> 3551
<211> 545
<212> DNA
<213> Homo sapiens

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<210> 3552
<211> 55
<212> PRT
<213> Homo sapiens

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<400> 3552
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Ala Lys Lys Asp Met Leu Ala Ala Leu Lys Ser Arg Gln Glu Ala Leu

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	20		25		30
Glu	Glu	Thr	Leu	Arg	Gln
			Arg	Leu	Glu
			Glu	Leu	Lys
			Lys	Lys	Leu
			Cys	Leu	
	35		40		45
Arg	Glu	Ala	Val	Ser	Leu
			Ser		
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<210> 3553

<211> 1412

<212> DNA

<213> Homo sapiens

<400> 3553

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 120
 gatgaccagc tcaacatcct gcccatctcc tcccacgttg ccaccatgga ggcctgcct
 180
 cccacagact cggatgagag tcttggtcct tctgatctgg agctgagggg gttgaaggag
 240
 agcttgcagg acaccagacc tgtgggtgtg ttggtggact gctgtaagac tctagaccag
 300
 gccaaagtgt tcttgaatt tatcaggagg atctctgaaa agaccctgag gagtactgtt
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 480
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 720
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 780
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 840
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 900
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 960
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 1020
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 1080
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 1140
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 1200
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 1260

gaacagagggc gtccttgtgg cagtgtattg ggggaaccact gaggcacag gaattagtgg
 1320
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 1412

<210> 3554

<211> 419

<212> PRT

<213> Homo sapiens

<400> 3554

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Gln	Asp	Val	Val	Gly	Arg	Phe	Asn	Glu	Arg	Phe	Ile	Leu	Ser	Leu	Ala
			20					25					30		
Ser	Cys	Lys	Lys	Cys	Leu	Val	Ile	Asp	Asp	Gln	Leu	Asn	Ile	Leu	Pro
		35					40					45			
Ile	Ser	Ser	His	Val	Ala	Thr	Met	Glu	Ala	Leu	Pro	Pro	Gln	Thr	Pro
	50					55					60				
Asp	Glu	Ser	Leu	Gly	Pro	Ser	Asp	Leu	Glu	Leu	Arg	Glu	Leu	Lys	Glu
	65				70				75					80	
Ser	Leu	Gln	Asp	Thr	Gln	Pro	Val	Gly	Val	Leu	Val	Asp	Cys	Cys	Lys
			85					90					95		
Thr	Leu	Asp	Gln	Ala	Lys	Ala	Val	Leu	Lys	Phe	Ile	Glu	Gly	Ile	Ser
		100						105					110		
Glu	Lys	Thr	Leu	Arg	Ser	Thr	Val	Ala	Leu	Thr	Ala	Ala	Arg	Gly	Arg
		115					120					125			
Gly	Lys	Ser	Ala	Ala	Leu	Gly	Leu	Ala	Ile	Ala	Gly	Ala	Val	Ala	Phe
	130					135					140				
Gly	Tyr	Ser	Asn	Ile	Phe	Val	Thr	Ser	Pro	Ser	Pro	Asp	Asn	Leu	His
			150						155					160	
Thr	Leu	Phe	Glu	Phe	Val	Phe	Lys	Gly	Phe	Asp	Ala	Leu	Gln	Tyr	Gln
			165					170						175	
Glu	His	Leu	Asp	Tyr	Glu	Ile	Ile	Gln	Ser	Leu	Asn	Pro	Glu	Phe	Asn
		180						185					190		
Lys	Ala	Val	Ile	Ile	Val	Asn	Val	Phe	Arg	Glu	His	Arg	Gln	Thr	Ile
		195				200						205			
Gln	Tyr	Ile	His	Pro	Ala	Asp	Ala	Val	Lys	Leu	Gly	Gln	Ala	Glu	Leu
		210				215					220				
Val	Val	Ile	Asp	Glu	Ala	Ala	Ala	Ile	Pro	Leu	Pro	Leu	Val	Lys	Ser
				230					235					240	
Leu	Leu	Gly	Pro	Tyr	Leu	Val	Phe	Met	Ala	Ser	Thr	Ile	Asn	Gly	Tyr
				245				250						255	
Glu	Gly	Thr	Gly	Arg	Ser	Leu	Ser	Leu	Lys	Leu	Ile	Gln	Gln	Leu	Arg
		260						265					270		
Gln	Gln	Ser	Ala	Gln	Ser	Gln	Val	Ser	Thr	Thr	Ala	Glu	Asn	Lys	Thr
		275				280						285			
Thr	Thr	Thr	Ala	Arg	Leu	Ala	Ser	Ala	Arg	Thr	Leu	His	Glu	Val	Ser
		290				295					300				
Leu	Gln	Glu	Ser	Ile	Arg	Tyr	Ala	Pro	Gly	Asp	Ala	Val	Glu	Lys	Trp
				310						315				320	
Leu	Asn	Asp	Leu	Leu	Cys	Leu	Asp	Cys	Leu	Asn	Ile	Thr	Arg	Ile	Val

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1038

<210> 3556

<211> 333

<212> PRT

<213> Homo sapiens

<400> 3556

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Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
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Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
 20           25           30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
 35           40           45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
 50           55           60
Gly Arg Pro Phe Val Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
 65           70           75
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
 85           90           95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
100           105           110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Ala Glu Ser Glu Met Ala
115           120           125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
130           135           140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145           150           155
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
165           170           175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Xaa Cys Arg Thr Xaa Val
180           185           190
Arg Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe
195           200           205
Arg Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu
210           215           220
His Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu
225           230           235
Leu Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu
245           250           255
Glu Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe
260           265           270
Leu Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala
275           280           285
Ala Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Val Pro
290           295           300
Ala Gly Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Ala Gln Pro
305           310           315
Ala Pro Gln Leu Pro Leu Asn Gly Cys Pro Thr Ile Leu
325           330

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<210> 3557

<211> 486

<212> DNA

<213> Homo sapiens

<400> 3557

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 120
 agaaagcaga gtaagtccaa aatccatgca gcacgcagcc tgagtgagat cgccatcgac
 180
 ctgaccgcaga cggggacgct gaagacctcg aagctggcca acatgggtag caaggggaag
 240
 atcatcagcg gcagcagcgg cagcctgctg tcttcaggat ctggtgccag gagacactgc
 300
 attctactcc caggttctca ggaatcagat agctcgagc cgccaagaa ggacatgctg
 360
 gctgccttga agtccaggca ggaagctctg gaggaacccc tgcgtcagag gctggaggaa
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 486

<210> 3558

<211> 162

<212> PRT

<213> Homo sapiens

<400> 3558

Ser Val Thr Arg Arg Thr Phe Gly His Ser Gly Ile Ala Val His Thr
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 Trp Tyr Ala Cys Pro Ala Leu Ile Lys Ser Ile Trp Ala Met Ala Ile
 20 25 30
 Ser Gln His Gln Phe Tyr Leu Asp Arg Lys Gln Ser Lys Ser Lys Ile
 35 40 45
 His Ala Ala Arg Ser Leu Ser Glu Ile Ala Ile Asp Leu Thr Glu Thr
 50 55 60
 Gly Thr Leu Lys Thr Ser Lys Leu Ala Asn Met Gly Ser Lys Gly Lys
 65 70 75 80
 Ile Ile Ser Gly Ser Ser Gly Ser Leu Leu Ser Ser Gly Ser Gly Ala
 85 90 95
 Arg Arg His Cys Ile Leu Leu Pro Gly Ser Gln Glu Ser Asp Ser Ser
 100 105 110
 Gln Ser Ala Lys Lys Asp Met Leu Ala Ala Leu Lys Ser Arg Gln Glu
 115 120 125
 Ala Leu Glu Glu Thr Leu Arg Gln Arg Leu Glu Glu Leu Lys Lys Leu
 130 135 140
 Cys Leu Arg Glu Ala Glu Leu Thr Gly Lys Leu Pro Val Glu Tyr Pro
 145 150 155 160
 Leu Asp

<210> 3559

<211> 673

<212> DNA

<213> Homo sapiens

<400> 3559

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 120
 gccgcgcaag caggggctat cgagcgggtc ctgagggatt acagcgacaa gcataggggt
 180
 actttcaaat ttgaatcaac agatgaagat aaaagaaaga aactctgtga aggcataattt
 240
 aaagtcctta taaaggacat cccaacaaca tgtcaagtgt cctgcctgga agtactccgc
 300
 attctctcca gagacaaaaa ggttttagtt cctgtgacaa ctaaggaaaa tatgcagata
 360
 ctgctgcgac tagccaagct aaatgagtta gatgattcct tggagaaagt atcagagttc
 420
 ccagttattg tggagtcatt aaaatgtctg tgtaatatag tgttcaacag tcagatggca
 480
 cagcagctca gcctggaact taatcttgct gcaaagctct gtaacctcct gagaaagtgc
 540
 aaggaccgga aatttatcaa tgacattaag tgctttgact tgcgcttgct cttcctcttg
 600
 tcacttttgc acaccgacat caggtcacia ttgcgctatg agctccaggg actaccgctg
 660
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 673

<210> 3560

<211> 195

<212> PRT

<213> Homo sapiens

<400> 3560

Met Asp Glu Glu Arg Ala Leu Tyr Ile Val Arg Ala Gly Glu Ala Gly
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 Ala Ile Glu Arg Val Leu Arg Asp Tyr Ser Asp Lys His Arg Ala Thr
 20 25 30
 Phe Lys Phe Glu Ser Thr Asp Glu Asp Lys Arg Lys Lys Leu Cys Glu
 35 40 45
 Gly Ile Phe Lys Val Leu Ile Lys Asp Ile Pro Thr Thr Cys Gln Val
 50 55 60
 Ser Cys Leu Glu Val Leu Arg Ile Leu Ser Arg Asp Lys Lys Val Leu
 65 70 75 80
 Val Pro Val Thr Thr Lys Glu Asn Met Gln Ile Leu Leu Arg Leu Ala
 85 90 95
 Lys Leu Asn Glu Leu Asp Asp Ser Leu Glu Lys Val Ser Glu Phe Pro
 100 105 110
 Val Ile Val Glu Ser Leu Lys Cys Leu Cys Asn Ile Val Phe Asn Ser
 115 120 125
 Gln Met Ala Gln Gln Leu Ser Leu Glu Leu Asn Leu Ala Ala Lys Leu
 130 135 140
 Cys Asn Leu Leu Arg Lys Cys Lys Asp Arg Lys Phe Ile Asn Asp Ile


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145             150             155             160
Lys Cys Phe Asp Leu Arg Leu Leu Phe Leu Leu Ser Leu Leu His Thr
                165             170             175
Asp Ile Arg Ser Gln Leu Arg Tyr Glu Leu Gln Gly Leu Pro Leu Leu
                180             185             190
Thr Gln Ile
                195

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<210> 3561

<211> 523

<212> DNA

<213> Homo sapiens

<400> 3561

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120
ggagggcatg agacgcctat tgcagagctg ctcaccagaa ggtaacagga atttagaaga
180
gaagctccta cctgcccccg atcatgcacg tggccactga ggatgccaga cgaggtgatg
240
ctgggtctcat agagaatgta cccgaaggac tgtccatttc ccccatgtac tggcaggttc
300
tccatgttga tgggcttttc agacttgatt ggctgcgtac agaagagatg gaggggtggg
360
caggctcagg aggagtgggg tcacagacag actctgcttg ggggctggca catgggggtg
420
aagcggaggt ttggtgggtg ttttctactt tgacttctca ttgcactaaa catacaactc
480
tccaggttga cggggaagag gagtggggca aaggggtgtg cac
523

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<210> 3562

<211> 106

<212> PRT

<213> Homo sapiens

<400> 3562

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Glu Asn Val Pro Glu Gly Leu Ser Ile Ser Pro Ile Asp Trp Gln Val
20             25             30
Leu His Val Asp Gly Leu Phe Arg Leu Asp Trp Leu Arg Thr Glu Glu
35             40             45
Met Glu Gly Trp Ala Gly Ser Gly Gly Val Gly Ser Gln Thr Asp Ser
50             55             60
Ala Trp Gly Leu Ala His Gly Val Glu Ala Glu Val Trp Trp Val Phe
65             70             75             80
Ser Thr Leu Thr Ser His Cys Thr Lys His Thr Thr Leu Gln Gly Asp
85             90             95
Gly Glu Glu Glu Trp Gly Lys Gly Val Cys
100             105

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<210> 3563
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 3563
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 120
 ccctgcgcgc cgtcgacggg gccccagtg ggcgcgggc tggacgcga gcagcgacg
 180
 gtgttcgcct tcgtgctctg cctgctcgtg gtgctggtgc tgttgatggt gcgctgcgtg
 240
 cgcctcctgc tcgaccccta cagccgcatg ccgcctcgt cctggaccga ccacaaggag
 300
 gcgctcgagc gcgggcagtt cgactacgcg ttggtgtgag ggcgcgggc ccccttagg
 359

<210> 3564
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 3564
 Met Ser Ala Thr Trp Thr Leu Ser Pro Glu Pro Leu Pro Pro Ser Thr
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 Gly Pro Pro Val Gly Ala Gly Leu Asp Ala Glu Gln Arg Thr Val Phe
 20 25 30
 Ala Phe Val Leu Cys Leu Leu Val Val Leu Val Leu Leu Met Val Arg
 35 40 45
 Cys Val Arg Ile Leu Leu Asp Pro Tyr Ser Arg Met Pro Ala Ser Ser
 50 55 60
 Trp Thr Asp His Lys Glu Ala Leu Glu Arg Gly Gln Phe Asp Tyr Ala
 65 70 75 80
 Leu Val

<210> 3565
 <211> 580
 <212> DNA
 <213> Homo sapiens

<400> 3565
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 aggacgagcg cgaacttcaa gtccagaag ccccgcttcc ctggagcccg cgcctgccc
 180
 cgctacgccc gccgggagcc gggcagagcg gccaaagtgt cgcagcccaa gaaaagaaag
 240
 cttgagtcgg ggggcggcgc cgaaggagg gagggaactg aagaggaaga tggcgcggag
 300

cgggaggcgg ccctggagcg accccggacg actaagcggg aacgggacca gctgtactac
 360
 gagtgctact cgagcgtttc ggtccacgag gagatgatcg cggaccgcgt ccgaccgat
 420
 gcctaccgct ggggtttccct tcggaactgg gcagcactgc gaggcaagac ggtactggac
 480
 gtggggcggg gcaccggcat tctgagcatc ttctgtgccc aggccggggc ccggcgcggtg
 540
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<210> 3566

<211> 193

<212> PRT

<213> Homo sapiens

<400> 3566

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Gln	Asn	Ser	Ser	Arg	Glu	Gln	Ala	Gln	Glu	Thr	Phe	Arg	Ala	Ala	Gly
			20					25					30		
Arg	Ala	Thr	Pro	Gln	Glu	Val	Gly	Arg	Thr	Ser	Ala	His	Phe	Lys	Ser
			35					40				45			
Gln	Lys	Pro	Pro	Phe	Pro	Gly	Ala	Arg	Ala	Val	Pro	Arg	Tyr	Ala	Arg
	50					55					60				
Arg	Glu	Pro	Gly	Arg	Ala	Ala	Lys	Met	Ser	Gln	Pro	Lys	Lys	Arg	Lys
65					70				75					80	
Leu	Glu	Ser	Gly	Gly	Gly	Ala	Glu	Gly	Gly	Glu	Gly	Thr	Glu	Glu	Glu
			85					90					95		
Asp	Gly	Ala	Glu	Arg	Glu	Ala	Ala	Leu	Glu	Arg	Pro	Arg	Thr	Thr	Lys
			100					105					110		
Arg	Glu	Arg	Asp	Gln	Leu	Tyr	Tyr	Glu	Cys	Tyr	Ser	Asp	Val	Ser	Val
			115				120					125			
His	Glu	Glu	Met	Ile	Ala	Asp	Arg	Val	Arg	Thr	Asp	Ala	Tyr	Arg	Trp
			130				135				140				
Val	Ser	Leu	Arg	Asn	Trp	Ala	Ala	Leu	Arg	Gly	Lys	Thr	Val	Leu	Asp
145					150					155				160	
Val	Gly	Ala	Gly	Thr	Gly	Ile	Leu	Ser	Ile	Phe	Cys	Ala	Gln	Ala	Gly
				165					170				175		
Ala	Arg	Arg	Val	Tyr	Ala	Val	Glu	Ala	Ser	Ala	Ile	Trp	Gln	Gln	Ala
			180					185					190		

Arg

<210> 3567

<211> 2811

<212> DNA

<213> Homo sapiens

<400> 3567

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 120

ataagcaggt ggaagagatc ctccgtctgg agaaagaaat cgaggacctg cagcgcatga
180
aggagcagca ggagctgtcg ctgaccgagg ctccctgca gaagctcgag gagcgcgagg
240
accaggagct ccgaggctg gagggaggaga tttttgcacc tgaaaaaggc agccatagtt
300
ttccagaagc aactcagagg tcagattgct cggagagttt acagacaatt gctggcagag
360
aaaaggagc aagaagaaaa gaagaacag gaagaggaag aaaagaagaa acgggaggaa
420
gaagaaagag aaagagagag agagcgaaga gaagccgagc tccgccccca gcaggaaagaa
480
gaaacgagga agcagcaaga actcgaagcc ttgcagaaga gccagaagga agctgaactg
540
accgtgaac tggagaaaca gaaggaaaat aagcaggtgg aagagatcct ccgtctggag
600
aaagaaatcg aggacctgca gcgcatgaag gagcagcagg agctgtcgct gaccgaggct
660
tccttcgaca agctgcagga gcggcgggac caggagctcc gcaggctgga ggaggaaagc
720
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840
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900
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960
cactcagacc agcgaacaag tggcatccgg accagcgatg actcttcaga ggaggaccca
1020
tacatgaacg acacggtggt gccaccagc ccagtgaggc acagcacggt gctgctcgcc
1080
ccatcagtcg aggactccgg gagcctacac aactcctcca gcggcgagtc cactactgc
1140
atgccccaga acgctgggga cttgccctcc ccagacggcg actacgacta cgaccaggat
1200
gactatgagg acggtgccat cactccggcg agcagcgatg ccttctccaa ctctacggc
1260
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1320
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1380
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1440
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1500
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1560
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1620
aagaagcgct ggtttgtcct ccgccagtc aagctgatgt actttgaaaa cgacagcgag
1680
gagaagctca agggcacctg agaagtgcga acggcaaaag agatcataga taacaccacc
1740

aaggagaatg ggatcgacat cattatggcc gataggactt tccacctgat tgcagagtcc
1800
ccagaagatg ccagccagtg gtccagctg ctgagtcagg tccacgcgtc cacggaccag
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1980
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2040
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2100
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2160
aagaaaacgt ggtttgtact caccacaat tccctggatt actacaagag ttcagagaag
2220
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2280
gagaagatat tcaaagagac aggctactgg aacgtcaccg tgtacggggc caagcactgt
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2400
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				325				330						335	
Val	Gln	Glu	Val	Asp	Thr	Thr	Glu	Gln	Leu	Lys	Arg	Ile	Ser	Arg	Met

340 345 350
 Arg Leu Val His Tyr Arg Tyr Lys Pro Glu Phe Ala Ala Ser Ala Gly
 355 360 365
 Ile Glu Ala Thr Ala Pro Glu Thr Gly Val Ile Ala Gln Glu Val Lys
 370 375 380
 Glu Ile Leu Pro Glu Ala Val Lys Asp Thr Gly Asp Met Val Phe Ala
 385 390 395 400
 Asn Gly Lys Thr Ile Glu Asn Phe Leu Val Asn Lys Glu Arg Ile
 405 410 415
 Phe Met Glu Asn Val Gly Ala Val Lys Glu Leu Cys Lys Leu Thr Asp
 420 425 430
 Asn Leu Glu Thr Arg Ile Asp Glu Leu Glu Arg Trp Ser His Lys Leu
 435 440 445
 Ala Lys Leu Arg Arg Leu Asp Ser Leu Lys Ser Thr Gly Ser Ser Gly
 450 455 460
 Ala Phe Ser His Ala Gly Ser Gln Phe Ser Arg Ala Gly Ser Val Pro
 465 470 475 480
 His Lys Lys Arg Pro Pro Lys Val Ala Ser Lys Ser Ser Ser Val Val
 485 490 495
 Pro Asp Gln Ala Cys Ile Ser Gln Arg Phe Leu Gln Gly Thr Ile Ile
 500 505 510
 Ala Leu Val Val Val Met Ala Phe Ser Val Val Ser Met Ser Thr Leu
 515 520 525
 Tyr Val Leu Ser Leu Arg Thr Glu Glu Asp Leu Val Asp Thr Asp Gly
 530 535 540
 Ser Phe Ala Val Ser Thr Ser Cys Leu Leu Ala Leu Leu Arg Pro Gln
 545 550 555 560
 Pro Pro Gly Gly Ser Glu Ala Leu Cys Pro Trp Ser Ser Gln Ser Phe
 565 570 575
 Gly Thr Thr Gln Leu Arg Gln Ser Pro Leu Thr Thr Gly Leu Pro Gly
 580 585 590
 Ile Gln Pro Ser Leu Leu Leu Val Thr Thr Ser Leu Thr Ser Ser Ala
 595 600 605
 Pro Gly Ser Ala Val Arg Thr Leu Asp Met Cys Ser Ser His Pro Cys
 610 615 620
 Pro Val Ile Cys Cys Ser Ser Pro Thr Thr Asn Pro Thr Thr Gly Pro
 625 630 635 640
 Ser Leu Gly Pro Ser Phe Asn Pro Gly His Val Leu Ser Pro Ser Pro
 645 650 655
 Ser Pro Ser Thr Asn Arg Ser Gly Pro Ser Gln Met Ala Leu Leu Pro
 660 665 670
 Val Thr Asn Ile Arg Ala Lys Ser Trp Gly Leu Ser Val Asn Gly Ile
 675 680 685
 Asp His Ser Lys His His Lys Ser Leu Glu Pro Leu Ala Ser Pro Ala
 690 695 700
 Val Pro Phe Pro Gly Gly Gln Gly Lys Ala Lys Asn Ser Pro Ser Leu
 705 710 715 720
 Gly Phe His Gly Arg Ala Arg Arg Gly Ala Leu Gln Ser Ser Val Gly
 725 730 735
 Pro Ala Glu Pro Thr Trp Ala Gln Gly Gln Ser Ala Ser Leu Leu Ala
 740 745 750
 Glu Pro Val Pro Ser Leu Thr Ser Ile Gln Val Leu Glu Asn Ser Met
 755 760 765
 Ser Ile Thr Ser Gln Tyr Cys Ala Pro Gly Asp Ala Cys Arg Pro Gly

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      770              775              780
Asn Phe Thr Tyr His Ile Pro Val Ser Ser Gly Thr Pro Leu His Leu
785              790              795              800
Ser Leu Thr Leu Gln Met Asn Ser Ser Ser Pro Val Ser Val Val Leu
      805              810              815
Cys Ser Leu Arg Ser Lys Glu Glu Pro Cys Glu Glu Gly Ser Leu Pro
      820              825              830
Gln Ser Leu His Thr His Gln Asp Thr Gln Gly Thr Ser His Arg Trp
      835              840              845
Pro Ile Thr Ile Leu Ser Phe Arg Glu Phe Thr Tyr His Phe Arg Val
      850              855              860
Ala Leu Leu Gly Gln Ala Asn Cys Ser Ser Glu Ala Leu Ala Gln Pro
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Ala Thr Asp Tyr His Phe His Phe Tyr Arg Leu Cys Asp
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<210> 3571
<211> 528
<212> DNA
<213> Homo sapiens

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120
acggcgctat ccatgctgcc cttgggcatg cgggaacccg ccgtcgggg cctcgcctcc
180
tcactctcgc atctgctggt cctcgggctg tatcttgggc cacagccgga ctcacggcct
240
gcactgctgc cgacggtgag cagcgaagta gcacaggctg cgctcaggac ggctctgcca
300
cgtgctagta ggctcctttt aggggggtgt tgagctgtga ctccaaggca aggtgcaacg
360
ctgggcgcag gatacccaac cgtgctttcg cagagctggt acaacagtgt gatgcaatgc
420
ctgctgttac cagaagaggg atccaggcca cacggaaggg agtcgtgtcg tggtttaccc
480
cggggacaac agatgtggtt aatgaaacct tgacagagaa tgaaaaaa
528

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<210> 3572
<211> 110
<212> PRT
<213> Homo sapiens

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<400> 3572
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1          5          10          15
His Ala Phe Leu Phe Thr Gly Gly Val Val Ser Ala Trp Asp Gln Val
20          25          30
Ser Tyr Phe Leu Phe Val Ile Phe Thr Ala Tyr Ala Met Leu Pro Leu
35          40          45
Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His

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50	55	60
Leu Leu Val Leu Gly Leu Tyr Leu Gly Pro Gln Pro Asp Ser Arg Pro		
65	70	75
Ala Leu Leu Pro Gln Val Ser Thr Gln Val Ala Gln Ala Ala Leu Arg		80
	85	90
Thr Ala Leu Pro Arg Ala Ser Arg Leu Leu Gly Gly Cys		95
	100	105
		110

<210> 3573

<211> 1236

<212> DNA

<213> Homo sapiens

<400> 3573

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tagcccccaga ttaagggggc agtttctttc ttccggcca ccagcgggca ggatcacccc
120
ccctgcctgc tccccaaagc ccagccttca gcccccccaa tcaatccagc ccacacacac
180
agtcccatatt ttccatcca ttctgttact tgtgtgttca ataaacctgg tggacacaca
240
gcttcacata cccacacact cacagccaca aaccccagaa gtcattgcaca tgcgacgca
300
ccttgtggca catgcacaca caaccacact tgtgtgcaaa gtggcagaca caccacaca
360
tgcatagaag caagtctctg gacctcttct gcattccaca gagggggctc ccctgtgtg
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480
cggcagttcc ctccagactt cagggaccag gaagctatgc agatgggtgc taaattctgc
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720
acagtgggag acctcctagc ccaggaccaa gtcaccgagg cagaggaaat tcttcaaaat
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840
gtgacgggtt ccagcgggca gggtatccca cccctaccc gggggaatag caagccgctt
900
tctgtcttgc tggccccgga ctccggccgc ctgccatcca tccctgagaa caggaaacct
960
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1020
gccgagagaa gagtctgtct caccgccagc aaactcagca ccctgaggcg gggcccgccg
1080
ggccgggggt ggagcagggc ctggctccgc cccggggggc gggacaaggg ggctgattcc
1140
ttgctctaac cctactgcgc gagaccgag ggccaagtcc tggccccgcc ccttcgaagg
1200

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tctttgagag ttttaactctn gccccgccct cttggg
1236

<210> 3574

<211> 361

<212> PRT

<213> Homo sapiens

<400> 3574

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			20					25					30		
Ile	Asn	Pro	Ser	His	Thr	His	Ser	Pro	Ile	Phe	Ser	Ile	His	Ser	Gly
		35					40					45			
Thr	Cys	Val	Phe	Asn	Lys	Pro	Gly	Gly	His	Thr	Ala	Ser	His	Thr	His
		50				55					60				
Thr	Leu	Thr	Ala	Thr	Asn	Pro	Arg	Ser	His	Ala	His	Ala	Asp	Ala	Pro
65					70					75					80
Cys	Gly	Thr	Cys	Thr	His	Asn	His	Thr	Cys	Val	Gln	Ser	Gly	Arg	His
					85				90					95	
Thr	His	Thr	Cys	Ile	Glu	Ala	Ser	Leu	Trp	Thr	Pro	Ser	Ala	Ser	His
			100				105						110		
Arg	Gly	Gly	Ser	Pro	Ala	Val	Phe	Asp	Trp	Phe	Phe	Glu	Ala	Ala	Cys
			115				120					125			
Pro	Ala	Ser	Val	Gln	Glu	Asp	Pro	Pro	Ile	Leu	Arg	Gln	Phe	Pro	Pro
			130			135					140				
Asp	Phe	Arg	Asp	Gln	Glu	Ala	Met	Gln	Met	Val	Pro	Lys	Phe	Cys	Phe
145					150					155					160
Pro	Phe	Asp	Val	Glu	Arg	Gly	Pro	Pro	Ser	Pro	Ala	Val	Gln	His	Phe
					165				170					175	
Thr	Phe	Ala	Leu	Thr	Asp	Leu	Ala	Gly	Asn	Arg	Arg	Phe	Gly	Phe	Cys
			180					185					190		
Arg	Leu	Arg	Ala	Gly	Thr	Gln	Ser	Cys	Leu	Cys	Ile	Leu	Ser	His	Leu
			195				200					205			
Pro	Trp	Phe	Glu	Val	Phe	Tyr	Lys	Leu	Leu	Asn	Thr	Val	Gly	Asp	Leu
			210			215						220			
Leu	Ala	Gln	Asp	Gln	Val	Thr	Glu	Ala	Glu	Glu	Leu	Leu	Gln	Asn	Leu
225					230					235					240
Phe	Gln	Gln	Ser	Leu	Ser	Gly	Pro	Gln	Ala	Ser	Val	Gly	Leu	Glu	Leu
					245				250					255	
Gly	Ser	Gly	Val	Thr	Val	Ser	Ser	Gly	Gln	Gly	Ile	Pro	Pro	Pro	Thr
			260					265					270		
Arg	Gly	Asn	Ser	Lys	Pro	Leu	Ser	Cys	Phe	Val	Ala	Pro	Asp	Ser	Gly
		275					280						285		
Arg	Leu	Pro	Ser	Ile	Pro	Glu	Asn	Arg	Asn	Leu	Thr	Glu	Leu	Val	Val
		290				295						300			
Ala	Val	Thr	Asp	Glu	Asn	Ile	Val	Gly	Leu	Phe	Ala	Ala	Leu	Leu	Ala
305					310					315					320
Glu	Arg	Arg	Val	Leu	Leu	Thr	Ala	Ser	Lys	Leu	Ser	Thr	Leu	Arg	Arg
					325				330					335	
Gly	Pro	Pro	Gly	Arg	Gly	Gly	Ser	Arg	Ala	Trp	Leu	Arg	Pro	Gly	Gly
			340					345					350		
Arg	Asp	Lys	Gly	Ala	Asp	Ser	Leu	Leu							

355

360

<210> 3575
 <211> 769
 <212> DNA
 <213> Homo sapiens

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 120
 cagtcaaagg tgctggagtt gtgtctgtat agaagtaagt cgtcccacca acagtttcct
 180
 ttggatcac ctgaccagaa gacggagtct gagaaacagg attattaaca gatgtagagg
 240
 cactagaagg caccatgtaa ctgtctggat ttggagtgtg actttctctt ctgggagcag
 300
 gagaagtatg tggagtaatc ttgggggaat gaagagggga agaccacgca gacaacgaca
 360
 ttcttgaaga ggaatgtaaa atgtttctta atggagcaat aattgggttt agagaacaa
 420
 tctggaaaat aaaatgcaaa cattcatttg gaagaaacat catctttggg atcgtaagt
 480
 caaagatgaa ggaataatt ttatcttgtt ttgttgtaga aaaagctctg attaaagcaa
 540
 atgtaaagtt tcttttttca aatgtactta tttccaaata tggtagcaga tttactgcaa
 600
 gaatagtctc ctccatcatca aggtttacat caggaaatatt aatgcaaga gtgacaaaa
 660
 atttaataaa ttaatggaag agtgggaagt aacagaattg tggctcttta taaaattatg
 720
 ccttttataa aagtttttct tttataaaa gcataattcc tttttttt
 769

<210> 3576
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 3576
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 Ser Thr Phe Glu Lys Arg Asn Phe Thr Phe Ala Leu Ile Arg Ala Phe
 20 25 30
 Ser Thr Thr Lys Gln Asp Lys Ile Ile Ser Phe Ile Phe Ala Leu Thr
 35 40 45
 Ile Pro Lys Met Met Phe Leu Pro Asn Glu Cys Leu His Phe Ile Phe
 50 55 60
 Gln Thr Cys Ser Leu Lys Pro Ile Ile Ala Pro Leu Arg Asn Ile Phe
 65 70 75 80
 Thr Ser Ser Ser Gly Met Ser Leu Ser Ala Gly Ser Ser Pro Leu His
 85 90 95
 Ser Pro Lys Ile Thr Pro His Thr Ser Pro Ala Pro Arg Arg Arg Ser

100										105					110						
His	Thr	Pro	Asn	Pro	Ala	Ser	Tyr	Met	Val	Pro	Ser	Ser	Ala	Ser	Thr						
115										120					125						
Ser	Val	Asn	Asn	Pro	Val	Ser	Gln	Thr	Pro	Ser	Ser	Gly	Gln	Val	Ile						
130										135					140						
Gln	Lys	Glu	Thr	Val	Gly	Gly	Thr	Thr	Tyr	Phe	Tyr	Thr	Asp	Thr	Thr						
145										150					155						
Pro	Ala	Pro	Leu	Thr	Gly	Met	Val	Phe	Pro	Asn	Tyr	His	Ile	Tyr	Pro						
165										170					175						
Pro	Thr	Ala	Pro	His	Val	Ala	Tyr	Met	Gln	Pro	Lys	Ala	Asn	Ala	Pro						
180										185					190						
Ser	Phe	Phe	Met	Ala	Asp	Glu	Leu	Arg	Gln	Glu	Leu	Ile									
195										200					205						

<210> 3577

<211> 1225

<212> DNA

<213> Homo sapiens

<400> 3577

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120	gtgattgggg	agagcatgta	cggggacttt	gaggaagctt	ttgaccatct
180	ctgactcgcca	ccaagaaccc	agaagaaatc	agaggcgggg	gactttctca
240	cttcttgtgc	gggacttcag	gcccacagac	caggaagaaa	tcaaaactct
300	atgtgtccca	ggttcttcat	cgacttcccg	gacatccttg	aacagcagag
360	acttaccttc	aaaaccactt	cgtgaagaa	gagagaagca	agtacgacta
420	cttcgcaggg	tggtgaacga	gagcaccctg	tgtctcatgg	ggcatgaacg
480	ctgaacctca	tctccctcct	ggccttgctg	gtgctggggc	gaacaaaaca
540	gtgccaccaa	ggtcacctgt	tactaccagc	ggtcacctta	gtcagtgatg
600	caactactac	gttgcccata	ctccagtcac	ctacagccag	ccttacccta
660	ctgtaactaa	ccttgagacc	tgaggggttc	cacagtggga	accccaatat
720	ctcaggttag	ggagctctct	ctagatgtag	gcatttgact	tttaaagggg
780	tgattctgct	tttttttttt	tttttctctt	gtgtacccat	tggaatgggt
840	tcatgagcca	accctcaaag	gacctgtatt	acagtgccac	gttggaatac
900	gcatgacctc	tccacatctt	tccaagatag	acactaacat	gtcatgtccc
960	acgtgggggt	tgagctctgt	gcagtaatcg	agattggggg	aatttgggca
1020					gcgcgtgaga

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 1225

<210> 3578
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 3578
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 Ile Ile Leu Asp Ser Leu Leu Phe Phe Tyr Asp Cys Ser Asn Asn Pro
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 Ile Ser Glu His Phe His Pro Thr Val Ile Gly Glu Ser Met Tyr Gly
 35 40 45
 Asp Phe Glu Glu Ala Phe Asp His Leu Gln Asn Arg Leu Ile Ala Thr
 50 55 60
 Lys Asn Pro Glu Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Ser Asn
 65 70 75 80
 Leu Leu Val Arg Asp Phe Arg Pro Thr Asp Gln Glu Glu Ile Lys Thr
 85 90 95
 Leu Glu Arg Tyr Met Cys Ser Arg Phe Phe Ile Asp Phe Pro Asp Ile
 100 105 110
 Leu Glu Gln Gln Arg Lys Leu Glu Thr Tyr Leu Gln Asn His Phe Ala
 115 120 125
 Glu Glu Glu Arg Ser Lys Tyr Asp Tyr Leu Met Ile Leu Arg Arg Val
 130 135 140
 Val Asn Glu Ser Thr Val Cys Leu Met Gly His Glu Arg Arg Gln Thr
 145 150 155 160
 Leu Asn Leu Ile Ser Leu Leu Ala Leu Arg Val Leu Gly Gly Thr Lys
 165 170 175
 His His Pro Pro Val Pro Pro Arg Ser Pro Val Thr Thr Ser Gly Pro
 180 185 190
 Leu Ser Gln
 195

<210> 3579
 <211> 755
 <212> DNA
 <213> Homo sapiens

<400> 3579
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 120
 cagatactcc agccaccgcg aaggttccag gaaaggacaa tgcctgcga gaaaatcagg
 180

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 240
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 300
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 360
 aacatctttt cctttgctct atgggaacat tttagggttt gttttgcaca gctggtttcc
 420
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 660
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<210> 3580

<211> 121

<212> PRT

<213> Homo sapiens

<400> 3580

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			20					25					30		
Glu	Thr	Lys	Gln	His	Glu	Lys	Trp	Leu	Ser	Gln	Pro	Thr	Cys	Ser	Asp
		35					40				45				
Met	Pro	Arg	Asn	Phe	Ser	Ser	Gly	Pro	Gly	Ser	Gly	Gly	Leu	Leu	Ile
		50				55					60				
Phe	Ser	Gln	Asp	Ile	Val	Leu	Ser	Trp	Asn	Leu	Ala	Gly	Gly	Trp	Ser
			70						75					80	
Ile	Cys	Ile	Trp	Ser	Ile	Ala	Arg	Leu	Ser	His	Leu	Ser	Ser	Asp	Gln
			85					90						95	
Lys	Cys	Ile	Ser	Lys	Ile	Ile	Thr	Ser	Thr	Lys	Thr	Ile	Ile	Asp	Cys
			100					105					110		
Glu	Gln	Thr	Phe	Ser	Val	Thr	Ser	Arg							
		115						120							

<210> 3581

<211> 2132

<212> DNA

<213> Homo sapiens

<400> 3581

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1740

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<210> 3582

<211> 138

<212> PRT

<213> Homo sapiens

<400> 3582

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 Ser Arg Pro Arg Pro Ser Thr Thr Ala Thr Ser Arg Cys Ser Ser Ala
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 Arg Trp Arg Arg Arg Thr Arg Gly Cys Thr Pro Ala Thr Cys Thr Ile
 85 90 95
 Thr Thr Ala Thr Ser Thr Arg Ala Trp Pro Ser Ala Trp Arg Ser Pro
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<210> 3583

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 3583

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<210> 3584

<211> 356

<212> PRT

<213> Homo sapiens

<400> 3584

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Ala Arg Glu Arg Lys Arg Lys Lys Arg Arg Ile Met Lys Ala Pro Ala
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Ala Glu Ala Val Ala Glu Gly Ala Ser Gly Arg His Gly Gln Gly Arg
   85                90                95
Ser Leu Glu Ala Glu Asp Lys Met Thr His Arg Ile Leu Arg Ala Ala
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Gln Glu Gly Asp Leu Pro Glu Leu Arg Arg Leu Leu Glu Pro His Glu
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Thr Pro Leu Met Cys Ala Ala Arg Ala Gly Gln Gly Ala Ala Val Ser
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Tyr Leu Leu Gly Arg Gly Ala Ala Trp Val Gly Val Cys Glu Leu Ser
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Gly Arg Asp Ala Ala Gln Leu Ala Glu Glu Ala Gly Phe Pro Glu Val
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Arg Ser Pro Thr Pro Ser Leu Gln Tyr Cys Glu Asn Cys Asp Thr His
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Phe Gln Asp Ser Asn His Arg Thr Ser Thr Ala His Leu Leu Ser Leu
   225                230                235                240
Ser Gln Gly Pro Gln Pro Pro Asn Leu Pro Leu Gly Val Pro Ile Ser
   245                250                255
Ser Pro Gly Phe Lys Leu Leu Leu Arg Gly Gly Trp Glu Pro Gly Met
   260                265                270
Gly Leu Gly Pro Arg Gly Glu Gly Arg Ala Asn Pro Ile Pro Thr Val
   275                280                285
Leu Lys Arg Asp Gln Glu Gly Leu Gly Tyr Arg Ser Ala Pro Gln Pro
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Arg Val Thr His Phe Pro Ala Trp Asp Thr Arg Ala Val Ala Gly Arg
   305                310                315                320
Glu Arg Pro Pro Arg Val Ala Thr Leu Ser Trp Arg Glu Glu Arg Arg
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<210> 3585

<211> 2782

<212> DNA

<213> Homo sapiens

<400> 3585

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<210> 3586

<211> 663

<212> PRT

<213> Homo sapiens

<400> 3586

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			20					25					30	
Arg	Ser	Cys	Trp	Arg	Lys	Trp	Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg
		35					40				45			
Met	Ile	Leu	Phe	Leu	Leu	Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Phe
	50					55				60				
Tyr	Ile	Asn	Leu	Ala	Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu
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														Asn

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  545              550              555
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Asp Arg Lys Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser
      580              585              590
Arg Phe Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val
      595              600              605
Gln Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe
      610              615              620
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp Pro
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<210> 3587

<211> 3148

<212> DNA

<213> Homo sapiens

<400> 3587

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<210> 3588

<211> 499

<212> PRT

<213> Homo sapiens

<400> 3588

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 Glu Asp Val Gln Glu Glu Thr Gln Leu Asp Leu Ser Gly Asp Ser Val
 35 40 45
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 50 55 60
 Met Lys Ile Glu Glu Tyr Ile Ser Lys Gln Ala Lys Ala Ser Glu Val
 65 70 75 80
 Met Gly Pro Val Glu Ala Ala Pro Glu Tyr Arg Val Ile Val Asp Ala
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 Asn Asn Leu Thr Val Glu Ile Glu Asn Glu Leu Asn Ile Ile His Lys
 100 105 110
 Phe Ile Arg Asp Lys Tyr Ser Lys Arg Phe Pro Glu Leu Glu Ser Leu
 115 120 125
 Val Pro Asn Ala Leu Asp Tyr Ile Arg Thr Val Lys Glu Leu Gly Asn
 130 135 140
 Ser Leu Asp Lys Cys Lys Asn Asn Glu Asn Leu Gln Gln Ile Leu Thr
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 Asn Ala Thr Ile Met Val Val Ser Val Thr Ala Ser Thr Thr Gln Gly
 165 170 175
 Gln Gln Leu Ser Glu Glu Glu Leu Glu Arg Leu Glu Glu Ala Cys Asp

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Glu Ser Arg Met Ser Phe Ile Ala Pro Asn Leu Ser Ile Ile Ile Gly
210              215              220
Ala Ser Thr Ala Ala Lys Ile Met Gly Val Ala Gly Gly Leu Thr Asn
225              230              235
Leu Ser Lys Met Pro Ala Cys Asn Ile Met Leu Leu Gly Ala Gln Arg
245              250              255
Lys Thr Leu Ser Gly Phe Ser Ser Thr Ser Val Leu Pro His Thr Gly
260              265              270
Tyr Ile Tyr His Ser Asp Ile Val Gln Ser Leu Pro Pro Asp Leu Arg
275              280              285
Arg Lys Ala Ala Arg Leu Val Ala Ala Lys Cys Thr Leu Ala Ala Arg
290              295              300
Val Asp Ser Phe His Glu Ser Thr Glu Gly Lys Val Gly Tyr Glu Leu
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Lys Asp Glu Ile Glu Arg Lys Phe Asp Lys Trp Gln Glu Pro Pro Pro
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Val Lys Gln Val Lys Pro Leu Pro Ala Pro Leu Asp Gly Gln Arg Lys
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Lys Arg Gly Gly Arg Arg Tyr Arg Lys Met Lys Glu Arg Leu Gly Leu
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Thr Glu Ile Arg Lys Gln Ala Asn Arg Met Ser Phe Gly Glu Ile Glu
370              375              380
Glu Asp Ala Tyr Gln Glu Asp Leu Gly Phe Ser Leu Gly His Leu Gly
385              390              395
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Lys Ala Arg Ile Ser Lys Thr Leu Gln Arg Thr Leu Gln Lys Gln Ser
420              425              430
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435              440              445
Ala Ser Ser Val Ala Phe Thr Pro Leu Gln Gly Leu Glu Ile Val Asn
450              455              460
Pro Gln Ala Ala Glu Lys Lys Val Ala Glu Ala Asn Gln Lys Tyr Phe
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<210> 3589

<211> 675

<212> DNA

<213> Homo sapiens

<400> 3589

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180

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<210> 3590

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3590

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Asp Pro Met Ser Pro Phe His Leu Ser Ser Val Ile Leu Cys Arg Pro
      35             40             45
Ser Ala Trp Pro Cys Leu Arg Ser Ser Ser Pro Pro Ala Ala Gln Gly
      50             55             60
Ser Phe Val Ser Ala Gln Glu Gly Pro Tyr Asn Pro Ser Trp Leu Trp
      65             70             75             80
Pro Gly Pro Cys Phe Val Ser Glu Leu Gly Gly Pro Ile Pro Lys His
      85             90             95
Trp Leu Gly Asn Ser Tyr Pro Ile Cys Cys Leu Gly Ser Ala Trp Phe
      100            105            110
Phe Thr His Ile Ser
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<210> 3591

<211> 669

<212> DNA

<213> Homo sapiens

<400> 3591

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120
cgatggtctt catcaggggt gattcctaata gaaaaaatac gaaatattgg aatctcagct
180

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 gcaaagatgc atgaggtgaa aggtaaagat ggagttggtg ctgtcatgga ttccatggaa
 300
 ctagagagac aaagaggaat cactattcag tcagcagcca cttacaccat gtggaaagat
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 480
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 669

<210> 3592

<211> 223

<212> PRT

<213> Homo sapiens

<400> 3592

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		20						25					30		
Lys	Gln	Val	Asn	Trp	Lys	Ala	Cys	Arg	Trp	Ser	Ser	Ser	Gly	Val	Ile
		35					40					45			
Pro	Asn	Glu	Lys	Ile	Arg	Asn	Ile	Gly	Ile	Ser	Ala	His	Ile	Asp	Ser
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Gly	Lys	Thr	Thr	Leu	Thr	Glu	Arg	Val	Leu	Tyr	Tyr	Thr	Gly	Arg	Ile
	65				70					75				80	
Ala	Lys	Met	His	Glu	Val	Lys	Gly	Lys	Asp	Gly	Val	Gly	Ala	Val	Met
			85					90						95	
Asp	Ser	Met	Glu	Leu	Glu	Arg	Gln	Arg	Gly	Ile	Thr	Ile	Gln	Ser	Ala
			100					105					110		
Ala	Thr	Tyr	Thr	Met	Trp	Lys	Asp	Val	Asn	Ile	Asn	Ile	Ile	Asp	Thr
		115				120						125			
Pro	Gly	His	Val	Asp	Phe	Thr	Ile	Glu	Val	Glu	Arg	Ala	Leu	Arg	Val
		130				135						140			
Leu	Asp	Gly	Ala	Val	Leu	Val	Leu	Cys	Ala	Val	Gly	Gly	Val	Gln	Cys
	145				150					155				160	
Gln	Thr	Met	Thr	Val	Asn	Arg	Gln	Met	Lys	Arg	Tyr	Asn	Val	Pro	Phe
			165						170					175	
Leu	Thr	Phe	Ile	Asn	Lys	Leu	Asp	Arg	Met	Gly	Ser	Asn	Pro	Ala	Arg
		180						185					190		
Ala	Leu	Gln	Gln	Met	Arg	Ser	Lys	Leu	Asn	His	Asn	Ala	Ala	Phe	Met
		195					200					205			
Gln	Ile	Pro	Met	Gly	Leu	Glu	Gly	Asn	Phe	Lys	Gly	Ile	Val	Asp	
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<210> 3593
 <211> 1005
 <212> DNA
 <213> Homo sapiens

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 180
 gtagtctcca agccgttgac cccattgcag gaagagatgg cgtctctact gcagcagatt
 240
 gagatagaga gaagcctgta ttcagaccac gagcttcgtg ctctggatga aaaccacgga
 300
 ctgggaaaga agaaagctga ccttcattgat gaagaagatg aacaggatat attgctggcg
 360
 caagatttgg aagatatgtg ggagcagaaa tttctacagt tcaaacttgg agctcgcata
 420
 acagaagctg atgaaaagaa tgaccgaaca tccctgaaca ggaagctaga caggaaacctt
 480
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 540
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 aacaacatg agccaagt cctaggaat gcacctgtg ggcactacac attcaagttc
 660
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 720
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 780
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 840
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 1005

<210> 3594
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 3594
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 20 25 30
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 35 40 45
 Arg Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys

50		55		60											
Pro	Leu	Thr	Pro	Leu	Gln	Glu	Met	Ala	Ser	Leu	Leu	Gln	Gln	Ile	
65				70					75					80	
Glu	Ile	Glu	Arg	Ser	Leu	Tyr	Ser	Asp	His	Glu	Leu	Arg	Ala	Leu	Asp
			85						90					95	
Glu	Asn	Gln	Arg	Leu	Ala	Lys	Lys	Lys	Ala	Asp	Leu	His	Asp	Glu	Glu
			100						105					110	
Asp	Glu	Gln	Asp	Ile	Leu	Leu	Ala	Gln	Asp	Leu	Glu	Asp	Met	Trp	Glu
			115						120					125	
Gln	Lys	Phe	Leu	Gln	Phe	Lys	Leu	Gly	Ala	Arg	Ile	Thr	Glu	Ala	Asp
			130						135					140	
Glu	Lys	Asn	Asp	Arg	Thr	Ser	Leu	Asn	Arg	Lys	Leu	Asp	Arg	Asn	Leu
			145						150					155	
Val	Leu	Leu	Val	Arg	Glu	Lys	Phe	Gly	Asp	Gln	Asp	Val	Trp	Ile	Leu
			165						170					175	
Pro	Gln	Ala	Glu	Trp	Gln	Pro	Gly	Glu	Thr	Leu	Arg	Gly	Thr	Ala	Glu
			180						185					190	
Arg	Thr	Leu	Ala	Thr	Leu	Ser	Glu	Asn	Asn	Met	Glu	Ala	Lys	Phe	Leu
			195						200					205	
Gly	Asn	Ala	Pro	Cys	Gly	His	Tyr	Thr	Phe	Lys	Phe	Pro	Gln	Ala	Met
			210						215					220	
Arg	Thr	Glu	Ser	Asn	Leu	Gly	Ala	Lys	Val	Phe	Phe	Phe	Lys	Ala	Leu
			225						230					235	
Leu	Leu	Thr	Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val
			245						250					255	
Trp	Val	Thr	Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu
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<210> 3595

<211> 1903

<212> DNA

<213> Homo sapiens

<400> 3595

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 180
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 540

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660
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720
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780
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1320
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1680
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1740
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1800
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accagacaaa taaatattag agacaaccac catcaaaaaa aaa
1903

<210> 3596

<211> 496

<212> PRT

<213> Homo sapiens

<400> 3596

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Gln Met Leu Leu Ala Gln Tyr Ile Glu Ser Phe Thr Gln Gly Ser Ile Glu			
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Ala His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys Gly Pro Ile			
	50	55	60
Val Glu Ser Tyr Ile Gly Phe Ile Glu Ser Tyr Arg Asp Pro Phe Gly			
	65	70	75
Ser Arg Gly Glu Phe Glu Gly Phe Val Ala Val Val Asn Lys Ala Met			
	85	90	95
Ser Ala Lys Phe Glu Arg Leu Val Ala Ser Ala Glu Gln Leu Leu Lys			
	100	105	110
Glu Leu Pro Trp Pro Pro Thr Phe Glu Lys Asp Lys Phe Leu Thr Pro			
	115	120	125
Asp Phe Thr Ser Leu Asp Val Leu Thr Phe Ala Gly Ser Gly Ile Pro			
	130	135	140
Ala Gly Ile Asn Ile Pro Asn Tyr Asp Asp Leu Arg Gln Thr Glu Gly			
	145	150	155
Phe Lys Asn Val Ser Leu Gly Asn Val Leu Ala Val Ala Tyr Ala Thr			
	165	170	175
Gln Arg Glu Lys Leu Thr Phe Leu Glu Glu Asp Asp Lys Asp Leu Tyr			
	180	185	190
Ile Leu Trp Lys Gly Pro Ser Phe Asp Val Gln Val Gly Leu His Glu			
	195	200	205
Leu Leu Gly His Gly Ser Gly Lys Leu Phe Val Gln Asp Glu Lys Gly			
	210	215	220
Ala Phe Asn Phe Asp Gln Glu Thr Val Ile Asn Pro Glu Thr Gly Glu			
	225	230	235
Gln Ile Gln Ser Trp Tyr Arg Ser Gly Glu Thr Trp Asp Ser Lys Phe			
	245	250	255
Ser Thr Ile Ala Ser Ser Tyr Glu Glu Cys Arg Ala Glu Ser Val Gly			
	260	265	270
Leu Tyr Leu Cys Leu His Pro Gln Val Leu Glu Ile Phe Gly Phe Glu			
	275	280	285
Gly Ala Asp Ala Glu Asp Val Ile Tyr Val Asn Trp Leu Asn Met Val			
	290	295	300
Arg Ala Gly Leu Leu Ala Leu Glu Phe Tyr Thr Pro Glu Ala Phe Asn			
	305	310	315
Trp Arg Gln Ala His Met Gln Ala Arg Phe Val Ile Leu Arg Val Leu			
	325	330	335
Leu Glu Ala Gly Glu Gly Leu Val Thr Ile Thr Pro Thr Thr Gly Ser			
	340	345	350
Asp Gly Arg Pro Asp Ala Arg Val Arg Leu Asp Arg Ser Lys Ile Arg			
	355	360	365
Ser Val Gly Lys Pro Ala Leu Glu Arg Phe Leu Arg Arg Leu Gln Val			
	370	375	380
Leu Lys Ser Thr Gly Asp Val Ala Gly Gly Arg Ala Leu Tyr Glu Gly			
	385	390	395
Tyr Ala Thr Val Thr Asp Ala Pro Pro Glu Cys Phe Leu Thr Leu Arg			
	405	410	415
Asp Thr Val Leu Leu Arg Lys Glu Ser Arg Lys Leu Ile Val Gln Pro			
	420	425	430
Asn Thr Arg Leu Glu Gly Asn Gly Ser Asp Val Gln Leu Leu Glu Tyr			

	435		440		445	
Glu	Ala	Ser	Ala	Ala	Gly	Leu
	450		455		460	
Glu	Asp	Gly	Pro	Glu	Leu	Glu
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Asp	Ala	Arg	Phe	Trp	Lys	Gly
	485		490		495	

<210> 3597

<211> 1090

<212> DNA

<213> Homo sapiens

<400> 3597

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120
gaaaatgggtg ttctgctgtg tgatttgatt aataagctta aacctggcgt cattaagaag
180
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240
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420
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660
gaaggttttg aaagtgcac agattcgga ttacattca agatgcagga ttataataaa
720
gatgatattg cgtatcgaag gatttcgggt gttgagccaa agactgcgtt acccttcaat
780
cgttttttac ccaacaaaag tagacagcca tcctatgtac cagcacctct gagaaagaaa
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1090

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<210> 3598

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 3598
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 35 40 45
 Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg
 50 55 60
 Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys
 65 70 75 80
 His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala
 85 90 95
 Asp Gly Thr Phe Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu
 100 105 110
 Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
 115 120 125
 Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
 130 135 140
 Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
 145 150 155

<210> 3599
 <211> 691
 <212> DNA
 <213> Homo sapiens

<400> 3599
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 180
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 420
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 480
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 540
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 600
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691

<210> 3600

<211> 98

<212> PRT

<213> Homo sapiens

<400> 3600

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             20             25             30
Met Val Glu Val Arg Ser Trp Ser Gly Ser Leu Val Gly Trp Leu Ala
             35             40             45
Pro Arg Pro Leu Ser Val Pro Ile Glu His Leu Leu Gly Ala Lys Asn
             50             55             60
Cys Cys Arg His Gly Gly Gln Trp Val Arg Arg Ala Val Pro Ala Val
65             70             75             80
Leu Ser Leu Val Gly Ala Ser Ser Leu His His Ala Val Tyr Leu Phe
             85             90             95
Leu Leu
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<210> 3601

<211> 2963

<212> DNA

<213> Homo sapiens

<400> 3601

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120
tgtccaagga catttggtc gcaggcacag agctgattaa ctctgttatgt atcttttgat
180
aataaggcag cgatcattaa gaaaaacgtg tagccaatga aataacatgt tctgggcccc
240
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300
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420
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600
cacagccggt actgtcccc gtgggacccc agcctggagc ccccatcctt ttggtcctg
660
cctgtggcca ctacagctctc aggtggccac atgcacatcc cctgtcctt cctgggcac
720
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1320
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<210> 3602

<211> 299

<212> PRT

<213> Homo sapiens

<400> 3602

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 Glu Ala Arg Glu Leu Met Tyr Ser Gly Ala Leu Leu Phe Phe Ser His
 35 40 45
 Gly Gln Gln Asn Ser Ala Ala Asp Leu Ser Met Leu Val Leu Glu Ser
 50 55 60
 Leu Glu Lys Ala Glu Val Glu Val Ala Asp Glu Leu Leu Glu Asn Leu
 65 70 75 80
 Ala Lys Val Phe Ser Leu Met Asp Pro Asn Ser Pro Glu Arg Val Thr
 85 90 95
 Phe Val Ser Arg Ala Leu Lys Trp Ser Ser Gly Gly Ser Gly Lys Leu
 100 105 110
 Gly His Pro Arg Leu His Gln Leu Leu Ala Leu Thr Leu Trp Lys Glu
 115 120 125
 Gln Asn Tyr Cys Glu Ser Arg Tyr His Phe Leu His Ser Ala Asp Gly
 130 135 140
 Glu Gly Cys Ala Asn Met Leu Val Glu Tyr Ser Thr Ser Arg Gly Phe
 145 150 155 160
 Arg Ser Glu Val Asp Met Phe Val Ala Gln Ala Val Leu Gln Phe Leu
 165 170 175
 Cys Leu Lys Asn Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr Thr
 180 185 190
 Gln Lys His Pro Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro Leu

195	200	205
Leu Asn Phe Ile Trp Phe Leu Leu Ala Val Asp Gly Gly Lys Leu		
210	215	220
Thr Val Phe Thr Val Leu Cys Glu Gln Tyr Gln Pro Ser Leu Arg Arg		
225	230	235
Asp Pro Met Tyr Asn Glu Tyr Leu Asp Arg Ile Gly Gln Leu Phe Phe		
	245	250
Gly Val Pro Pro Lys Gln Thr Ser Ser Tyr Gly Gly Leu Leu Gly Asn		
	260	265
Leu Leu Thr Ser Leu Met Gly Ser Ser Glu Gln Glu Asp Gly Glu Glu		
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<210> 3603

<211> 1082

<212> DNA

<213> Homo sapiens

<400> 3603

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1020

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 1082

<210> 3604

<211> 146

<212> PRT

<213> Homo sapiens

<400> 3604

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 20 25 30
 Val Ala Ala Gln Glu Glu Pro Asp Lys Glu Gly Lys Glu Lys Pro His
 35 40 45
 Ala Gly Val Ser Pro Arg Gly Val Lys Arg Gln Arg Arg Ser Ser Ser
 50 55 60
 Gly Gly Ser Gln Glu Lys Arg Gly Arg Pro Ser Gln Glu Pro Pro Leu
 65 70 75 80
 Ala Pro Pro His Arg Arg Arg Arg Ser Arg Gln His Pro Gly Pro Leu
 85 90 95
 Pro Pro Thr Asn Ala Ala Pro Thr Val Pro Gly Pro Val Glu Pro Leu
 100 105 110
 Leu Leu Pro Pro Pro Pro Pro Ser Leu Ala Pro Ala Gly Pro Ala
 115 120 125
 Val Ala Ala Pro Leu Pro Ala Pro Ser Thr Arg Pro Ser Ser Pro Ser
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 Arg Leu
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<210> 3605

<211> 2004

<212> DNA

<213> Homo sapiens

<400> 3605

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<210> 3606

<211> 324

<212> PRT

<213> Homo sapiens

<400> 3606

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      20           25           30
Lys Gly Asp Tyr Tyr Glu Ala His Gln Met Tyr Arg Thr Leu Phe Phe
      35           40           45
Arg Tyr Met Ser Gln Ser Lys His Thr Glu Ala Arg Glu Leu Met Tyr
      50           55           60
Ser Gly Ala Leu Leu Phe Phe Ser His Gly Gln Gln Asn Ser Ala Ala
      65           70           75           80
Asp Leu Ser Met Leu Val Leu Glu Ser Leu Glu Lys Ala Glu Val Glu
      85           90           95
Val Ala Asp Glu Leu Leu Glu Asn Leu Ala Lys Val Phe Ser Leu Met
      100          105          110
Asp Pro Asn Ser Pro Glu Arg Val Thr Phe Val Ser Arg Ala Leu Lys
      115          120          125
Trp Ser Ser Gly Gly Ser Gly Lys Leu Gly His Pro Arg Leu His Gln
      130          135          140
Leu Leu Ala Leu Thr Leu Trp Lys Glu Gln Asn Tyr Cys Glu Ser Arg
      145          150          155          160
Tyr His Phe Leu His Ser Ala Asp Gly Glu Gly Cys Ala Asn Met Leu
      165          170          175
Val Glu Tyr Ser Thr Ser Arg Gly Phe Arg Ser Glu Val Asp Met Phe
      180          185          190
Val Ala Gln Ala Val Leu Gln Phe Leu Cys Leu Lys Asn Lys Ser Ser
      195          200          205
Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro Ser Ile Glu
      210          215          220
Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile Trp Phe Leu
      225          230          235          240
Leu Leu Ala Val Asp Gly Gly Lys Leu Thr Val Phe Thr Val Leu Cys
      245          250          255
Glu Gln Tyr Gln Pro Ser Leu Arg Arg Asp Pro Met Tyr Asn Glu Tyr
      260          265          270
Leu Asp Arg Ile Gly Gln Leu Phe Phe Gly Val Pro Pro Lys Gln Thr
      275          280          285
Ser Ser Tyr Gly Gly Leu Leu Gly Asn Leu Leu Thr Ser Leu Met Gly
      290          295          300
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<210> 3607

<211> 1726

<212> DNA

<213> Homo sapiens

<400> 3607

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360
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420
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1620

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<210> 3608

<211> 436

<212> PRT

<213> Homo sapiens

<400> 3608

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Glu	Val	Lys	Trp	Ser	Val	Arg	Met	Thr	Leu	Cys	Ala	Gly	Ile	Cys	Ser
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Tyr	Glu	Gly	Lys	Gly	Gly	Met	Cys	Ser	Ile	Arg	Leu	Ser	Glu	Pro	Leu
	50					55					60				
Leu	Lys	Leu	Arg	Pro	Arg	Lys	Asp	Leu	Val	Glu	Thr	Leu	Leu	His	Glu
65					70					75					
Met	Ile	His	Ala	Tyr	Leu	Phe	Val	Thr	Asn	Asn	Asp	Lys	Asp	Arg	Glu
			85						90					95	
Gly	His	Gly	Pro	Glu	Phe	Cys	Lys	His	Met	His	Arg	Ile	Asn	Ser	Leu
			100					105					110		
Thr	Gly	Ala	Asn	Ile	Thr	Val	Tyr	His	Thr	Phe	His	Asp	Glu	Val	Asp
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Glu	Tyr	Arg	Arg	His	Trp	Trp	Arg	Cys	Asn	Gly	Pro	Cys	Gln	His	Arg
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Pro	Pro	Tyr	Tyr	Gly	Tyr	Val	Lys	Arg	Ala	Thr	Asn	Arg	Glu	Pro	Ser
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Tyr	Ile	Lys	Ile	Lys	Glu	Pro	Glu	Asn	Tyr	Ser	Lys	Lys	Gly	Lys	Gly
		180					185						190		
Lys	Ala	Lys	Leu	Gly	Lys	Glu	Pro	Val	Leu	Ala	Ala	Glu	Asn	Lys	Asp
		195					200					205			
Lys	Pro	Asn	Arg	Gly	Glu	Ala	Gln	Leu	Val	Ile	Pro	Phe	Ser	Gly	Lys
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225					230					235				240	
Ile	Thr	Ser	His	Ala	Ile	Asn	Lys	Thr	Gln	Asp	Leu	Leu	Asn	Gln	Asn
			245						250					255	
His	Ser	Ala	Asn	Ala	Val	Arg	Pro	Asn	Ser	Lys	Ile	Lys	Val	Lys	Phe
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Glu	Gln	Asn	Gly	Ser	Ser	Lys	Asn	Ser	His	Leu	Val	Ser	Pro	Ala	Val
		275					280					285			
Ser	Asn	Ser	His	Gln	Asn	Val	Leu	Ser	Asn	Tyr	Phe	Pro	Arg	Val	Ser
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Phe	Ala	Asn	Gln	Lys	Ala	Phe	Arg	Gly	Val	Asn	Gly	Ser	Pro	Arg	Ile
305					310					315					320
Ser	Val	Thr	Val	Gly	Asn	Ile	Pro	Lys	Asn	Ser	Val	Ser	Ser	Ser	Ser
				325					330					335	
Gln	Arg	Arg	Val	Ser	Ser	Ser	Lys	Ile	Ser	Leu	Arg	Asn	Ser	Ser	Lys

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Val	Thr	Glu	Ser	Ala	Ser	Val	Met	Pro	Ser	Gln	Asp	Val	Ser	Gly	Ser		
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Glu	Asp	Thr	Phe	Pro	Asn	Lys	Arg	Pro	Arg	Leu	Glu	Asp	Lys	Thr	Val		
370						375						380					
Phe	Asp	Asn	Phe	Phe	Ile	Lys	Lys	Glu	Gln	Ile	Lys	Ser	Ser	Gly	Asn		
385						390						395					
Asp	Pro	Lys	Tyr	Ser	Thr	Thr	Ala	Gln	Asn	Ser	Ser	Ser	Ser	Ser	Ser		
405						410						415					
Ser	Gln	Ser	Lys	Met	Val	Asn	Cys	Pro	Val	Cys	Gln	Asn	Glu	Val	Leu		
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Gly	Val	Ser	Asp														
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<210> 3609

<211> 1286

<212> DNA

<213> Homo sapiens

<400> 3609

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<210> 3610

<211> 268

<212> PRT

<213> Homo sapiens

<400> 3610

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 35 40 45
 Arg Asp Tyr Phe Leu Lys Phe Ala Tyr Ile Val Asp Leu Asp Ser Asp
 50 55 60
 Thr Ala Asp Lys Phe Leu Gln Leu Xaa Trp Asn Gln Arg Cys Gln Glu
 65 70 75 80
 Gly Ala Val Ser Tyr Gln Xaa Tyr Pro Leu Ser Pro Thr Arg Phe Thr
 85 90 95
 His Cys Glu Gln Val Leu Gly Glu Gly Ala Leu Asp Arg Gly Thr Tyr
 100 105 110
 Tyr Trp Glu Val Glu Ile Ile Glu Gly Trp Val Ser Met Gly Val Met
 115 120 125
 Ala Ala Asp Phe Ser Pro Gln Glu Pro Tyr Asp Arg Gly Arg Leu Gly
 130 135 140
 Arg Asn Ala His Ser Cys Cys Leu Gln Trp Asn Gly Arg Ser Phe Ser
 145 150 155 160
 Val Trp Phe His Gly Leu Glu Ala Pro Leu Pro His Pro Phe Ser Pro
 165 170 175
 Thr Val Gly Val Cys Leu Glu Tyr Ala Asp Arg Ala Leu Ala Phe Tyr
 180 185 190
 Ala Val Arg Asp Gly Lys Met Ser Leu Leu Arg Arg Leu Lys Ala Ser
 195 200 205
 Arg Pro Arg Arg Gly Gly Ile Pro Ala Ser Pro Ile Asp Pro Phe Gln
 210 215 220
 Ser Arg Leu Asp Ser His Phe Ala Gly Leu Phe Thr His Arg Leu Lys
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 Pro Ala Phe Phe Leu Glu Ser Val Asp Ala His Leu Gln Ile Gly Pro
 245 250 255
 Leu Lys Lys Ser Cys Ile Ser Val Leu Lys Arg Arg
 260 265

<210> 3611

<211> 816

<212> DNA

<213> Homo sapiens

<400> 3611

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 420
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<210> 3612

<211> 272

<212> PRT

<213> Homo sapiens

<400> 3612

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			20					25					30		
Lys	Val	Lys	Pro	Arg	Lys	Ile	Phe	Gln	Trp	Arg	Gln	Leu	Glu	Asn	Leu
			35				40					45			
Tyr	Phe	Arg	Glu	Lys	Lys	Phe	Ser	Val	Glu	Val	His	Asp	Pro	Arg	Arg
	50					55					60				
Ala	Ser	Val	Thr	Arg	Arg	Thr	Phe	Gly	His	Ser	Gly	Ile	Ala	Val	His
	65				70				75				80		
Thr	Trp	Tyr	Ala	Cys	Pro	Ala	Leu	Ile	Lys	Ser	Ile	Trp	Ala	Met	Ala
			85					90					95		
Ile	Ser	Gln	His	Gln	Phe	Tyr	Leu	Asp	Arg	Lys	Gln	Ser	Lys	Ser	Lys
			100				105					110			
Ile	His	Ala	Ala	Arg	Ser	Leu	Ser	Glu	Ile	Ala	Ile	Asp	Leu	Thr	Glu

	115						120							125							
Thr	Gly	Leu	Lys	Thr	Ser	Lys	Leu	Ala	Asn	Met	Gly	Ser	Lys	Gly							
	130					135				140											
Lys	Ile	Ile	Ser	Gly	Ser	Ser	Gly	Ser	Leu	Leu	Ser	Ser	Gly	Ser							
145					150					155				160							
Glu	Ser	Asp	Ser	Ser	Gln	Ser	Ala	Lys	Lys	Asp	Met	Leu	Ala	Ala							
				165					170					175							
Lys	Ser	Arg	Gln	Glu	Ala	Leu	Glu	Glu	Thr	Leu	Arg	Gln	Arg	Leu							
		180						185				190									
Glu	Leu	Lys	Lys	Leu	Cys	Leu	Arg	Glu	Ala	Glu	Leu	Thr	Gly	Lys							
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Pro	Val	Glu	Tyr	Pro	Leu	Asp	Pro	Gly	Glu	Glu	Pro	Pro	Ile	Val							
	210					215					220										
Arg	Arg	Ile	Gly	Thr	Ala	Phe	Lys	Leu	Asp	Glu	Gln	Lys	Ile	Leu							
225					230					235				240							
Lys	Gly	Glu	Glu	Ala	Glu	Leu	Glu	Arg	Leu	Glu	Arg	Glu	Phe	Ala							
				245					250					255							
Gln	Ser	Gln	Ile	Thr	Glu	Ala	Ala	Arg	Arg	Leu	Ala	Ser	Asp	Asn							
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<210> 3613

<211> 659

<212> DNA

<213> Homo sapiens

<400> 3613

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120					
cacctggatc	cctgcagccc	agccttgaat	gcgtctggat	taggggaaag	acgagaaacg
180					
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240					
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300					
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360					
aactcgtctc	atttatcaag	tcctctgggc	tgggaatctc	actgaattcc	aaacgcggga
420					
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480					
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540					
tacagtcctt	tcgaccattg	ccttggagca	ccgcacacag	cgcacgcgac	tccggccgcg
600					
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<210> 3614

<211> 123

<212> PRT

<213> Homo sapiens

<400> 3614

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      20           25           30
Gly Leu Gly Ile Ser Leu Asn Ser Lys Arg Arg Lys Glu Glu Thr Phe
      35           40           45
Pro Thr Arg Cys Gly Cys Asp Ala Ser Gln Gly Pro Gln Gly His Cys
      50           55           60
Pro Arg Ala His Arg Pro Pro Leu Thr Ala Thr Gly Ala Trp Ile Arg
      65           70           75           80
Ser Tyr Ile Val Gln Ser Phe Arg Pro Leu Pro Trp Ser Thr Arg Thr
      85           90           95
Arg Ala Arg Ile Ser Gly Arg Ala His Thr His Ser Tyr Thr Arg Thr
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Gln Thr Arg Ser Glu Lys Ser Pro Pro Pro
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<210> 3615

<211> 1388

<212> DNA

<213> Homo sapiens

<400> 3615

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120
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180
gcagagggtg attctgctgc tgagatgaat ggggaggagg aagagagtga ggaggagcgg
240
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300
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360
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660
gacctcagct ctgaatggtg ggacgacaaa ctgcacgcca gaggcagctc caggtcttgg
720
gactccctgc cggccagcaa gaggaagaag gcacctctgg tttctggccc atacatcgtg
780
tacatgcttc aagagatcgg catcctggag gactggacag ccatcaaaaa ggctagggca
840
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900

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<210> 3616

<211> 290

<212> PRT

<213> Homo sapiens

<400> 3616

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 Glu Arg Ser Gly Ser Gln Thr Glu Ser Glu Glu Glu Ser Ser Glu Met
 35 40 45
 Asp Asp Glu Asp Tyr Glu Arg Arg Arg Ser Glu Cys Val Ser Glu Met
 50 55 60
 Leu Asp Leu Glu Lys Gln Phe Ser Glu Leu Lys Glu Lys Leu Phe Arg
 65 70 75 80
 Glu Arg Leu Ser Gln Leu Arg Leu Arg Leu Glu Glu Val Gly Ala Glu
 85 90 95
 Arg Ala Pro Glu Tyr Thr Glu Pro Leu Gly Gly Leu Gln Arg Ser Leu
 100 105 110
 Lys Ile Arg Ile Gln Val Ala Gly Ile Tyr Lys Gly Phe Cys Leu Asp
 115 120 125
 Val Ile Arg Asn Lys Tyr Glu Cys Glu Leu Gln Gly Ala Lys Gln His
 130 135 140
 Leu Glu Ser Glu Lys Leu Leu Tyr Asp Thr Leu Gln Gly Glu Leu
 145 150 155 160
 Gln Glu Arg Ile Gln Arg Leu Glu Glu Asp Arg Gln Ser Leu Asp Leu
 165 170 175
 Ser Ser Glu Trp Trp Asp Asp Lys Leu His Ala Arg Gly Ser Ser Arg
 180 185 190
 Ser Trp Asp Ser Leu Pro Pro Ser Lys Arg Lys Lys Ala Pro Leu Val
 195 200 205
 Ser Gly Pro Tyr Ile Val Tyr Met Leu Gln Glu Ile Gly Ile Leu Glu
 210 215 220
 Asp Trp Thr Ala Ile Lys Lys Ala Arg Ala Ala Val Ser Pro Gln Lys

225		230		235		240
Arg	Lys	Ser	Asp	Asp	Arg	Thr
			245		250	
Ala	Arg	Leu	Leu	Trp	Cys	Cys
			260		265	
Ala	Trp	Thr	Pro	Pro	Leu	Pro
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Trp	Ser					
	290					

<210> 3617

<211> 804

<212> DNA

<213> Homo sapiens

<400> 3617

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120
aggatgggat ggtagtagtg aaggacatag gatgggggta gagtgtggag actttttgaa
180
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420
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<210> 3618

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3618

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Ala	Glu	Glu	Ile	Cys	Glu	Ser	Ser	Ser	Lys	Met	Ile	Thr	Phe	Ile	Asp

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                20                25                30
Leu Ala Gly His His Lys Tyr Leu His Thr Thr Ile Phe Gly Leu Thr
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Ser Tyr Cys Pro Asp Cys Ala Leu Leu Val Ser Ala Asn Thr Gly
                50                55                60
Ile Ala Gly Thr Thr Arg Glu His Leu Gly Leu Ala Leu Ala Leu Lys
        65                70                75                80
Val Pro Phe Phe Ile Val Val Ser Lys Ile Asp Leu Cys Ala Lys Thr
                85                90                95
Thr Val Glu Arg Thr Val Arg Gln Leu Glu Arg Val Leu Lys Gln Pro
                100                105                110
Gly Cys His Lys Val Pro Met Leu Val Thr Ser Glu Asp Asp Ala Val
                115                120                125
Thr Ala Ala Gln Gln Phe Ala Gln Ser Pro Asn Val Thr Pro Ile Phe
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Thr Leu Ser Ser
145

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<210> 3619

<211> 948

<212> DNA

<213> Homo sapiens

<400> 3619

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780
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840
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900

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948

<210> 3620

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3620

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			20					25					30		
Ser	Ser	Ser	Ser	Met	Ala	Thr	Pro	Leu	Ser	Cys	Cys	Pro	Thr	Trp	Ala
		35					40					45			
Pro	Gly	Ala	Ser	Ser	Gln	Pro	Cys	Ser	Thr	Tyr	Pro	Pro	Pro	Arg	Thr
	50					55					60				
Thr	Thr	Leu	Ser	Thr	Ser	Thr	Ser	Trp	Ser	Cys	Leu	Leu	Leu	Pro	Cys
	65				70					75				80	
Ala	Ser	Cys	Pro	Ser	Arg	Cys	Ser	Cys	Gln	Thr	Trp	Pro	Ser	Ser	Pro
			85						90					95	
Thr	Ala	Ser	Thr	Pro	Thr	Thr	Ser	Cys	Thr	Ser	Phe	Met	Thr	Thr	Cys
			100					105					110		
Cys	His	Ser	Ser	Thr	Pro	Cys	Gly	Ser	Phe	Pro	Ala	Trp	Pro	Thr	Arg
		115					120					125			
His	Gly	Ser	Ser	Ser	Trp	Arg	Ala	Gly	Ala	Arg	Val	His	Thr	Ser	Thr
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Ser	Thr	Ser	Cys	Ser	Ala	Pro	Ser	Ser	Leu	Ser	Cys	Gly	His	Ser	
	145				150					155					

<210> 3621

<211> 2934

<212> DNA

<213> Homo sapiens

<400> 3621

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180
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240
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540

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<211> 228

<212> PRT

<213> Homo sapiens

<400> 3622

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			20					25					30		
Glu	Ser	Gly	Phe	Asp	Pro	Asn	Ile	Arg	Asp	Ser	Arg	Gly	Arg	Thr	Gly
		35					40					45			
Leu	His	Leu	Ala	Ala	Ala	Arg	Gly	Asn	Val	Asp	Ile	Cys	Gln	Leu	Leu
		50				55				60					
His	Lys	Phe	Gly	Ala	Asp	Leu	Leu	Ala	Thr	Asp	Tyr	Gln	Gly	Asn	Thr
				70					75					80	
Ala	Leu	His	Leu	Cys	Gly	His	Val	Asp	Thr	Ile	Gln	Phe	Leu	Val	Ser
			85					90						95	
Asn	Gly	Leu	Lys	Ile	Asp	Ile	Cys	Asn	His	Gln	Gly	Ala	Thr	Pro	Leu
		100						105					110		
Val	Leu	Ala	Lys	Arg	Arg	Gly	Val	Asn	Lys	Asp	Val	Ile	Arg	Leu	Leu
		115				120					125				
Glu	Ser	Leu	Glu	Glu	Gln	Glu	Val	Lys	Gly	Phe	Asn	Arg	Gly	Thr	His
		130				135					140				
Ser	Lys	Leu	Glu	Thr	Met	Gln	Thr	Ala	Glu	Ser	Glu	Ser	Ala	Met	Glu
				150						155				160	
Ser	His	Ser	Leu	Leu	Asn	Pro	Asn	Leu	Gln	Gln	Gly	Glu	Gly	Val	Leu

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                165                170                175
Ser Ser Phe Arg Thr Thr Trp Gln Glu Phe Val Glu Asp Leu Gly Phe
                180                185                190
Trp Arg Val Leu Leu Leu Ile Phe Val Ile Ala Leu Leu Ser Leu Gly
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Ile Ala Tyr Tyr Val Ser Gly Val Leu Pro Phe Val Glu Asn Gln Pro
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Glu Leu Val His
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<210> 3623

<211> 586

<212> DNA

<213> Homo sapiens

<400> 3623

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<210> 3624

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3624

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20     25     30
Arg Asp Ile Thr Lys Glu Glu Ile Ser Lys Phe Ser Lys Ala Glu Trp
35     40     45
Glu Lys Lys Arg Met Asp Lys Ala Ile Gly Tyr Ser Phe Ala Ile Val
50     55     60
Gly Ile Asn Ile Thr Asp Leu Ala Tyr Asn Leu Leu Val Ser Gly Ala
65     70     75     80
Leu Lys Thr His Phe Tyr Asn Ile Ala Pro Glu Ala Pro Thr Leu Ser

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85										90										95											
His	Phe	Gln	Gln	Thr	Phe	Cys	Tyr	Leu	Met	His	Glu	Phe	His	Lys	Phe	His	Phe	Gln	Gln	Thr	Phe	Cys	Tyr	Leu	Met	His	Glu	Phe	His	Lys	Phe
100										105										110											
Trp	Ile	Glu	Glu	Asp	Pro	Met	Asp	Ile	Met	Glu	Phe	Asn	Arg	Val	Arg	Trp	Ile	Glu	Glu	Asp	Pro	Met	Asp	Ile	Met	Glu	Phe	Asn	Arg	Val	Arg
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Ala	Leu	Cys	Pro	His	Phe	Ala	Ala	Ser	Glu	Gly	Leu	Ile	Asn	Met	Ala	Leu	Cys	Pro	His	Phe	Ala	Ala	Ser	Glu	Gly	Leu	Ile	Asn	Met		
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<210> 3625

<211> 4799

<212> DNA

<213> Homo sapiens

<400> 3625

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<210> 3626

<211> 551

<212> PRT

<213> Homo sapiens

<400> 3626

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			20					25					30		
Trp	Gly	Pro	Ser	Ser	Ser	Leu	Met	Ser	Glu	Ile	Ala	Asp	Leu	Thr	Tyr
			35				40					45			
Asn	Val	Val	Ala	Phe	Ser	Glu	Ile	Met	Ser	Met	Ile	Trp	Lys	Arg	Leu
			50				55				60				
Asn	Asp	His	Gly	Lys	Asn	Trp	Arg	His	Val	Tyr	Lys	Ala	Met	Thr	Leu
			65			70				75				80	
Met	Glu	Tyr	Leu	Ile	Lys	Thr	Gly	Ser	Glu	Arg	Val	Ser	Gln	Gln	Cys
				85				90					95		
Lys	Glu	Asn	Met	Tyr	Ala	Val	Gln	Thr	Leu	Lys	Asp	Phe	Gln	Tyr	Val
			100					105					110		
Asp	Arg	Asp	Gly	Lys	Asp	Gln	Gly	Val	Asn	Val	Arg	Glu	Lys	Ala	Lys
			115				120					125			
Gln	Leu	Val	Ala	Leu	Leu	Arg	Asp	Glu	Asp	Arg	Leu	Arg	Glu	Glu	Arg
			130			135					140				
Ala	His	Ala	Leu	Lys	Thr	Lys	Glu	Lys	Leu	Ala	Gln	Thr	Ala	Thr	Ala
					150					155				160	
Ser	Ser	Ala	Ala	Val	Gly	Ser	Gly	Pro	Pro	Pro	Glu	Ala	Glu	Gln	Ala
			165					170						175	
Trp	Pro	Gln	Ser	Ser	Gly	Glu	Glu	Glu	Leu	Gln	Leu	Gln	Leu	Ala	Leu
			180					185					190		
Ala	Met	Ser	Lys	Glu	Glu	Ala	Asp	Gln	Glu	Glu	Arg	Ile	Arg	Arg	Gly
			195				200					205			
Asp	Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr
			210			215					220				
Gly	Gly	Lys	Glu	Glu	Ser	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr
					230					235				240	
Ala	Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro
					245				250					255	
Met	Ala	Ala	Ala	Val	Pro	Thr	Ala	Ala	Pro	Thr	Ser	Asp	Pro	Trp	Gly

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                260                265                270
Gly Pro Pro Val Pro Pro Ala Ala Asp Pro Trp Gly Gly Pro Ala Pro
275                280                285
Thr Pro Ala Ser Gly Asp Pro Trp Arg Pro Ala Ala Pro Ala Gly Pro
290                295                300
Ser Val Asp Pro Trp Gly Gly Thr Pro Ala Pro Ala Ala Gly Glu Gly
305                310                315
Pro Thr Pro Asp Pro Trp Gly Ser Ser Asp Gly Gly Val Pro Val Ser
320                325                330
Gly Pro Ser Ala Ser Asp Pro Trp Thr Pro Ala Pro Ala Phe Ser Asp
335                340                345
Pro Trp Gly Gly Ser Pro Ala Lys Pro Ser Thr Asn Gly Thr Thr Thr
350                355                360
Ala Gly Gly Phe Asp Thr Glu Pro Asp Glu Phe Ser Asp Phe Asp Arg
365                370                375
Leu Arg Thr Ala Leu Pro Thr Ser Gly Ser Ser Ala Gly Glu Leu Glu
380                385                390
Leu Leu Ala Gly Glu Val Pro Ala Arg Ser Pro Gly Ala Phe Asp Met
395                400                405
Ser Gly Val Arg Gly Ser Leu Ala Glu Ala Val Gly Ser Pro Pro Pro
410                415                420
Ala Ala Thr Pro Thr Pro Thr Pro Thr Arg Lys Thr Pro Glu Ser
425                430                435
Phe Leu Gly Pro Asn Ala Ala Leu Val Asp Leu Asp Ser Leu Val Ser
440                445                450
Arg Pro Gly Pro Thr Pro Pro Gly Ala Lys Ala Ser Asn Pro Phe Leu
455                460                465
Pro Gly Gly Gly Pro Ala Thr Gly Pro Ser Val Thr Asn Pro Phe Gln
470                475                480
Pro Ala Pro Pro Ala Thr Leu Thr Leu Asn Gln Leu Arg Leu Ser Pro
485                490                495
Val Pro Pro Val Pro Gly Ala Pro Pro Thr Tyr Ile Ser Pro Leu Gly
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Gly Gly Pro Gly Leu Pro Pro Met Met Pro Pro Gly Pro Pro Ala Pro
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Asn Thr Asn Pro Phe Leu Leu
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<210> 3627

<211> 1760

<212> DNA

<213> Homo sapiens

<400> 3627

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300

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caccctcaag aagtcagtat ggtgcggaat ttaattcaga aagatagaac ctttgcgtgt
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<210> 3628

<211> 440

<212> PRT

<213> Homo sapiens

<400> 3628

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 35 40 45
 Thr Ser Leu Pro Thr Ser His Thr Tyr Leu Gly Ala Asp Met Glu Glu
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 Phe His Gly Arg Thr Leu His Asp Asp Asp Ser Cys Gln Val Ile Pro
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 Val Leu Pro Gln Val Met Met Ile Leu Ile Pro Gly Gln Thr Leu Pro
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 165 170 175
 Gln Ala Lys Val Gln Ile Leu Pro Glu Cys Val Leu Pro Ser Thr Met
 180 185 190
 Ser Ala Val Gln Leu Glu Ser Leu Asn Lys Cys Gln Ile Phe Pro Ser
 195 200 205
 Lys Pro Val Ser Arg Glu Asp Gln Cys Ser Tyr Lys Trp Trp Gln Lys
 210 215 220
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 245 250 255
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 275 280 285
 Asp Asp Val Leu Arg Ile Gln Leu Leu Lys Ile Gly Ser Ala Ile Gln
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 305 310 315 320
 Cys Lys Gln Cys Gln Glu Thr Glu Ile Thr Thr Lys Asn Glu Ile Phe
 325 330 335
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 340 345 350
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 355 360 365
 Ile Gly Arg Pro Ser Thr Glu His Ser Trp Phe Pro Gly Tyr Ala Trp
 370 375 380
 Thr Val Ala Gln Cys Lys Ile Cys Ala Ser His Ile Gly Trp Lys Phe
 385 390 395 400
 Thr Ala Thr Lys Lys Asp Met Ser Pro Gln Lys Phe Trp Gly Leu Thr

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Pro Asp Lys Val Ile Leu Cys Leu
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<210> 3629
 <211> 695
 <212> DNA
 <213> Homo sapiens

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<210> 3630
 <211> 139
 <212> PRT
 <213> Homo sapiens

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<400> 3630
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Ser Tyr Phe Leu Phe Val Ile Phe Thr Ala Tyr Ala Met Leu Pro Leu
35      40      45
Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His
50      55      60
Leu Leu Val Leu Gly Leu Tyr Leu Gly Pro Gln Pro Asp Ser Arg Pro
65      70      75      80
Ala Leu Leu Pro Gln Leu Ala Ala Asn Ala Val Leu Phe Leu Cys Gly

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                20                25                30
Ile Thr Thr Glu Gly Lys Tyr Trp Lys Ser Arg Ile Glu Ile Val Ile
      35      40      45
Arg Glu Tyr His Lys Trp Arg Thr Tyr Phe Lys Lys Arg Leu Gln Gln
      50      55      60
His Lys Asp Glu Asp Leu Ser Ser Leu Val Gln Asp Asp Asp Met Leu
      65      70      75      80
Tyr Trp His Lys His Gly Asp Gly Trp Lys Thr Pro Val Pro Met Glu
      85      90      95
Glu Asp Pro Leu Leu Asp Thr Asp Met Leu Met Ser Glu Phe Ser Asp
      100      105      110
Thr Leu Phe Ser Thr Leu Ser Ser His Gln Pro Val Ala Trp Pro Asn
      115      120      125
Pro Arg Glu Ile Ala His Leu Gly Asn Ala Asp Met Ile Gln Pro Gly
      130      135      140
Leu Ile Pro Leu Gln Pro Asn Leu Asp Phe Met Asp Thr Phe Glu Pro
      145      150      155      160
Phe Gln Asp Leu Phe Ser Ser Ser Arg Ser Ile Phe Gly Ser Met Leu
      165      170      175
Pro Ala Ser Ala Ser Ala Pro Val Pro Asp Pro Asn Asn Pro Pro Ala
      180      185      190
Gln Glu Ser Ile Leu Pro Thr Thr Ala Leu Pro Thr Val Ser Leu Pro
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Asp Ser Leu Ile Ala Pro Pro Thr Ala Pro Ser Leu Ala Arg
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<210> 3633

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 3633

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120
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180
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240
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300
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360
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420
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480
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540
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600
cgggagcaca tcctggccac gggaagctat gatgaacaca tcctactgtg ggacacacga
660

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 720
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 780
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 840
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 960
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<210> 3634

<211> 277

<212> PRT

<213> Homo sapiens

<400> 3634

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		20					25						30		
Glu	Ile	Val	Tyr	Ser	Gly	Gly	Asp	Asp	Gly	Leu	Leu	Arg	Gly	Trp	Asp
		35				40						45			
Thr	Arg	Val	Pro	Gly	Lys	Phe	Leu	Phe	Thr	Ser	Xaa	Lys	Thr	His	His
		50			55						60				
Xaa	Gly	Val	Cys	Ser	Ile	Gln	Ser	Ser	Pro	His	Arg	Glu	His	Ile	Leu
65					70				75				80		
Ala	Thr	Gly	Ser	Tyr	Asp	Glu	His	Ile	Leu	Leu	Trp	Asp	Thr	Arg	Asn
			85					90					95		
Met	Lys	Gln	Pro	Leu	Ala	Asp	Thr	Pro	Val	Gln	Gly	Gly	Val	Trp	Arg
			100					105					110		
Ile	Lys	Trp	His	Pro	Phe	His	His	His	Leu	Leu	Leu	Ala	Ala	Cys	Met

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<210> 3636

<211> 278

<212> PRT

<213> Homo sapiens

<400> 3636

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Ala Arg Leu Gln Gln Val Asp Pro Val Leu Leu Lys Asp Glu Pro Gln
35 40 45
Gln Thr Ala Ala Gln Met Gly Cys Ala Pro Ile Gln Pro Leu Ala Met
50 55 60
Pro Gln Ala Leu Pro Leu Ala Ala Gly Pro Leu Pro Pro Gly Ser Ile
65 70 75 80
Ala Asn Leu Thr Glu Leu Gln Gly Val Ile Val Gly Gln Pro Val Leu
85 90 95
Gly Gln Ala Gln Leu Ala Gly Leu Gly Gln Gly Ile Leu Thr Glu Thr
100 105 110
Gln Gln Gly Leu Met Val Ala Ser Pro Ala Gln Thr Leu Asn Asp Thr
115 120 125
Leu Asp Asp Ile Met Ala Ala Val Ser Gly Arg Ala Ser Ala Met Ser
130 135 140
Asn Thr Pro Thr His Ser Ile Ala Ala Ser Ile Ser Gln Pro Gln Thr
145 150 155 160
Pro Thr Pro Ser Pro Ile Ile Ser Pro Ser Ala Met Leu Pro Ile Tyr
165 170 175
Pro Ala Ile Asp Ile Asp Ala Gln Thr Glu Ser Asn His Asp Thr Ala
180 185 190
Leu Thr Leu Ala Cys Ala Gly Gly His Glu Glu Leu Val Gln Thr Leu
195 200 205
Leu Glu Arg Gly Ala Ser Ile Glu His Arg Asp Lys Gly Phe Thr
210 215 220
Pro Leu Ile Leu Ala Ala Thr Ala Gly His Val Gly Val Val Glu Ile
225 230 235 240
Leu Leu Asp Asn Gly Ala Asp Ile Glu Ala Gln Ser Glu Arg Thr Lys
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Asp Thr Pro Leu Ser Leu Ala Cys Ser Gly Gly Arg Gln Glu Val Val
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Glu Leu Leu Leu Ala Arg
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<210> 3637

<211> 2128

<212> DNA

<213> Homo sapiens

<400> 3637

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120
cctgccaacc cctgctcttc caggtcgggc cccgggggtc tgccgctgtt agggacagag
180
gcaaagaagg gcaggacggt ccgggtttccc gtggatgttc ccgccgaga aagacagcaa
240
gttgtgtgtg cggccgggac gggggaggga aggtagccgc cggccgcag ccatggacca
300
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360
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420
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480
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1680

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 1980
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<210> 3638

<211> 200

<212> PRT

<213> Homo sapiens

<400> 3638

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 20 25 30
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 35 40 45
 Arg Cys Ser Tyr Pro Val His Asp Glu Ser Arg Gln Met Met Val Met
 50 55 60
 Val Glu Glu Cys Gly Arg Tyr Ala Ser Phe Gln Gly Ile Pro Ser Ala
 65 70 75 80
 Glu Trp Arg Ile Cys Thr Ile Val Thr Gly Leu Gly Cys Gly Leu Leu
 85 90 95
 Leu Leu Val Ala Leu Thr Ala Leu Met Gly Cys Cys Val Ser Asp Leu
 100 105 110
 Ile Ser Arg Thr Val Gly Arg Val Ala Gly Gly Ile Gln Phe Leu Gly
 115 120 125
 Gly Leu Leu Ile Gly Ala Gly Cys Ala Leu Tyr Pro Leu Gly Trp Asp
 130 135 140
 Ser Glu Glu Val Arg Gln Thr Cys Gly Tyr Thr Ser Gly Gln Phe Asp
 145 150 155 160
 Leu Gly Lys Cys Glu Ile Gly Trp Ala Tyr Tyr Cys Thr Gly Ala Gly
 165 170 175
 Ala Thr Ala Ala Met Leu Leu Cys Thr Trp Leu Ala Cys Phe Ser Gly
 180 185 190
 Lys Lys Gln Lys His Tyr Pro Tyr
 195 200

<210> 3639

<211> 726

<212> DNA

<213> Homo sapiens

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 120
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 180
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 240
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 300
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 480
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 540
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 600
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 660
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 720
 taagat
 726

<210> 3640

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3640

Met	Leu	His	Ala	Ala	Arg	Lys	Arg	Asp	His	Val	Pro	Phe	Arg	Lys	Met
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Ser	Leu	Ile	Met	Lys	Glu	Met	Pro	Trp	Arg	Thr	Gln	His	Pro	Asn	Phe
			20					25					30		
Ser	Leu	Leu	Asn	Pro	Leu	Lys	Gly	Glu	Ile	Phe	Leu	Leu	Pro	Ala	Arg
			35				40					45			
Val	Tyr	Gly	Asp	Asp	Thr	Leu	Arg	Pro	Cys	Trp	Cys	Trp	Lys	Asn	His
			50				55				60				
Leu	Trp	Gln	Cys	His	Phe	Leu	Arg	Lys	Thr	Tyr	Gln	Ser	Phe	Ala	Met
					70					75				80	
Phe	Thr	Ile	Asp	Lys	Lys	Arg	Asp	Met	Gln	Ser	Val	Lys	Cys	Ile	Thr
					85				90					95	
Leu	Ile	Ile	Cys	Leu	His										
					100										

<210> 3641

<211> 455

<212> DNA

<213> Homo sapiens

<400> 3641
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 120
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 180
 gagctcgaga cgctcgcgcg ctacacctct gggccccctgt gcgtggggaa gtcaggaaga
 240
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 300
 ggaggtggcc gaagggaaga ggggtgggca ggggctgctc tgcacctctc agcagagcgg
 360
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 455

<210> 3642

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3642

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Pro	Arg	Gly	Arg	Ala	Gly	Gly	Ala	Ala	Pro	Gly	Gly	Glu	Glu	Met	Ser
			20					25					30		
Gln	Ser	Pro	Glu	Glu	Ser	Arg	Ser	Ser	His	Ala	Ser	Arg	Asp	Leu	Ala
		35					40					45			
Pro	Leu	Glu	Arg	Arg	Ser	Gly	Arg	Gly	Ala	Arg	Asp	Ala	Arg	Ala	Leu
	50					55				60					
Thr	Ser	Trp	Ala	Pro	Val	Arg	Gly	Glu	Val	Arg	Lys	Lys	Thr	Pro	Ser
	65				70				75				80		
Glu	Val	Thr	Val	Pro	Thr	Arg	Val	Asp	Ser	Pro	Arg	Pro	Asp	His	Ala
			85					90					95		
Arg	Arg	Trp	Pro	Lys	Gly	Arg	Gly	Trp	Gly	Arg	Gly	Cys	Ser	Ala	Pro
			100				105					110			
Ser	Ser	Arg	Ala	Ala	Ser	Leu	Gln	Val	Phe	Ala	Leu	Ala	Arg	Arg	Ser
		115				120					125				
Pro	Arg	Glu	Gln	Phe	Gly	Thr	Val	Arg	Ile	Gly	Phe	Arg	Glu	Pro	Ala
	130					135					140				
Phe	Lys	Thr	Arg												
145															

<210> 3643

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 3643

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120
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420
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480
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1680

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 1920
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 1980
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 2220
 aaaaaaaaaa aaaaaaaaaa aaa
 2243

<210> 3644

<211> 560

<212> PRT

<213> Homo sapiens

<400> 3644

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Gln	Val	Ala	Ser	Lys	Ala	Glu	Glu	Asn	Leu	Leu	Met	Val	Leu	Gly
		20					25					30		
Asp	Met	Ser	Asp	Arg	Arg	Ala	Ala	Val	Ile	Phe	Ala	Asp	Thr	Leu
		35				40					45			
Leu	Leu	Phe	Glu	Gly	Ile	Ala	Arg	Ile	Val	Glu	Thr	His	Gln	Pro
	50				55					60				
Val	Glu	Thr	Tyr	Tyr	Gly	Pro	Gly	Arg	Leu	Tyr	Thr	Leu	Ile	Lys
65				70				75					80	
Leu	Gln	Val	Glu	Cys	Asp	Arg	Gln	Val	Glu	Lys	Val	Val	Asp	Lys
			85					90					95	
Ile	Lys	Gln	Arg	Asp	Tyr	His	Gln	Gln	Phe	Arg	His	Val	Gln	Asn
		100					105					110		
Leu	Met	Arg	Asn	Ser	Thr	Thr	Glu	Lys	Ile	Glu	Pro	Arg	Glu	Leu
	115						120					125		
Pro	Ile	Leu	Thr	Glu	Val	Thr	Leu	Met	Asn	Ala	Arg	Ser	Glu	Leu
	130					135					140			
Leu	Arg	Phe	Leu	Lys	Lys	Arg	Ile	Ser	Ser	Asp	Phe	Glu	Val	Gly
145				150						155				160
Ser	Met	Ala	Ser	Glu	Glu	Val	Lys	Gln	Glu	His	Gln	Lys	Cys	Leu
			165					170					175	
Lys	Leu	Leu	Asn	Asn	Cys	Leu	Leu	Ser	Cys	Thr	Met	Gln	Glu	Leu
		180						185				190		
Gly	Leu	Tyr	Val	Thr	Met	Glu	Glu	Tyr	Phe	Met	Arg	Glu	Thr	Val
		195				200						205		
Lys	Ala	Val	Ala	Leu	Asp	Thr	Tyr	Glu	Lys	Gly	Gln	Leu	Thr	Ser

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225              230              235              240
Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala Met Ile Asn Leu Ala
      245              250              255
Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val Leu Cys Asn Lys Leu
      260              265              270
Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp Ile Gln Arg Gly Val
      275              280              285
Thr Ser Ala Val Asn Ile Met His Ser Ser Leu Gln Gln Gly Lys Phe
      290              295              300
Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala Lys Met Ser Phe Leu
305              310              315              320
Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu Asn Ile Ser Thr Leu
      325              330              335
Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu Phe Ser Gln Gly Ile
      340              345              350
Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser Cys Leu Ser Asp Leu
      355              360              365
Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu Gln Glu Gly Leu Thr
      370              375              380
Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val Gln Pro Trp Ile Asn
385              390              395              400
Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu Glu Glu Phe Asn Asp
      405              410              415
Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe Ile Leu Asn Leu Glu
      420              425              430
Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser Pro Val Ile Tyr Asp
      435              440              445
Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala Val Glu Leu Glu Lys
      450              455              460
Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly Gly Leu Gln Phe Asp
465              470              475              480
Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr Thr Val Thr Thr Trp
      485              490              495
Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln Met Ala Thr Ile Leu
      500              505              510
Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr Trp Gly Pro Asn Ser
      515              520              525
Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Gln Val Leu
      530              535              540
Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile Lys Arg Leu Arg Leu
545              550              555              560

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<210> 3645

<211> 823

<212> DNA

<213> Homo sapiens

<400> 3645

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ccagggtttt gtagatggat tcttcaaaaa ctcttttgag gtattgcctg ggcttctcag
120

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tcgggttgat ttctcatct tctatttgat gggctaactg ctctatggaa ggaagatctt
 180
 cctcctcctt ggaggctaag atttgcgta actctttcct gagatcaata aaacgatcgt
 240
 ggaacagggc caggcaccac ggctcggta agtagctata gagatctgtg atcagggttt
 300
 catcgtagcc agcacacagg ttgttgagga gttgctcgtg ctggccaac aagcgatgt
 360
 agttggaggc ggggaagggc tcctagaaa ggcacgtgat ggtttccacc attttatact
 420
 tgttaatatg aattcggaag taagtccat ttttcgact cgcggttact agttctaaac
 480
 cataattagg ctgggccatt tgtacctca agggagttgg aatggcaggc ttggcaatat
 540
 gcagataatg gtaagacca ggaagaatgc ccccttgaat ctgggtccc ttgtacatgg
 600
 ggatgagccg gtcaagatta gctggtggct cggtcacagg ctcaagggtt ggatcaaaag
 660
 gatgtagcat agctgctgcc agctgaaagc caatttcttt ggaactgaag ttgctggtgg
 720
 gccattcat ttgagtagta tctattggag aatttggtga gggagccagc agctctgatg
 780
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 823

<210> 3646

<211> 243

<212> PRT

<213> Homo sapiens

<400> 3646

Met	Asn	Gly	Pro	Thr	Ser	Asn	Phe	Ser	Ser	Lys	Glu	Ile	Gly	Phe	Gln
1				5					10					15	
Leu	Ala	Ala	Ala	Met	Leu	His	Leu	Phe	Asp	Pro	Thr	Leu	Glu	Pro	Val
			20					25					30		
Thr	Glu	Pro	Pro	Ala	Asn	Leu	Asp	Arg	Leu	Ile	Pro	Met	Tyr	Lys	Gly
		35				40					45				
Ala	Lys	Ile	Gln	Gly	Gly	Ile	Leu	Pro	Gly	Ser	Tyr	His	Tyr	Leu	His
	50					55				60					
Ile	Ala	Lys	Pro	Ala	Ile	Pro	Thr	Pro	Leu	Glu	Val	Gln	Met	Ala	Gln
	65				70				75				80		
Pro	Asn	Tyr	Gly	Leu	Glu	Leu	Val	Thr	Gly	Ser	Ala	Lys	Asn	Gly	Thr
			85					90					95		
Tyr	Phe	Arg	Ile	His	Ile	Asn	Lys	Tyr	Lys	Met	Val	Glu	Thr	Ile	Thr
			100					105					110		
Cys	Leu	Ser	Arg	Glu	Pro	Phe	Pro	Ala	Ser	Asn	Tyr	Ile	Arg	Leu	Phe
		115					120					125			
Gly	Gln	His	Glu	Gln	Leu	Leu	Asn	Asn	Leu	Cys	Ala	Arg	Tyr	Asp	Glu
		130				135				140					
Asn	Leu	Ile	Thr	Asp	Leu	Tyr	Ser	Tyr	Phe	Thr	Glu	Pro	Trp	Cys	Leu
	145				150				155				160		
Ala	Leu	Phe	His	Asp	Arg	Phe	Ile	Asp	Leu	Arg	Lys	Glu	Leu	Arg	Gln
			165					170					175		
Ile	Leu	Ala	Ser	Lys	Glu	Glu	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Leu


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                180                185                190
Ala His Gln Ile Glu Asp Glu Glu Ile Asn Pro Thr Glu Lys Pro Arg
                195                200                205
Gln Tyr Leu Lys Arg Val Phe Glu Glu Ser Ile Tyr Lys Thr Leu Val
                210                215                220
Glu Arg Ser Thr Leu Asp Tyr Leu His Tyr Asn Arg Tyr His Leu Pro
225                230                235                240
Met Tyr Ala

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```

<210> 3647
<211> 584
<212> DNA
<213> Homo sapiens

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<400> 3647
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gcgcgggatgc ctttgagcgc ggtgacttct cactgcgtat cgagccgctg gaggtcgcog
120
acgagggcac ctactcctgc cacctgcacc accattactg tggcctgcac gaacgccgcg
180
tcttcaccct gacggtcgcc gaaccccaag cggagccgcc cccccggggc tctccgggca
240
acggctccag ccacagcggc gccccaggcc cagggtgaagg aggcctccct gggaccggg
300
aaggcgggag cccacccca cgggggttgc tctgcgcccg ctgtcccttg cccgaggccc
360
gcggatccca gcgggnnggc cgtggcccgc gtcggggcgc aggtcttctg ggtacctgac
420
gccgctccga ccccgcttc cccgcagacc ccacactggc gcgcggccac aacgtcatca
480
atgtcatcgt ccccgagagc cgagcccact tcttcagca gctgggctac gtgctggcca
540
cgctgctgct cttcactcct ctactgggtca ctgtcctcct ggcc
584

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<210> 3648
<211> 63
<212> PRT
<213> Homo sapiens

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<400> 3648
Thr Arg Arg Ala Ser Ala Ala Pro Thr Gly Pro Phe Phe Cys Ala Thr
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Ala Trp Leu Trp Ala Arg Met Pro Leu Ser Ala Val Thr Ser His Cys
20          25          30
Val Ser Ser Arg Trp Arg Ser Pro Thr Arg Ala Pro Thr Pro Ala Thr
35          40          45
Cys Thr Thr Ile Thr Val Ala Cys Thr Asn Ala Ala Ser Ser Thr
50          55          60

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```

<210> 3649
<211> 648

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<212> DNA

<213> Homo sapiens

<400> 3649

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 120
 tgctcattgt ttgctgtgct cccctttttt tttcagggtg ctattttcgc agatgtcaaa
 180
 gaagttctgt taactgatgg gaatgaaaag gccatcagaa atgtgcaaga catcatcaca
 240
 aggaatcaga aggctggtgt gtttaagacc cagaaaaatat caagctgcgt tttacgatgg
 300
 gataatgaga cagatgtctc tcaactggaa ggacattttg acattgttat gtgtgctgac
 360
 tgctgttttc tggaccagta cagagccagc cttgttgatg caataaagag attactccag
 420
 cccaggggga aagcgatggt atttgcccca cgccgagggg atacttttaa ccagttttgc
 480
 aatctagctg aaaaagctgg tttctgtatc caaagacatg aaaattatga tgaacacatt
 540
 tcaaacttcc actccaagtt gaaaaaggaa aaccgggaca tatatgaaga aaaccttcac
 600
 taccgcgcctc tgcttatttt gaccaaacat ggatagaaga ttaagctt
 648

<210> 3650

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3650

Met	Ile	Leu	Lys	Ala	Cys	His	Ser	Cys	Phe	His	Phe	His	Thr	Asp	Lys
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His	Ile	Cys	Ser	Leu	Phe	Ala	Val	Leu	Pro	Phe	Phe	Phe	Gln	Val	Ala
			20					25					30		
Ile	Ser	Ala	Asp	Val	Lys	Glu	Val	Leu	Leu	Thr	Asp	Gly	Asn	Glu	Lys
		35					40					45			
Ala	Ile	Arg	Asn	Val	Gln	Asp	Ile	Ile	Thr	Arg	Asn	Gln	Lys	Ala	Gly
		50				55					60				
Val	Phe	Lys	Thr	Gln	Lys	Ile	Ser	Ser	Cys	Val	Leu	Arg	Trp	Asp	Asn
				70						75				80	
Glu	Thr	Asp	Val	Ser	Gln	Leu	Glu	Gly	His	Phe	Asp	Ile	Val	Met	Cys
			85					90						95	
Ala	Asp	Cys	Leu	Phe	Leu	Asp	Gln	Tyr	Arg	Ala	Ser	Leu	Val	Asp	Ala
			100					105					110		
Ile	Lys	Arg	Leu	Leu	Gln	Pro	Arg	Gly	Lys	Ala	Met	Val	Phe	Ala	Pro
			115				120					125			
Arg	Arg	Gly	Asn	Thr	Leu	Asn	Gln	Phe	Cys	Asn	Leu	Ala	Glu	Lys	Ala
		130				135					140				
Gly	Phe	Cys	Ile	Gln	Arg	His	Glu	Asn	Tyr	Asp	Glu	His	Ile	Ser	Asn
			145		150					155				160	
Phe	His	Ser	Lys	Leu	Lys	Lys	Glu	Asn	Pro	Asp	Ile	Tyr	Glu	Glu	Asn

	165		170		175
Leu His Tyr	Pro Pro Leu Leu Ile	Leu Thr Lys His Gly			
	180		185		

<210> 3651
 <211> 2469
 <212> DNA
 <213> Homo sapiens

<400> 3651
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 120
 tttgaagggg ccactgtggt catcctgaac atgcccaagg gaacagagtt tgggattgac
 180
 tataactcct gggaggtcgg gcccaagttc cggggcgctga agatgatccc tccaggcatc
 240
 cacttcctcc actacagctc tgtggacaag gctaataccga aggaagtagg ccctcgtatg
 300
 ggtttcttcc ttagcctgca ccagcggggg ctgacagtgc tgcgtggag cactcagg
 360
 gaagaggtag acctgtcccc agccccagag tctgaggtgg aggccatgag ggccaacctc
 420
 caggagctgg accagttcct ggggccttac ccatatgcc aacctgaaga gtggatctca
 480
 ctcaccaact tcatacagca agccacagtg gagaagctac agcccagaaa tcgacagatc
 540
 tgtgcctttt ccgatgtgct acctgtgctc tccatgaagc acaccaagga ccgctggggg
 600
 cagaatctac ccgctgtggt cattgagtgc aaaagctacc aagagggcct ggcccgggta
 660
 ccagagatga agcccagagc cgggacagag atccgcttct cagagctgcc caccgagatg
 720
 ttcccagagg gtgccacgcc agctgagata accaagcaca gcatggacct gagctatgcc
 780
 ctgggagact tgctcatcaa gcagttcccc agcagcccc aggatgtgct tggatgaatc
 840
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 900
 cggctcctgc acctcctgtg ccggtcagaa gcagccatga tgaagcaca caccctctac
 960
 atcaacctca tgtccatcct gtaccaccag cttgggtgaga tccccgtga cttctctgta
 1020
 gacattgtct cccaagacaa ctccctcacc agcaccttac aggtttttctt ttccctctgc
 1080
 tgcagcattg ccgtggatgc caccctgaga aagaaagctg aaaagttcca agctcacctg
 1140
 accaagaagt tcgggtggga ctttgctgag gaacctgagg actgtgcccc ggtggtgggtg
 1200
 gagctccctg agggcatcga gatgggctaa ctgggggagc gctctcagct gcgagggggc
 1260
 ccttcccaca gggctgcagt cctggcctct ccatttactt ctccccatcc tgggacctgc
 1320

cagggcagca atctctccag gtcctgcaaa gatggagcca gaattccctt tttcactgat
 1380
 aaatatatatt cttcattgcc aaagaggctg tacccatcct gaaggcacat ttgtgggttc
 1440
 cccatcagcc aggccctgggt gctaacctgg ctgaatttca cacaggctct tacacacaca
 1500
 cgctcctagg agacatctgc ctacacggca accatatttc ctctgaatga gaaggaattg
 1560
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 1620
 cctggattgc ccaggggggc tgagaagttg gttggtgact ttttttgcgg ttaaatgaag
 1680
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 1800
 ttcaatctag caggtggtca gcttcagctt tctccatcga aatcccatc tctgtgccag
 1860
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 1920
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 1980
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 2100
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 2160
 aatgagctcc tggttctctg ggagtccttc gtgctgtgtg gcagggttcc tctctagaca
 2220
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 2280
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 2340
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 2460
 aaaaaaaaaa
 2469

<210> 3652

<211> 384

<212> PRT

<213> Homo sapiens

<400> 3652

Met	Ala	Ala	Val	Gln	Met	Asp	Pro	Glu	Leu	Ala	Lys	Arg	Leu	Phe	Phe
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Glu	Gly	Ala	Thr	Val	Val	Ile	Leu	Asn	Met	Pro	Lys	Gly	Thr	Glu	Phe
			20					25					30		
Gly	Ile	Asp	Tyr	Asn	Ser	Trp	Glu	Val	Gly	Pro	Lys	Phe	Arg	Gly	Val
		35					40					45			
Lys	Met	Ile	Pro	Pro	Gly	Ile	His	Phe	Leu	His	Tyr	Ser	Ser	Val	Asp

50					55					60					
Lys	Ala	Asn	Pro	Lys	Glu	Val	Gly	Pro	Arg	Met	Gly	Phe	Phe	Leu	Ser
65					70					75				80	
Leu	His	Gln	Arg	Gly	Leu	Thr	Val	Leu	Arg	Trp	Ser	Thr	Leu	Arg	Glu
				85					90					95	
Glu	Val	Asp	Leu	Ser	Pro	Ala	Pro	Glu	Ser	Glu	Val	Glu	Ala	Met	Arg
			100					105					110		
Ala	Asn	Leu	Gln	Glu	Leu	Asp	Gln	Phe	Leu	Gly	Pro	Tyr	Pro	Tyr	Ala
		115					120					125			
Thr	Leu	Lys	Lys	Trp	Ile	Ser	Leu	Thr	Asn	Phe	Ile	Ser	Glu	Ala	Thr
	130					135						140			
Val	Glu	Lys	Leu	Gln	Pro	Glu	Asn	Arg	Gln	Ile	Cys	Ala	Phe	Ser	Asp
	145				150					155				160	
Val	Leu	Pro	Val	Leu	Ser	Met	Lys	His	Thr	Lys	Asp	Arg	Val	Gly	Gln
			165						170					175	
Asn	Leu	Pro	Arg	Cys	Gly	Ile	Glu	Cys	Lys	Ser	Tyr	Gln	Glu	Gly	Leu
		180						185					190		
Ala	Arg	Leu	Pro	Glu	Met	Lys	Pro	Arg	Ala	Gly	Thr	Glu	Ile	Arg	Phe
		195					200					205			
Ser	Glu	Leu	Pro	Thr	Gln	Met	Phe	Pro	Glu	Gly	Ala	Thr	Pro	Ala	Glu
		210				215					220				
Ile	Thr	Lys	His	Ser	Met	Asp	Leu	Ser	Tyr	Ala	Leu	Glu	Thr	Val	Leu
	225				230					235				240	
Ile	Lys	Gln	Phe	Pro	Ser	Ser	Pro	Gln	Asp	Val	Leu	Gly	Glu	Leu	Gln
			245						250					255	
Phe	Ala	Phe	Val	Cys	Phe	Leu	Leu	Gly	Asn	Val	Tyr	Glu	Ala	Phe	Glu
			260					265					270		
His	Trp	Lys	Arg	Leu	Leu	His	Leu	Leu	Cys	Arg	Ser	Glu	Ala	Ala	Met
		275					280					285			
Met	Lys	His	His	Thr	Leu	Tyr	Ile	Asn	Leu	Met	Ser	Ile	Leu	Tyr	His
		290				295					300				
Gln	Leu	Gly	Glu	Ile	Pro	Ala	Asp	Phe	Phe	Val	Asp	Ile	Val	Ser	Gln
				310						315				320	
Asp	Asn	Phe	Leu	Thr	Ser	Thr	Leu	Gln	Val	Phe	Phe	Ser	Ser	Ala	Cys
			325						330					335	
Ser	Ile	Ala	Val	Asp	Ala	Thr	Leu	Arg	Lys	Lys	Ala	Glu	Lys	Phe	Gln
			340					345					350		
Ala	His	Leu	Thr	Lys	Lys	Phe	Arg	Trp	Asp	Phe	Ala	Ala	Glu	Pro	Glu
		355					360					365			
Asp	Cys	Ala	Pro	Val	Val	Val	Glu	Leu	Pro	Glu	Gly	Ile	Glu	Met	Gly
		370				375						380			

<210> 3653

<211> 283

<212> DNA

<213> Homo sapiens

<400> 3653

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gcattataacc aatcagagct tcttttctgtg ctgctgaaat ggaacgggtgc catcaggccc

120

tcttctccac tggagatgct ccttcagctc agcaggacgc tagctcggaa ctcagactgc

180

acattttttgc ggattgggag gagggccgac gccgtggcgg gatagtctct ggagctgcct
 240
 tttgggggtg tttgcctggt ggcattttca gtactccacg cgt
 283

<210> 3654
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 3654
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 Ile Pro Ile Arg Ala Ser Phe Ala Ala Glu Met Glu Arg Cys His
 20 25 30
 Gln Ala Val Phe Ser Thr Gly Asp Ala Pro Ser Ala Gln Gln Asp Ala
 35 40 45
 Ser Ser Glu Leu Arg Leu His Ile Phe Ala Asp Trp Glu Glu Gly Arg
 50 55 60
 Arg Arg Gly Arg Ile Val Ser Gly Ala Ala Phe Trp Gly Cys Leu Pro
 65 70 75 80
 Val Gly Ile Phe Ser Thr Pro Arg
 85

<210> 3655
 <211> 3477
 <212> DNA
 <213> Homo sapiens

<400> 3655
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 120
 gaggtagagg ttgctctggt gcagctggag gaagaacagg gaacctaggg ttggggagag
 180
 atgtatagag gaaaactccc ccaggcacac agcctccgct ctggaccaac gcaggcttca
 240
 gtgagtacac acaagggaac tgatgtcaag gccettttcta tgacctttcc cattctagca
 300
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 360
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 420
 aaaaacaaat aaaataaata aataaataaa taaactaaag ccttattatgc caggcgtgat
 480
 cacatgcccc acactcccct ccatcccagc actatgcaca gttcacggct catatgcaca
 540
 gtggaagaca cgtgggacaa gagcaaagca caagtgcac atggtccctc tctaaccact
 600
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 660
 ttataataat cctcattcac atttctagtt tctgagggaa gagagaaaga gaaaggaaga
 720

agtggaagt gcggaacccc aatgagtagg gcacagaaag gagggcgagc agagacagca
780
agaggtcagg taagccaagg agcagcggag caggtcaatc agggaagttc tgggcaccct
840
ggggctcagg g gatctcagg ggggaacta tcacagatca ggacagcaag gttccaggag
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960
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1080
cagagcccca ccacaagtc agcaatgaat gtgtcctcag tctccccaga gcggtggctc
1140
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1380
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1560
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1920
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1980
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2340

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<210> 3656

<211> 429

<212> PRT

<213> Homo sapiens

<400> 3656

Met	Ala	Ser	Leu	Lys	Glu	Leu	Ala	Pro	Thr	Gly	Arg	Ile	Met	Asn	Ser
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Cys	Met	Ala	Ser	Leu	Phe	Pro	Ala	Trp	Glu	Pro	Pro	Leu	Ile	Thr	Leu
				20				25				30			
Lys	Ala	Gly	Thr	Gly	Ser	Met	Arg	Ser	Gly	Phe	Pro	Ala	Lys	Ser	Ala
		35					40				45				
Met	Trp	Arg	Tyr	Arg	Gly	Thr	Pro	Phe	Ser	Lys	Ala	Val	Glu	His	Ile
	50					55				60					
Asn	Lys	Thr	Ile	Ala	Pro	Ala	Leu	Val	Ser	Lys	Lys	Leu	Asn	Val	Thr

65					70					75					80
Glu	Gln	Glu	Lys	Ile	Asp	Lys	Leu	Met	Ile	Glu	Met	Asp	Gly	Thr	Glu
				85					90					95	
Asn	Lys	Ser	Lys	Phe	Gly	Ala	Asn	Ala	Ile	Leu	Gly	Val	Ser	Leu	Ala
				100				105						110	
Val	Cys	Lys	Ala	Gly	Ala	Val	Glu	Lys	Gly	Val	Pro	Leu	Tyr	Arg	His
				115				120				125			
Ile	Ala	Asp	Leu	Ala	Gly	Asn	Ser	Glu	Val	Ile	Leu	Pro	Val	Pro	Ala
				130				135				140			
Phe	Asn	Val	Ile	Asn	Gly	Gly	Ser	His	Ala	Gly	Asn	Lys	Leu	Ala	Met
				145				150			155				160
Gln	Glu	Phe	Met	Ile	Leu	Pro	Val	Gly	Ala	Ala	Asn	Phe	Arg	Glu	Ala
				165				170						175	
Met	Arg	Ile	Gly	Ala	Glu	Val	Tyr	His	Asn	Leu	Lys	Asn	Val	Ile	Lys
				180				185					190		
Glu	Lys	Tyr	Gly	Lys	Asp	Ala	Thr	Asn	Val	Gly	Asp	Glu	Gly	Gly	Phe
				195				200				205			
Ala	Pro	Asn	Ile	Leu	Glu	Asn	Lys	Glu	Gly	Leu	Glu	Leu	Lys	Thr	
				210			215				220				
Ala	Ile	Gly	Lys	Ala	Gly	Tyr	Thr	Asp	Lys	Val	Val	Ile	Gly	Met	Asp
				225			230			235				240	
Val	Ala	Ala	Ser	Glu	Phe	Phe	Arg	Ser	Gly	Lys	Tyr	Asp	Leu	Asp	Phe
				245					250					255	
Lys	Ser	Pro	Asp	Asp	Pro	Ser	Arg	Tyr	Ile	Ser	Pro	Asp	Gln	Leu	Ala
				260				265					270		
Asp	Leu	Tyr	Lys	Ser	Phe	Ile	Lys	Asp	Tyr	Pro	Val	Val	Ser	Ile	Glu
				275			280					285			
Asp	Pro	Phe	Asp	Gln	Asp	Asp	Trp	Gly	Ala	Trp	Gln	Lys	Phe	Thr	Ala
				290			295				300				
Ser	Ala	Gly	Ile	Gln	Val	Val	Gly	Asp	Asp	Leu	Thr	Val	Thr	Asn	Pro
				310						315				320	
Lys	Arg	Ile	Ala	Gln	Ala	Val	Asn	Glu	Lys	Ser	Cys	Asn	Cys	Leu	Leu
				325					330					335	
Leu	Lys	Val	Asn	Gln	Ile	Gly	Ser	Val	Thr	Glu	Ser	Leu	Gln	Ala	Cys
				340				345				350			
Lys	Leu	Ala	Gln	Ala	Asn	Gly	Trp	Gly	Val	Met	Val	Ser	His	Arg	Ser
				355			360				365				
Gly	Glu	Thr	Glu	Asp	Thr	Phe	Ile	Ala	Asp	Leu	Val	Val	Gly	Leu	Cys
				370			375				380				
Thr	Gly	Gln	Ile	Lys	Thr	Gly	Ala	Pro	Cys	Arg	Ser	Glu	Arg	Leu	Ala
				385			390			395				400	
Lys	Tyr	Asn	Gln	Leu	Leu	Arg	Ile	Glu	Glu	Glu	Leu	Gly	Ser	Lys	Ala
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<210> 3657

<211> 337

<212> DNA

<213> Homo sapiens

<400> 3657

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 120
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 180
 gttcattttc ggctcaaggc ttacacgtgc aggtgtgcca catgttcatt ttcggtctaa
 240
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 300
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 337

<210> 3658

<211> 99

<212> PRT

<213> Homo sapiens

<400> 3658

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Leu	Arg	Val	His	Phe	Arg	Leu	Lys	Ala	Tyr	Thr	Cys	Arg	Cys	Val	Thr
		20					25					30			
Cys	Ser	Phe	Ser	Ala	Gln	Gly	Val	His	Val	Gln	Val	Cys	Tyr	Val	Phe
		35				40					45				
Ile	Phe	Gly	Ser	Arg	Leu	Thr	Arg	Ala	Gly	Val	Pro	His	Val	His	Phe
	50				55					60					
Arg	Leu	Lys	Ala	Tyr	Met	Cys	Arg	Cys	Val	Thr	Cys	Ser	Leu	Ser	Ala
65				70					75					80	
Gln	Arg	Val	His	Val	Gln	Val	Cys	His	Met	Phe	Ile	Phe	Gly	Ser	Arg
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Arg Thr Arg

<210> 3659

<211> 1025

<212> DNA

<213> Homo sapiens

<400> 3659

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 gttgaaaata agacggccca gatattaaat cttcagcaac atttatctgc ccttgaaaaa
 180
 gatattaaac acaatgagga acttctttaa aggtgccaac tacattataa agaactaaag
 240
 atgaaaataa gaaaaatat ttctgaaatt cgggaacttg agaacataga agaaccaccg
 300
 tctgtagata ttgcaacttt ggaagatgaa gctcaggaaa ataaaagcaa aatgaaaaatg
 360
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 420
 gaagcagaaa ataagtatga tgcaattaaa ttcaaaaatta atcaactatc ggagctagca
 480

gaccacctta aggatgaatt aaaccttgct gattctgaag tggataacca aaaacgaggg
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 aaacgacatt atgaaaaaaaa acaaaaagaa cacttgagata ccttaataaa aaagaacga
 600
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 660
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 720
 aggcagaaga tacaggcaga acatgctagt catggagatc gagaggaaa aatgaggcag
 780
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 840
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 900
 aggtgtttga ctttacgatg caaattatac ttgacaact tactatctca gcgggcctat
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 1025

<210> 3660

<211> 341

<212> PRT

<213> Homo sapiens

<400> 3660

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 35 40 45
 Leu Asn Leu Gln Gln His Leu Ser Ala Leu Glu Lys Asp Ile Lys His
 50 55 60
 Asn Glu Glu Leu Leu Lys Arg Cys Gln Leu His Tyr Lys Glu Leu Lys
 65 70 75 80
 Met Lys Ile Arg Lys Asn Ile Ser Glu Ile Arg Glu Leu Glu Asn Ile
 85 90 95
 Glu Glu His Gln Ser Val Asp Ile Ala Thr Leu Glu Asp Glu Ala Gln
 100 105 110
 Glu Asn Lys Ser Lys Met Lys Met Val Glu Glu His Met Glu Gln Gln
 115 120 125
 Lys Glu Asn Met Glu His Leu Lys Ser Leu Lys Ile Glu Ala Glu Asn
 130 135 140
 Lys Tyr Asp Ala Ile Lys Phe Lys Ile Asn Gln Leu Ser Glu Leu Ala
 145 150 155 160
 Asp Pro Leu Lys Asp Glu Leu Asn Leu Ala Asp Ser Glu Val Asp Asn
 165 170 175
 Gln Lys Arg Gly Lys Arg His Tyr Glu Lys Lys Gln Lys Glu His Leu
 180 185 190
 Asp Thr Leu Asn Lys Lys Lys Arg Glu Leu Asp Met Lys Glu Lys Glu
 195 200 205
 Leu Glu Glu Lys Met Ser Gln Ala Arg Gln Ile Cys Pro Glu Arg Ile

210	215	220
Glu Val Glu Lys Ser Ala Ser Ile Leu Asp Lys Glu Ile Asn Arg Leu		
225	230	235
Arg Gln Lys Ile Gln Ala Glu His Ala Ser His Gly Asp Arg Glu Glu		240
	245	250
Ile Met Arg Gln Tyr Gln Glu Ala Arg Glu Thr Tyr Leu Asp Leu Asp		255
	260	265
Ser Lys Val Arg Thr Leu Lys Lys Phe Ile Lys Leu Leu Gly Glu Ile		270
	275	280
Met Glu His Arg Phe Lys Thr Tyr Gln Gln Phe Arg Arg Cys Leu Thr		285
	290	295
Leu Arg Cys Lys Leu Tyr Phe Asp Asn Leu Leu Ser Gln Arg Ala Tyr		300
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Cys Gly Lys Met Asn Phe Asp His Lys Asn Glu Thr Leu Ser Ile Ser		315
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Val Gln Pro Gly Glu		335
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<210> 3661

<211> 1117

<212> DNA

<213> Homo sapiens

<400> 3661

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 180
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 300
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 360
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 420
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 480
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 540
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 600
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 660
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 900

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 960
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 1020
 ttcaagcctc catttgcctgt ttttttactg atggaaagtc tatgatcgat ggcgatggaaa
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 1117

<210> 3662

<211> 371

<212> PRT

<213> Homo sapiens

<400> 3662

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			20				25						30		
Pro	Ser	Val	Tyr	Pro	Tyr	Lys	Leu	Tyr	Arg	Leu	Leu	Pro	Met	Lys	Cys
		35					40					45			
Lys	Arg	Ala	Pro	Tyr	Lys	Ser	Tyr	Arg	Asn	Ser	Ser	Tyr	Glu	Asn	Ala
	50					55					60				
Arg	Glu	Asn	Ser	Gln	Met	Asn	Glu	Ser	Ala	Pro	Gly	Thr	Tyr	Val	Val
	65				70				75					80	
Gln	Asn	Pro	His	Ser	Ser	Glu	Leu	Pro	Thr	Leu	Asn	Phe	Gln	Asp	Thr
			85						90					95	
Val	Asn	Thr	Leu	Thr	Asn	Ser	Pro	Ala	Ile	Pro	Leu	Glu	Thr	Ser	Ala
			100					105					110		
Cys	Gln	Asp	Ile	Pro	Thr	Ser	Ala	Asn	Val	Gln	Asn	Ala	Glu	Gly	Thr
		115				120						125			
Lys	Trp	Gly	Glu	Glu	Ala	Leu	Lys	Met	Asp	Leu	Asp	Asn	Asn	Phe	Tyr
	130					135					140				
Ser	Thr	Glu	Val	Ser	Val	Ser	Ser	Thr	Glu	Asn	Ala	Val	Ser	Ser	Asp
	145				150				155						160
Leu	Arg	Ala	Gly	Asp	Val	Pro	Val	Leu	Ser	Leu	Ser	Asn	Ser	Ser	Glu
			165					170						175	
Asn	Ala	Ala	Ser	Val	Ile	Ser	Tyr	Ser	Gly	Ser	Ala	Pro	Ser	Val	Ile
		180						185					190		
Val	His	Ser	Ser	Gln	Phe	Ser	Ser	Val	Ile	Met	His	Ser	Asn	Ala	Ile
		195					200					205			
Ala	Ala	Met	Thr	Ser	Ser	Asn	His	Arg	Ala	Phe	Ser	Asp	Pro	Ala	Val
	210					215						220			
Ser	Gln	Ser	Leu	Lys	Asp	Asp	Ser	Lys	Pro	Glu	Pro	Asp	Lys	Val	Gly
	225				230					235				240	
Arg	Phe	Ala	Ser	Arg	Pro	Lys	Ser	Ile	Lys	Glu	Lys	Lys	Lys	Thr	Thr
			245						250					255	
Ser	His	Thr	Arg	Gly	Glu	Ile	Pro	Glu	Glu	Ser	Asn	Tyr	Val	Ala	Asp
		260				265							270		
Pro	Gly	Gly	Ser	Leu	Ser	Lys	Thr	Thr	Asn	Ile	Ala	Glu	Glu	Thr	Ser
		275					280						285		
Lys	Ile	Glu	Thr	Tyr	Ile	Ala	Lys	Pro	Ala	Leu	Pro	Gly	Thr	Ser	Thr
	290					295					300				
Asn	Ser	Asn	Val	Ala	Pro	Leu	Cys	Gln	Ile	Thr	Val	Lys	Ile	Gly	Asn

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305              310              315              320
Glu Ala Ile Val Lys Arg His Ile Leu Gly Ser Lys Leu Phe Tyr Lys
              325              330              335
Arg Gly Arg Arg Pro Lys Tyr Gln Met Gln Glu Glu Leu Leu Pro Gln
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Gly Asn Asp Pro Glu Pro Ser Gly Asp Ser Pro Leu Gly Leu Cys Gln
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Ser Glu Cys
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<210> 3663
<211> 481
<212> DNA
<213> Homo sapiens

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<400> 3663
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481

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<210> 3664
<211> 138
<212> PRT
<213> Homo sapiens

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<400> 3664
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20     25     30
Met Ser Asp Asn Val Asp Arg Cys Phe Glu Thr Cys Pro Pro Arg Thr
35     40     45
Phe Leu Pro Ala Leu Tyr Lys Ile Phe Leu Asp Glu Ser Ala Pro Asp
50     55     60
Asn Val Leu Glu Val Thr Ala Arg Ala Ile Thr Tyr Tyr Leu Asp Val
65     70     75     80
Ser Ala Glu Cys Thr Arg Arg Ile Val Gly Val Asp Gly Ala Ile Lys
85     90     95
Ala Leu Cys Asn Arg Leu Val Val Val Glu Leu Asn Asn Arg Thr Ser

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	100		105		110										
Arg	Asp	Leu	Ala	Glu	Gln	Cys	Val	Lys	Val	Ser	Ile	Thr	Tyr	Trp	Leu
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Ile	Thr	Tyr	Phe	Ser	Gln	Thr	Ser	Gln	Gly						
	130						135								

<210> 3665

<211> 6633

<212> DNA

<213> Homo sapiens

<400> 3665

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180
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1260

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cagctagtgg catgtctccc agatgtggta cttcaggaac tctttttcaa actcacatca
720
cagtatcatc ggagattgtc taagaggcag cctcctgaca ccacaccatt gcgaacatcg
780
gaggatctga taaatgcctg tagtcattat ggcttaattt atccatgggt tcacgtcgta
840

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atatcatctg attcttttagc tgataaaaaa tatacagaag atcttttcaa attacagtct
 900
 cttatatgtg gtccttcatt tgacatagct tccattattc cgttcttgga gccactttca
 960
 gaagacacta ttgccggcct cagtgtccat gttctgtgtc gtacacgctt gaaagagtat
 1020
 gaacagtgtca tagacatact gtttagagaga tgcccggagg cagtcattcc atatgtcta
 1080
 catgaactga aagaagagaa ccggactctg tgggtgaaaa aactgttgcc tgaactttgt
 1140
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 1200
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 1226

<210> 3670

<211> 385

<212> PRT

<213> Homo sapiens

<400> 3670

Met	Ser	Gly	Leu	Ser	Met	Ala	Glu	Val	Leu	Ala	Arg	Thr	Asp	Trp	Thr
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Val	Glu	Asp	Gly	Leu	Gln	Lys	Tyr	Glu	Arg	Gly	Leu	Ile	Phe	Tyr	Ile
		20						25				30			
Asn	His	Ser	Leu	Tyr	Glu	Asn	Leu	Asp	Glu	Glu	Leu	Asn	Glu	Glu	Leu
		35				40					45				
Ala	Ala	Lys	Val	Val	Gln	Met	Phe	Tyr	Val	Ala	Glu	Pro	Lys	Gln	Val
	50				55					60					
Pro	His	Ile	Leu	Cys	Ser	Pro	Ser	Met	Lys	Asn	Ile	Asn	Pro	Leu	Thr
65				70				75					80		
Ala	Met	Ser	Tyr	Leu	Arg	Lys	Met	Asp	Thr	Ser	Gly	Phe	Ser	Ser	Ile
			85					90					95		
Leu	Val	Thr	Leu	Ser	Lys	Ala	Ala	Val	Ala	Leu	Lys	Met	Gly	Asp	Leu
		100						105					110		
Asp	Val	Tyr	Arg	Asn	Glu	Met	Lys	Ser	His	Pro	Glu	Met	Lys	Leu	Val
		115				120						125			
Cys	Gly	Phe	Ile	Leu	Glu	Pro	Arg	Leu	Leu	Ile	Gln	His	Arg	Lys	Gly
	130					135				140					
Gln	Ile	Val	Pro	Thr	Glu	Leu	Ala	Thr	His	Leu	Lys	Glu	Thr	Gln	Pro
145				150						155				160	
Gly	Leu	Leu	Val	Ala	Ser	Val	Leu	Gly	Leu	Gln	Lys	Asn	Ser	Lys	Ile
			165					170						175	
Gly	Ile	Glu	Glu	Ala	Asp	Ser	Phe	Phe	Lys	Val	Leu	Cys	Gly	Lys	Asp
		180						185					190		
Glu	Asp	Thr	Ile	Pro	Gln	Leu	Leu	Ile	Asp	Phe	Trp	Glu	Ala	Gln	Leu
		195					200					205			
Val	Ala	Cys	Leu	Pro	Asp	Val	Val	Leu	Gln	Glu	Leu	Phe	Phe	Lys	Leu
	210					215				220					
Thr	Ser	Gln	Tyr	Ile	Trp	Arg	Leu	Ser	Lys	Arg	Gln	Pro	Pro	Asp	Thr
225				230						235				240	
Thr	Pro	Leu	Arg	Thr	Ser	Glu	Asp	Leu	Ile	Asn	Ala	Cys	Ser	His	Tyr
			245					250						255	
Gly	Leu	Ile	Tyr	Pro	Trp	Val	His	Val	Val	Ile	Ser	Ser	Asp	Ser	Leu

	260		265		270
Ala	Asp Lys Asn Tyr Thr Glu Asp Leu Ser Lys Leu Gln Ser Leu Ile				
	275		280		285
Cys	Gly Pro Ser Phe Asp Ile Ala Ser Ile Ile Pro Phe Leu Glu Pro				
	290		295		300
Leu	Ser Glu Asp Thr Ile Ala Gly Leu Ser Val His Val Leu Cys Arg				
	305		310		315
Thr	Arg Leu Lys Glu Tyr Glu Gln Cys Ile Asp Ile Leu Leu Glu Arg				
		325		330	335
Cys	Pro Glu Ala Val Ile Pro Tyr Ala Asn His Glu Leu Lys Glu Glu				
		340		345	350
Asn	Arg Thr Leu Trp Trp Lys Lys Leu Leu Pro Glu Leu Cys Gln Arg				
		355		360	365
Ile	Lys Cys Gly Gly Glu Lys Tyr Gln Leu Tyr Leu Ser Ser Leu Lys				
	370		375		380

Ala
385

<210> 3671

<211> 828

<212> DNA

<213> Homo sapiens

<400> 3671

nntacagcta agattcattt catacgtttg atgcttagct gaaaaattac aataaattct
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120
agggcatctg gggtaagtaa aaacaaacac atagagcctg cctggagaag ctcatggtct
180
gatggaaaga taagcaagaa gagttaattt ctaatcaata tgataaaaag gtcagagagc
240
agtttctgaa aaacatgttt ttgagttgag tcttgaaaga caaggagatg ttagtaaagc
300
agagaagggg gaattcattc tagaaagatc agacaatgtg tgggaagggc agagtctgaa
360
aagagcatgc cccatttgga gaagcatcaa gaagccacg cgttagaagc accggcccca
420
tgagacaaag acacagctag agagattgac taggccatgt cggaatgtcc tcttatttta
480
tacatacata agcatataga tacatatagc caaagttacc tttttaatga tcttttttac
540
ccagtgtatt ctggaggctg aatgggcaca tatgaacatc tccgagaggt tgtgtttggc
600
aaaagtgaag atgagcatta tcccctttgg aaatcagtca ttggagggat gatggctggt
660
gttatttggc agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa
720
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca tgcatttgca
780
aaaatcttag ctgaaggagg aatacgaggg ctttgggcag gctgggta
828

<210> 3672

<211> 124
 <212> PRT
 <213> Homo sapiens

<400> 3672
 Met Ser Glu Cys Pro Leu Ile Leu Tyr Ile His Lys His Ile Asp Thr
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 Tyr Ser Gln Ser Tyr Leu Phe Asn Asp Leu Phe Tyr Pro Val Tyr Ser
 20 25 30
 Gly Gly Arg Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly
 35 40 45
 Lys Ser Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly
 50 55 60
 Met Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 65 70 75 80
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly Lys
 85 90 95
 Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile Leu Ala
 100 105 110
 Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val
 115 120

<210> 3673
 <211> 1052
 <212> DNA
 <213> Homo sapiens

<400> 3673
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 60
 gttcattctg ggagcgctgc tgggtggcat tattatgcat gtataaaagtc attcagtgat
 120
 gagcagtggt acagcttcaa tgatcaacat gtcagcagga taacacaaga ggacattaag
 180
 aaaacacatg gtggatcttc aggaagcaga ggatattatt ctatgtcttt cgcaagttcc
 240
 acaaatgcat atatgctgat ctatagactg aaggatccag ccagaaatgc aaaatttcta
 300
 gaagtggatg aataccaga acatattaaa aacttggtgc agaagagag agagttggaa
 360
 gaacaagaaa agagacaacg agaaattgag cgcaatacat gcaagataaa attattctgt
 420
 ttgcatccta caaaacaagt aatgatggaa aataaattgg aggttcataa ggataagaca
 480
 ttaaaggaag cagtagaaat ggcttataag atgatggatt tagaagaggt aataccctgt
 540
 gattgctgtc gccttgtaa atatgatgag ttatcatgatt atctagaacg gtcatatgaa
 600
 ggagaagaag atacaccaat ggggcttcta ctagggtggcg tcaagtcaac atatatgttt
 660
 gatctgtgtg tggagacgag aaagcctgat caggttttcc aatcttataa acctggaggg
 720
 gagccatttt acaccatttt tagttggctt gtacttagaa ttttctctgag aaagggtttt
 780

tttttattgt agcaatgaac ataatttaca ttttgtatat ggtcttaca tgtagaataa
 840
 ttttgacagg ttgagaagta ctcagcacca gcttgggaatt aagttctaga ttacttgcaa
 900
 agagttgtgt acataatttt aaaaacaaca aaaaacaaca aagttcttag cttacgggtct
 960
 tcagtggggtt ttttctctc cagtgggcggt tactgaatca ttctggatgc tgtcaatccc
 1020
 taaagttatc aattgctctc ttaggaagat ct
 1052

<210> 3674

<211> 263

<212> PRT

<213> Homo sapiens

<400> 3674

Xaa	Ile	Ser	Lys	Ser	Gly	Leu	Glu	Lys	Asn	Ser	Leu	Ile	Tyr	Glu	Leu
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Phe	Ser	Val	Met	Val	His	Ser	Gly	Ser	Ala	Ala	Gly	Gly	His	Tyr	Tyr
			20					25					30		
Ala	Cys	Ile	Lys	Ser	Phe	Ser	Asp	Glu	Gln	Trp	Tyr	Ser	Phe	Asn	Asp
			35				40					45			
Gln	His	Val	Ser	Arg	Ile	Thr	Gln	Glu	Asp	Ile	Lys	Lys	Thr	His	Gly
	50					55					60				
Gly	Ser	Ser	Gly	Ser	Arg	Gly	Tyr	Tyr	Ser	Ser	Ala	Phe	Ala	Ser	Ser
65				70						75				80	
Thr	Asn	Ala	Tyr	Met	Leu	Ile	Tyr	Arg	Leu	Lys	Asp	Pro	Ala	Arg	Asn
				85					90					95	
Ala	Lys	Phe	Leu	Glu	Val	Asp	Glu	Tyr	Pro	Glu	His	Ile	Lys	Asn	Leu
			100					105					110		
Val	Gln	Lys	Glu	Arg	Glu	Leu	Glu	Gln	Glu	Lys	Arg	Gln	Arg	Glu	
		115				120					125				
Ile	Glu	Arg	Asn	Thr	Cys	Lys	Ile	Lys	Leu	Phe	Cys	Leu	His	Pro	Thr
	130				135					140					
Lys	Gln	Val	Met	Met	Glu	Asn	Lys	Leu	Glu	Val	His	Lys	Asp	Lys	Thr
145				150						155				160	
Leu	Lys	Glu	Ala	Val	Glu	Met	Ala	Tyr	Lys	Met	Met	Asp	Leu	Glu	Glu
			165					170					175		
Val	Ile	Pro	Leu	Asp	Cys	Cys	Arg	Leu	Val	Lys	Tyr	Asp	Glu	Phe	His
			180					185					190		
Asp	Tyr	Leu	Glu	Arg	Ser	Tyr	Glu	Gly	Glu	Glu	Asp	Thr	Pro	Met	Gly
		195					200					205			
Leu	Leu	Leu	Gly	Gly	Val	Lys	Ser	Thr	Tyr	Met	Phe	Asp	Leu	Leu	Leu
	210					215						220			
Glu	Thr	Arg	Lys	Pro	Asp	Gln	Val	Phe	Gln	Ser	Tyr	Lys	Pro	Gly	Gly
225				230						235				240	
Glu	Pro	Phe	Tyr	Thr	Ile	Phe	Ser	Trp	Ser	Val	Leu	Arg	Ile	Phe	Leu
				245					250					255	
Arg	Lys	Val	Phe	Phe	Leu	Leu									
				260											

<210> 3675

<211> 837

<212> DNA

<213> Homo sapiens

<400> 3675

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nntccggaga tgtgaagaag gggggcgagc ggacaggaag atgaagggaag caaagctgcc
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cgccgcggga caggcgtcta ggtgaacaag aaaatgaccg aagaacaca cccagacgat
120
gacagctata ttgtgcgtgt caaggctgtg gttatgacca gagatgactc cagcggggga
180
tggttccac aggaaggagg cgggatcagt cgcgtcgggg tctgtaaggt catgcacccc
240
gaaggcaatg gacgaagcgg ctttctcatc catggtgaac gacagaaaga caaactgggtg
300
gtattggaat gctatgtaag aaaggacttg gtctacacca aagccaatcc aacgtttcat
360
cactggaagg tcgataatag gaagtttga cttactttcc aaagccctgc tgatgccgga
420
gcctttgaca ggggagtaag gaaagcaatc gaagacctta tagaagaagt agaaaatgat
480
tctggcgggc ccagaagcct cctggcctac ccactgtcct cctgtaatca gaggccagg
540
gtgtacagct gccactgaaa aggaaggga tctgtgacct ctggagccct gggttcggttt
600
aggccttggt ctatgggtaa gtgagtagta ggcattgtgt tacatctgat cgtggcctgg
660
agggcccttg ggcagtcagt tctcatggtg ggcttgacta gagtccacag atgcaaacac
720
aaaaattctc cactgcagca catccaggta tcaaatcaga ggggttaaaga agccatagac
780
agggcccttg gaagaagaa atatcaagca aggcattgta ataccaaatt cagatct
837

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<210> 3676

<211> 154

<212> PRT

<213> Homo sapiens

<400> 3676

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Met Thr Glu Glu Thr His Pro Asp Asp Asp Ser Tyr Ile Val Arg Val
1          5          10          15
Lys Ala Val Val Met Thr Arg Asp Asp Ser Ser Gly Gly Trp Phe Pro
20          25          30
Gln Glu Gly Gly Ile Ser Arg Val Gly Val Cys Lys Val Met His
35          40          45
Pro Glu Gly Asn Gly Arg Ser Gly Phe Leu Ile His Gly Glu Arg Gln
50          55          60
Lys Asp Lys Leu Val Val Leu Glu Cys Tyr Val Arg Lys Asp Leu Val
65          70          75          80
Tyr Thr Lys Ala Asn Pro Thr Phe His His Trp Lys Val Asp Asn Arg
85          90          95
Lys Phe Gly Leu Thr Phe Gln Ser Pro Ala Asp Ala Arg Ala Phe Asp
100         105         110
Arg Gly Val Arg Lys Ala Ile Glu Asp Leu Ile Glu Glu Val Glu Asn

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      115              120              125
Asp Ser Gly Gly Pro Arg Arg Leu Leu Ala Tyr Pro Leu Ser Ser Cys
    130              135              140
Asn Gln Arg Pro Arg Val Tyr Ser Cys His
    145              150

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<210> 3677
<211> 418
<212> DNA
<213> Homo sapiens

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<400> 3677
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ttcatgccaag agctcgtaaa gaatctccta ggcgagatgc ctctgtgggt ctgccagagt
120
tgccgaagaag gcattggagga agatgaaagg cagacaggtc gagaacatgc agtggcgatc
180
tccttgctac acacatcctg caaatcacag tcttgaggag atgactctca ttcgtcctcg
240
tcttctctct catcctctc atcctcgtcc tctcttctct gccctgggaa ctccggagagc
300
tgggatccta gctcgtctct gtcggcacat aagctctcgg gcctctggaa ttcccacat
360
tccagtgggg ccattgccagg cagctctctt gggagtcctc ctaccatccc tggcgcgcc
418

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<210> 3678
<211> 139
<212> PRT
<213> Homo sapiens

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<400> 3678
Xaa Glu Glu Gly Pro Ser Gln Asn Gly Leu Val Leu Gln Gly Glu Lys
 1          5              10              15
Leu Pro Pro Asp Phe Met Pro Lys Leu Val Lys Asn Leu Leu Gly Glu
    20          25          30
Met Pro Leu Trp Val Cys Gln Ser Cys Arg Lys Ser Met Glu Glu Asp
    35          40          45
Glu Arg Gln Thr Gly Arg Glu His Ala Val Ala Ile Ser Leu Ser His
    50          55          60
Thr Ser Cys Lys Ser Gln Ser Cys Gly Asp Asp Ser His Ser Ser Ser
    65          70          75          80
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Pro Gly
    85          90          95
Asn Ser Gly Asp Trp Asp Pro Ser Ser Phe Leu Ser Ala His Lys Leu
    100          105          110
Ser Gly Leu Trp Asn Ser Pro His Ser Ser Gly Ala Met Pro Gly Ser
    115          120          125
Ser Leu Gly Ser Pro Pro Thr Ile Pro Gly Ala
    130          135

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```

<210> 3679
<211> 567

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<212> DNA

<213> Homo sapiens

<400> 3679

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 cgccctcaggc agctgctccc catgcttctt cagggaacaa gtatcttcac tggccctaag
 120
 gagatcgagc agatcaaggc ccagctggag acagccctga agtgaggagaa ctatgagggtg
 180
 aagctgcggc tgctgctgca cctggaggaa ctgcagatgg agcatgatat cgggcactat
 240
 gacctggagt cggtgcccat gacctgggac cctgtggacc agaaccccag gctgctcacg
 300
 ctggagggttc ctggagtgac tgagagccgc ccctcagtgc tacggggcga ccacctgttt
 360
 gcccttttgt cctcgagac acaccaggag gaccccatca catataagggt ctttgtgac
 420
 aaggtggaat tggaccgtgt caagctgagc ttttccatga gcctcctgag cgcctttgtg
 480
 gatgggctga ccttcaagggt gaactttacc ttcaaccgcc agccgctgag agtccagcac
 540
 cgtgcctggg agttgacagg gcgctgg
 567

<210> 3680

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3680

Arg	Val	Lys	Gly	Tyr	Asp	Leu	Glu	Leu	Ser	Met	Ala	Leu	Gly	Thr	Tyr
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Tyr	Pro	Pro	Pro	Arg	Leu	Arg	Gln	Leu	Pro	Met	Leu	Leu	Gln	Gly	
			20				25					30			
Thr	Ser	Ile	Phe	Thr	Ala	Pro	Lys	Glu	Ile	Ala	Glu	Ile	Lys	Ala	Gln
		35					40					45			
Leu	Glu	Thr	Ala	Leu	Lys	Trp	Arg	Asn	Tyr	Glu	Val	Lys	Leu	Arg	Leu
	50				55					60					
Leu	Leu	His	Leu	Glu	Glu	Leu	Gln	Met	Glu	His	Asp	Ile	Arg	His	Tyr
	65			70					75					80	
Asp	Leu	Glu	Ser	Val	Pro	Met	Thr	Trp	Asp	Pro	Val	Asp	Gln	Asn	Pro
			85					90						95	
Arg	Leu	Leu	Thr	Leu	Glu	Val	Pro	Gly	Val	Thr	Glu	Ser	Arg	Pro	Ser
		100						105					110		
Val	Leu	Arg	Gly	Asp	His	Leu	Phe	Ala	Leu	Leu	Ser	Ser	Glu	Thr	His
		115				120						125			
Gln	Glu	Asp	Pro	Ile	Thr	Tyr	Lys	Gly	Phe	Val	His	Lys	Val	Glu	Leu
	130				135					140					
Asp	Arg	Val	Lys	Leu	Ser	Phe	Ser	Met	Ser	Leu	Leu	Ser	Arg	Phe	Val
	145			150						155				160	
Asp	Gly	Leu	Thr	Phe	Lys	Val	Asn	Phe	Thr	Phe	Asn	Arg	Gln	Pro	Leu
				165				170						175	
Arg	Val	Gln	His	Arg	Ala	Trp	Glu	Leu	Thr	Gly	Arg	Trp			

180

185

<210> 3681
 <211> 788
 <212> DNA
 <213> Homo sapiens

<400> 3681
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 ccccgccctcc acttccttcg gatgaggccc tgctgcactg tgcctggaa ggaaagctcc
 120
 gagaccggga ggagagcctt cagcagctgc gggacagcct ggggctgagc atggagcagc
 180
 gcggcggagg tcgcctgcga ggcgcctggc caggcctgag cctctgccac catggccatt
 240
 gtgcagactc tgccagtgc actggagcct gctcctgaag ctgccactgc cccacaagct
 300
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 360
 cctccccgcc accacggccc tcctggggccc acctctctcc gccagcagga tggcctgcta
 420
 cggggtggct atgaggcaca ggagccgctg tgcccagctg tgccccctag gaaggctgtc
 480
 cctgtcacca gcttcaccta catcaatgag gacttccgga cagagtcacc cccagccca
 540
 agcagtgatg ttgaggatgc ccgagagcag cgggcacaca atgcccacct ccgcggccca
 600
 ccaccaaaag tcattccctgt ctctggaaag ctggagaaga acatagagaa gatcctgatc
 660
 cgcccaacag ccttcaagcc agtgctgccc aaacctcgag gggctccgct cctgectagc
 720
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 780
 gggggccc
 788

<210> 3682
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 3682
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 Ala Ala Thr Ala Pro Gln Ala Pro Val Met Gly Ser Val Ser Ser Leu
 20 25 30
 Ile Ser Gly Arg Pro Cys Pro Gly Gly Pro Ala Pro Pro Arg His His
 35 40 45
 Gly Pro Pro Gly Pro Thr Phe Phe Arg Gln Gln Asp Gly Leu Leu Arg
 50 55 60
 Gly Gly Tyr Glu Ala Gln Glu Pro Leu Cys Pro Ala Val Pro Pro Arg
 65 70 75 80
 Lys Ala Val Pro Val Thr Ser Phe Thr Tyr Ile Asn Glu Asp Phe Arg

85						90						95					
Thr	Glu	Ser	Pro	Pro	Ser	Pro	Ser	Ser	Asp	Val	Glu	Asp	Ala	Arg	Glu		
100						105						110					
Gln	Arg	Ala	His	Asn	Ala	His	Leu	Arg	Gly	Pro	Pro	Pro	Lys	Leu	Ile		
115						120						125					
Pro	Val	Ser	Gly	Lys	Leu	Glu	Lys	Asn	Ile	Glu	Lys	Ile	Leu	Ile	Arg		
130						135						140					
Pro	Thr	Ala	Phe	Lys	Pro	Val	Leu	Pro	Lys	Pro	Arg	Gly	Ala	Pro	Ser		
145						150						155					
Leu	Pro	Ser	Phe	Met	Gly	Pro	Arg	Ala	Thr	Gly	Leu	Ser	Gly	Ser	Gln		
165						170						175					
Gly	Ser	Leu	Thr	Gln	Leu	Phe	Gly	Gly									
180						185											

<210> 3683

<211> 4421

<212> DNA

<213> Homo sapiens

<400> 3683

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120	cgagggtgaa	gcccgccggc	ccgcgaactg	gactggtgga	tctctcacag	ctggggccccc
180	ggaactccgat	ctccgcgcgc	tccgccacca	tcaggggcggy	atccggctct	ggtgttttgat
240	ggaggggggtg	tgggtgtagg	aaaggaatcc	cgctccctctc	cacctttttt	cgctcttcggg
300	gcttcagact	cagggaactc	gctcatggct	ttcttgtatg	agaagaagaa	attcaaatctc
360	caaaactactt	tcaccttgga	ggagctgact	cggttccctc	tcgtgaaccg	ggctcctcttc
420	tgcgaagtccc	ggctgctgga	tggaggggat	tttgtcagct	tgtcgtcaag	ggaggaggta
480	cagggaactc	gtgtgcgggt	gcgaaaagag	ttcaccttcg	tgtgtaagat	gagtgtcaac
540	ccggccaccg	gcctgctgga	cccctgtgtc	ttccgtgtgt	ctgtgcgcaa	ggagctgaaa
600	ggcgggaagg	cttatctcaa	gctgggcttc	gctgacttga	acctggccga	gtttgcgggc
660	tcgggctcca	cggtgcgcgt	ctgcctgtct	gagggatatg	acacgaagaa	cactcgccag
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<210> 3684

<211> 384

<212> PRT

<213> Homo sapiens

<400> 3684

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Thr	Leu	Glu	Glu	Leu	Thr	Ala	Val	Pro	Phe	Val	Asn	Gly	Val	Leu	Phe
			20					25					30		
Cys	Lys	Val	Arg	Leu	Leu	Asp	Gly	Gly	Asp	Phe	Val	Ser	Leu	Ser	Ser
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Arg	Glu	Glu	Val	Gln	Glu	Asn	Cys	Val	Arg	Trp	Arg	Lys	Arg	Phe	Thr
		50				55					60				
Phe	Val	Cys	Lys	Met	Ser	Ala	Asn	Pro	Ala	Thr	Gly	Leu	Leu	Asp	Pro
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Cys	Val	Phe	Arg	Val	Ser	Val	Arg	Lys	Glu	Leu	Lys	Gly	Gly	Lys	Ala
			85					90						95	
Tyr	Ser	Lys	Leu	Gly	Phe	Ala	Asp	Leu	Asn	Leu	Ala	Glu	Phe	Ala	Gly
			100				105						110		
Ser	Gly	Ser	Thr	Val	Arg	Cys	Cys	Leu	Leu	Glu	Gly	Tyr	Asp	Thr	Lys
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Asn	Thr	Arg	Gln	Asp	Asn	Ser	Ile	Leu	Lys	Val	Thr	Ile	Gly	Met	Phe
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Leu	Leu	Ser	Gly	Asp	Pro	Cys	Phe	Lys	Thr	Pro	Pro	Ser	Thr	Ala	Lys
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			165					170						175	
Gly	Gly	Gly	Thr	Ser	Ser	Gly	Gly	Ser	Ser	Thr	Asn	Ser	Leu	Thr	Gly
		180					185					190			
Ser	Arg	Pro	Pro	Lys	Ala	Arg	Pro	Thr	Ile	Leu	Ser	Ser	Gly	Leu	Pro
		195					200					205			
Glu	Glu	Pro	Asp	Gln	Asn	Leu	Ser	Ser	Pro	Glu	Glu	Val	Phe	His	Ser
		210				215					220				
Gly	His	Ser	Arg	Asn	Ser	Ser	Tyr	Ala	Ser	Gln	Gln	Ser	Lys	Ile	Ser
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Gly	Tyr	Ser	Thr	Glu	His	Ser	His	Ser	Ser	Ser	Leu	Ser	Asp	Leu	Thr
			245						250					255	
His	Arg	Arg	Asn	Thr	Ser	Thr	Ser	Ser	Ser	Ala	Ser	Gly	Gly	Leu	Gly
			260				265						270		
Met	Thr	Val	Glu	Gly	Pro	Glu	Gly	Ser	Glu	Arg	Glu	His	Arg	Pro	Pro
		275					280						285		
Glu	Lys	Pro	Pro	Arg	Pro	Pro	Arg	Pro	Leu	His	Leu	Ser	Asp	Arg	Ser
		290				295					300				
Phe	Arg	Arg	Lys	Lys	Asp	Ser	Val	Glu	Ser	His	Pro	Thr	Trp	Val	Asp
305				310					315					320	
Asp	Thr	Arg	Ile	Asp	Ala	Asp	Ala	Ile	Val	Glu	Lys	Ile	Val	Gln	Ser

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 1293

<210> 3686
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 3686
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 Pro Val Cys Cys Glu Thr Asp His Arg Pro Ala Gln Arg Ser Pro Arg
 35 40 45
 Arg Val Pro Cys Leu Cys Pro Pro Arg Arg Arg His Pro Pro Arg Ser
 50 55 60
 Phe Thr Ser Cys Thr Phe Ser Gly Ser Arg Ser His Ile His Pro Thr
 65 70 75 80
 Trp Arg Ser Pro His Asp Val Pro Gly Ser Val Leu Ala Pro Ala Ala
 85 90 95
 Ala Leu Gly Asn Arg Ile Gly Lys Arg Ser Pro Arg Val Asp Ala
 100 105 110

<210> 3687
 <211> 566
 <212> DNA
 <213> Homo sapiens

<400> 3687
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 360
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<210> 3688

<211> 57
 <212> PRT
 <213> Homo sapiens

<400> 3688
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 Glu Tyr Pro Pro Gly Leu Leu Val Ala Val His Leu Phe Ala Leu Met
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 Xaa Leu His Val Ser Ala Ala Pro His
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<210> 3689
 <211> 1562
 <212> DNA
 <213> Homo sapiens

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<210> 3690

<211> 504

<212> PRT

<213> Homo sapiens

<400> 3690

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			20					25					30		
Thr	Asp	Glu	Ala	Glu	Lys	Arg	Ser	Arg	Lys	Pro	Glu	Lys	Glu	Pro	Arg
		35				40						45			
Arg	Ser	Gly	Arg	Ala	Thr	Asn	His	Asp	Ser	Cys	Asp	Ser	Cys	Lys	Glu
		50				55					60				
Gly	Gly	Asp	Leu	Leu	Cys	Cys	Asp	His	Cys	Pro	Ala	Ala	Phe	His	Leu
65					70				75					80	
Gln	Cys	Cys	Asn	Pro	Pro	Leu	Ser	Glu	Glu	Met	Leu	Pro	Pro	Gly	Glu
			85						90					95	
Trp	Met	Cys	His	Arg	Cys	Thr	Val	Arg	Arg	Lys	Lys	Arg	Glu	Gln	Lys
			100					105					110		
Lys	Glu	Leu	Gly	His	Val	Asn	Gly	Leu	Val	Asp	Lys	Ser	Gly	Lys	Arg
		115				120						125			
Thr	Thr	Ser	Pro	Ser	Ser	Asp	Thr	Asp	Leu	Leu	Asp	Arg	Ser	Ala	Ser
		130				135						140			
Lys	Thr	Glu	Leu	Lys	Ala	Ile	Ala	His	Ala	Arg	Ile	Leu	Glu	Arg	Arg
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Ala	Ser	Arg	Pro	Gly	Thr	Pro	Thr	Ser	Ser	Ala	Ser	Thr	Glu	Thr	Pro
			165					170					175		
Thr	Ser	Glu	Gln	Asn	Asp	Val	Asp	Glu	Asp	Ile	Ile	Asp	Val	Asp	Glu
		180						185					190		
Glu	Pro	Val	Ala	Ala	Glu	Pro	Asp	Tyr	Val	Gln	Pro	Gln	Leu	Arg	Arg
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Pro	Phe	Glu	Leu	Leu	Ile	Ala	Ala	Ala	Met	Glu	Arg	Asn	Pro	Thr	Gln

210 215 220
 Phe Gln Leu Pro Asn Glu Leu Thr Cys Thr Thr Ala Leu Pro Gly Ser
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 Ser Lys Arg Arg Arg Lys Glu Glu Thr Thr Gly Lys Asn Val Lys Lys
 245 250 255
 Thr Gln His Glu Leu Asp His Asn Gly Leu Val Pro Leu Pro Val Lys
 260 265 270
 Val Cys Phe Thr Cys Asn Arg Ser Cys Arg Val Ala Pro Leu Ile Gln
 275 280 285
 Cys Asp Tyr Cys Pro Leu Leu Phe His Met Asp Cys Leu Glu Pro Pro
 290 295 300
 Leu Thr Ala Met Pro Leu Gly Arg Trp Met Cys Pro Asn His Ile Glu
 305 310 315 320
 His Val Val Leu Asn Gln Lys Asn Met Thr Leu Ser Asn Arg Cys Gln
 325 330 335
 Val Phe Asp Arg Phe Gln Asp Thr Val Ser Gln His Val Val Lys Val
 340 345 350
 Asp Phe Leu Asn Arg Ile His Lys Lys His Pro Pro Asn Arg Arg Val
 355 360 365
 Leu Gln Ser Val Lys Arg Arg Ser Leu Lys Val Pro Asp Ala Ile Lys
 370 375 380
 Ser Gln Tyr Gln Phe Pro Pro Pro Leu Ile Ala Pro Ala Ala Ile Arg
 385 390 395 400
 Asp Gly Glu Leu Ile Cys Asn Gly Ile Pro Glu Glu Ser Gln Met His
 405 410 415
 Leu Leu Asn Ser Glu His Leu Ala Thr Gln Ala Glu Gln Gln Glu Trp
 420 425 430
 Leu Cys Ser Val Val Ala Leu Gln Cys Ser Ile Leu Lys His Leu Ser
 435 440 445
 Ala Lys Gln Met Pro Ser His Trp Asp Ser Glu Gln Thr Glu Lys Ala
 450 455 460
 Asp Ile Lys Pro Val Ile Val Thr Asp Ser Ser Val Thr Thr Ser Leu
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 Gln Thr Ala Asp Lys Thr Pro Thr Pro Ser His Tyr Pro Leu Ser Cys
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 Pro Ser Gly Ile Ser Thr Gln Asn
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<210> 3691

<211> 418

<212> DNA

<213> Homo sapiens

<400> 3691

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 300

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<210> 3692

<211> 94

<212> PRT

<213> Homo sapiens

<400> 3692

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			20					25					30		
Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Phe	Tyr	Val	Leu	Arg	Gln
		35					40					45			
Arg	Ile	Ala	Arg	Ile	Arg	Cys	Gln	Leu	Lys	Ala	Val	Cys	Gln	Pro	Arg
	50				55				60						
Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	Lys	Cys	His	Pro
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<210> 3693

<211> 2641

<212> DNA

<213> Homo sapiens

<400> 3693

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<210> 3694

<211> 390

<212> PRT

<213> Homo sapiens

<400> 3694

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 35 40 45
 Ala Val Phe Ala Gly Met Lys Arg Pro Cys Glu Glu Thr Thr Ser Glu
 50 55 60
 Ser Asp Met Asp Glu Thr Ile Asp Val Gly Ser Glu Asn Asn Tyr Ser
 65 70 75 80
 Gly Gln Ser Thr Ser Ser Val Ile Arg Leu Asn Ser Pro Thr Thr Thr
 85 90 95
 Ser Gln Ile Met Ala Arg Lys Lys Arg Arg Gly Ile Ile Glu Lys Arg
 100 105 110
 Arg Arg Asp Arg Ile Asn Asn Ser Leu Ser Glu Leu Arg Arg Leu Val
 115 120 125
 Pro Thr Ala Phe Glu Lys Gln Gly Ser Ala Lys Leu Glu Lys Ala Glu
 130 135 140
 Ile Leu Gln Met Thr Val Asp His Leu Lys Met Leu Gln Ala Thr Gly
 145 150 155 160
 Gly Lys Gly Tyr Phe Asp Ala His Ala Leu Ala Met Asp Phe Met Ser
 165 170 175
 Ile Gly Phe Arg Glu Cys Leu Thr Glu Val Ala Arg Tyr Leu Ser Ser
 180 185 190
 Val Glu Gly Leu Asp Ser Ser Asp Pro Leu Arg Val Arg Leu Val Ser
 195 200 205
 His Leu Ser Thr Cys Ala Thr Gln Arg Glu Ala Ala Ala Met Thr Ser
 210 215 220
 Ser Met Ala His His Xaa Ser Ser Ala Pro Pro Ala Ser Leu Gly Arg
 225 230 235 240
 Arg Leu Pro Pro Pro Ala Arg Ser Pro Ala Pro Ala Gln Arg Pro Pro
 245 250 255
 Cys Leu Arg Val Asn Pro Leu Ser Pro Leu His Asn Phe Arg Ser Ala
 260 265 270
 Ser Ala His Gly Ser Ala Leu Leu Thr Ala Thr Phe Ala His Ala Asp

	275		280		285										
Ser	Ala	Leu	Arg	Met	Pro	Ser	Thr	Gly	Ser	Val	Ala	Pro	Cys	Val	Pro
	290		295		300										
Pro	Leu	Ser	Thr	Ser	Leu	Leu	Ser	Leu	Ser	Ala	Thr	Val	His	Ala	Ala
	305		310		315									320	
Ala	Ala	Ala	Ala	Thr	Ala	Ala	Ala	His	Ser	Phe	Pro	Leu	Ser	Phe	Ala
			325						330					335	
Gly	Ala	Phe	Pro	Met	Leu	Pro	Pro	Asn	Ala	Ala	Ala	Val	Ala	Ala	
			340					345					350		
Ala	Thr	Ala	Ile	Ser	Pro	Pro	Leu	Ser	Val	Ser	Ala	Thr	Ser	Ser	Pro
			355					360					365		
Gln	Gln	Thr	Ser	Ser	Gly	Thr	Asn	Asn	Lys	Pro	Tyr	Arg	Pro	Trp	Gly
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<210> 3695

<211> 1615

<212> DNA

<213> Homo sapiens

<400> 3695

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<210> 3696

<211> 146

<212> PRT

<213> Homo sapiens

<400> 3696

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 20 25 30
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 35 40 45
 Cys Asn Ser Trp Ser Ser Pro Gln Leu Gln Ser Ser Leu Pro Glu Pro
 50 55 60
 His Asp Arg Pro Leu Ala Leu Pro Leu Ser Asp Ser Gln Ile Gln Trp
 65 70 75 80
 Phe Tyr Gln Ala Leu Asn Leu Ser Leu Pro Leu Pro Asn Phe His Ala
 85 90 95
 Gly Thr Glu Pro Asp Gly Leu Asp Pro Met Val Thr Leu Ser Leu Asn
 100 105 110
 Leu Gly Leu Ser Phe Ala Glu Leu Arg Arg Met Tyr Leu Phe Leu Asn
 115 120 125
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 Pro Ser
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<210> 3697

<211> 550

<212> DNA

<213> Homo sapiens

<400> 3697

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 180
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 420
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<210> 3698

<211> 183

<212> PRT

<213> Homo sapiens

<400> 3698

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Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	Trp	Gly	Trp
		20						25					30		
Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	Gln	Pro	Arg	Cys
		35				40						45			
Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	Lys	Cys	His	Pro	Gly
	50					55					60				
Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	Asn	Glu	Cys	Gly	Leu	Lys
	65				70					75				80	
Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	Asn	Thr	Tyr	Gly	Ser	Tyr	Lys
				85					90					95	
Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser
			100					105						110	
Ser	Ala	Leu	Thr	Cys	Ser	Met	Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val
		115					120					125			
Val	Lys	Gly	Gln	Ile	Arg	Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	Gln	Leu
		130				135					140				
Ala	Pro	Asp	Gly	Arg	Thr	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Gly
				150						155				160	
Arg	Ala	Ser	Cys	Pro	Lys	Phe	Arg	Gln	Cys	Val	Asn	Thr	Phe	Gly	Ser
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Tyr	Ile	Cys	Lys	Cys	His	Lys									
						180									

<210> 3699

<211> 510

<212> DNA

<213> Homo sapiens

<400> 3699

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 360
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<210> 3700

<211> 127

<212> PRT

<213> Homo sapiens

<400> 3700

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			20					25					30		
Ala	Val	Asn	Lys	Val	His	Ala	Phe	Gly	Lys	Arg	Gly	Asn	Ala	Leu	Arg
		35					40					45			
Arg	Asp	Pro	Asn	Leu	Pro	Val	His	Ile	Arg	Gly	Trp	Leu	His	Lys	Gln
	50					55				60					
Asp	Ser	Ser	Gly	Leu	Arg	Leu	Trp	Lys	Arg	Arg	Trp	Phe	Val	Leu	Ser
65					70					75				80	
Gly	His	Cys	Leu	Phe	Tyr	Tyr	Lys	Asp	Ser	Arg	Glu	Glu	Ser	Val	Leu
			85						90					95	
Gly	Ser	Val	Leu	Leu	Pro	Ser	Tyr	Asn	Ile	Arg	Pro	Asp	Gly	Pro	Gly
			100					105					110		
Ala	Pro	Arg	Gly	Arg	Arg	Phe	Thr	Phe	Thr	Ala	Glu	His	Pro	Gly	
		115					120						125		

<210> 3701

<211> 733

<212> DNA

<213> Homo sapiens

<400> 3701

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 120
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 420
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 480
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<210> 3702

<211> 236

<212> PRT

<213> Homo sapiens

<400> 3702

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			20				25						30		
Ser	Asn	Leu	Lys	Glu	His	Lys	Lys	Thr	His	Thr	Ala	Asp	Lys	Val	Phe
	35						40					45			
Thr	Cys	Asp	Glu	Cys	Gly	Lys	Ser	Phe	Asn	Met	Gln	Arg	Lys	Leu	Val
	50				55					60					
Lys	His	Arg	Ile	Arg	His	Thr	Gly	Glu	Arg	Pro	Tyr	Ser	Cys	Ser	Ala
65					70				75						80
Cys	Gly	Lys	Cys	Phe	Gly	Gly	Ser	Gly	Asp	Leu	Arg	Arg	His	Val	Arg
			85					90					95		
Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys	Glu	Ile	Cys	Asn	Lys	Cys
			100				105						110		
Phe	Thr	Arg	Ser	Ala	Val	Leu	Arg	Arg	His	Lys	Lys	Met	His	Cys	Lys
	115				120						125				
Ala	Gly	Asp	Glu	Ser	Pro	Asp	Val	Leu	Glu	Glu	Leu	Ser	Gln	Ala	Ile
	130				135						140				
Glu	Thr	Ser	Asp	Leu	Glu	Lys	Ser	Gln	Ser	Ser	Asp	Ser	Phe	Ser	Gln
145				150					155						160
Asp	Thr	Ser	Val	Thr	Leu	Met	Pro	Val	Ser	Val	Lys	Leu	Pro	Val	His

165										170										175											
Pro	Val	Glu	Asn	Ser	Val	Ala	Glu	Phe	Asp	Ser	His	Ser	Gly	Gly	Ser	Pro	Val	Glu	Asn	Ser	Val	Ala	Glu	Phe	Asp	Ser	His	Ser	Gly	Gly	Ser
180										185										190											
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Glu	Lys	Leu	Ser	Leu	Asp	Pro	Gly	Lys	Leu	Ala	Lys	Pro	Gln	Ile	His	Pro	Val	Glu	Asn	Ser	Val	Ala	Glu	Phe	Asp	Ser	His	Ser	Gly	Gly	Ser
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<210> 3703

<211> 3294

<212> DNA

<213> Homo sapiens

<400> 3703

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300	cgacgctttc	cccgggaagac	cctggggccc	tctgatctct	cccttctctc	tttggcccc
360	ggcacctctc	ctgtagggctc	ccttggtctc	ctagctccca	ttcccccaac	gctgttggcc
420	cctggcacc	tgctggggcc	caagcgtgag	gtggacatgc	acccccctct	gccccagcct
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600	gccctcacac	cccagcaagt	gcagcagatt	cttatcatca	gagaggttct	gccaggagcc
660	aaatgtgatt	ataccataca	ggtgcagcta	aggttctgtc	tctgtgagac	cagctgcccc
720	caggaagatt	attttcccc	caacctcttt	gtcaagggtc	atgggaaact	gtgccccctg
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840	aacatcacac	ccctggctcg	actctcagcc	actgttccca	acaccattgt	gggtcaattgg
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<210> 3704

<211> 619

<212> PRT

<213> Homo sapiens

<400> 3704

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			20					25					30		
Leu	His	Leu	Leu	Lys	Ser	Ser	Cys	Ala	Pro	Ser	Val	Gln	Met	Lys	Ile
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Lys	Glu	Leu	Tyr	Arg	Arg	Arg	Phe	Pro	Arg	Lys	Thr	Leu	Gly	Pro	Ser
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Asp	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Thr	Ser	Pro	Val	Gly	Ser
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Pro	Gly	Pro	Leu	Ala	Pro	Ile	Pro	Pro	Thr	Leu	Leu	Ala	Pro	Gly	Thr
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Leu	Leu	Gly	Pro	Lys	Arg	Glu	Val	Asp	Met	His	Pro	Pro	Leu	Pro	Gln
			100					105					110		
Pro	Val	His	Pro	Asp	Val	Thr	Met	Lys	Pro	Leu	Pro	Phe	Tyr	Glu	Val
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Tyr	Gly	Glu	Leu	Ile	Arg	Pro	Thr	Thr	Leu	Ala	Ser	Thr	Ser	Ser	Gln
		130				135					140				
Arg	Phe	Glu	Glu	Ala	His	Phe	Thr	Phe	Ala	Leu	Thr	Pro	Gln	Gln	Val
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Gln	Gln	Ile	Leu	Thr	Ser	Arg	Glu	Val	Leu	Pro	Gly	Ala	Lys	Cys	Asp
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Tyr	Thr	Ile	Gln	Val	Gln	Leu	Arg	Phe	Cys	Leu	Cys	Glu	Thr	Ser	Cys
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Pro	Gln	Glu	Asp	Tyr	Phe	Pro	Pro	Asn	Leu	Phe	Val	Lys	Val	Asn	Gly
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Lys	Leu	Cys	Pro	Leu	Pro	Gly	Tyr	Leu	Pro	Pro	Thr	Lys	Asn	Gly	Ala
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Glu	Pro	Lys	Arg	Pro	Ser	Arg	Pro	Ile	Asn	Ile	Thr	Pro	Leu	Ala	Arg

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225                230                235                240
Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp Ser Ser Glu
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Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg Gln Leu Thr
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Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile Arg Asn Pro
                275                280                285
Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala Asp Pro Asp
                290                295                300
Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met Cys Pro Leu
305                310                315                320
Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr Cys Ala His
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Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn Glu Lys Lys
                340                345                350
Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro Tyr Glu Ser
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Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser Cys Ser Asp
370                375                380
Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys Pro Met Lys
385                390                395                400
Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Gly Tyr Gly Leu
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Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro Ser Glu Asn
                420                425                430
Lys Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser Ser Ser Asp
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Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val Thr Ser Ala
450                455                460
Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr Ser Gly His
465                470                475                480
Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr Leu Gly Gly
                485                490                495
Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro Ala Phe Pro
500                505                510
Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe Leu Gln Thr
515                520                525
Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu Asp Glu Gln
530                535                540
Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro Ser His Phe
545                550                555                560
Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys Ser Ala Thr
                565                570                575
Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala Pro Gly Gly
580                585                590
Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly Pro Ser Leu
595                600                605
Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp
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<210> 3705

<211> 1737

<212> DNA

<213> Homo sapiens

<400> 3705
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<210> 3706

<211> 191

<212> PRT

<213> Homo sapiens

<400> 3706

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			20					25				30			
Ser	Arg	Gln	Gly	Gln	Gly	Thr	Glu	Ala	Gly	Met	Glu	Ala	Gly	Thr	Glu
		35				40					45				
Ala	Gly	Thr	Glu	Ala	Gly	Arg	Val	Gly	Gly	Val	Thr	Val	Glu	Gln	Gly
	50					55				60					
Lys	Ser	Leu	Ile	Asn	Tyr	Glu	Pro	His	Gly	Thr	Arg	Thr	Ala	Gly	Phe
65				70					75				80		
Thr	Ala	His	Pro	Pro	Lys	Ser	Thr	Ser	Val	Cys	Val	Cys	Xaa	Arg	Gln
			85					90					95		
His	Ile	Cys	Thr	Cys	Val	Cys	Met	Cys	Val	Arg	Lys	Cys	Val	Pro	Arg
		100					105					110			
Gln	His	Ile	Cys	Met	Cys	Ala	Cys	Val	Cys	Ile	Arg	Thr	Ala	Ile	Cys
		115				120					125				
Thr	Cys	Val	His	Val	Gln	Thr	Ala	Tyr	Leu	Cys	Thr	Cys	Val	Cys	Pro
	130				135				140						
Gly	Asn	Ile	Cys	Thr	Cys	Val	Ser	Val	Glu	Ala	Ala	Leu	Ser	Val	Cys
145				150					155			160			
Val	Ser	Arg	Ser	Ile	Ser	Ala	Cys	Val	Cys	Val	Ser	Xaa	Thr	Ala	Tyr
			165					170				175			
Leu	Cys	Met	Arg	Val	Cys	Val	Arg	Thr	Ala	Val	Cys	Val	Cys	Val	
			180					185				190			

<210> 3707

<211> 585

<212> DNA

<213> Homo sapiens

<400> 3707

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 180
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 240
 aaaatatggg gcatttcatt ggatgctgaaaatgcatttg ataacattca acttccttac
 300

atgataaaaa ccctcaagaa actgggtata gaaggaatgt atctcaacgt aataaaagcc
 360
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<210> 3708

<211> 106

<212> PRT

<213> Homo sapiens

<400> 3708

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Ile	Gln	Gln	Lys	Glu	Arg	Thr	Lys	Ile	Trp	Gly	Ile	Ser	Leu	Asp	Ala
			20					25					30		
Glu	Asn	Ala	Phe	Asp	Asn	Ile	Gln	Leu	Pro	Tyr	Met	Ile	Lys	Thr	Leu
		35					40					45			
Lys	Lys	Leu	Gly	Ile	Glu	Gly	Met	Tyr	Leu	Asn	Val	Ile	Lys	Ala	Val
	50				55				60						
Tyr	Asp	Arg	Pro	Xaa	Val	Ser	Ile	Ile	Leu	Asn	Gly	Glu	Asn	Leu	Gln
65				70					75					80	
Glu	Leu	Gln	Thr	Phe	Gly	Leu	Arg	Ser	Gly	Thr	Gln	Gln	Gly	Cys	Pro
			85					90						95	
Leu	Ser	Pro	Gln	Leu	Leu	Asn	Ile	Val	Leu						
			100					105							

<210> 3709

<211> 3768

<212> DNA

<213> Homo sapiens

<400> 3709

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3768

<210> 3710

<211> 70

<212> PRT

<213> Homo sapiens

<400> 3710

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		20					25					30			
Cys	Asp	Val	Ile	Leu	Val	Ala	Gly	Asp	Arg	Arg	Ile	Pro	Ala	His	Arg
		35				40					45				
Leu	Val	Leu	Ser	Ser	Val	Ser	Asp	Tyr	Phe	Ala	Ala	Met	Phe	Thr	Asn
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<210> 3711

<211> 1366

<212> DNA

<213> Homo sapiens

<400> 3711

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<210> 3712

<211> 368

<212> PRT

<213> Homo sapiens

<400> 3712

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 Leu Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp Arg
 35 40 45
 Leu Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg Arg
 50 55 60
 Glu Leu Leu Ser Leu Pro Ala Ala Ser Leu Ala Asp Gln Asp Ile Phe
 65 70 75 80
 Asn Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro Cys
 85 90 95
 Val Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys Tyr
 100 105 110
 Ser Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys Lys
 115 120 125
 Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr Leu
 130 135 140
 Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe Val
 145 150 155 160
 Cys Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala Leu
 165 170 175
 Ala Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln Gln
 180 185 190
 Leu Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro Pro
 195 200 205
 Pro Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp
 210 215 220
 Arg Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro Met

225		230		235		240									
Ser	Leu	Ala	Leu	Tyr	Leu	Thr	Asp	Ala	Glu	Ala	Gln	Gln	Phe	Leu	His
				245				250						255	
Phe	Val	Glu	Ala	Ser	Pro	Val	Leu	Ala	Ala	Arg	Gln	Asp	Val	Ala	Tyr
				260				265					270		
His	Val	Val	Tyr	Arg	Glu	Gly	Pro	Leu	Tyr	Pro	Val	Asn	Gln	Leu	Arg
				275				280					285		
Asn	Val	Ala	Leu	Ala	Gln	Ala	Leu	Thr	Pro	Tyr	Val	Phe	Leu	Ser	Asp
				290				295				300			
Ile	Asp	Phe	Leu	Pro	Ala	Tyr	Ser	Leu	Tyr	Asp	Tyr	Leu	Arg	Ala	Ser
				305				310				315			320
Ile	Glu	Gln	Leu	Gly	Leu	Gly	Ser	Arg	Arg	Lys	Ala	Ala	Leu	Val	Val
				325				330					335		
Pro	Ala	Phe	Glu	Thr	Leu	Arg	Tyr	Arg	Phe	Ser	Phe	Pro	His	Ser	Lys
				340				345					350		
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<210> 3713

<211> 1719

<212> DNA

<213> Homo sapiens

<400> 3713

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900

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<210> 3714

<211> 488

<212> PRT

<213> Homo sapiens

<400> 3714

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 35 40 45
 Ser Glu Asn Glu Thr Ser Asp Arg Glu Asp Gly Pro Pro Lys Gly His
 50 55 60
 His Val Thr Asp Ser Glu Asn Asp Glu Pro Leu Asn Leu Asn Ala Ser
 65 70 75 80
 Asp Ser Glu Ser Glu Glu Leu His Arg Gln Lys Asp Ser Asp Ser Glu
 85 90 95
 Ser Glu Glu Arg Ala Glu Pro Pro Ala Ser Asp Ser Glu Asn Glu Asp
 100 105 110
 Val Asn Gln His Gly Ser Asp Ser Glu Ser Glu Glu Thr Arg Lys Leu
 115 120 125
 Pro Gly Ser Asp Ser Glu Asn Glu Glu Leu Leu Asn Gly His Ala Ser
 130 135 140
 Asp Ser Glu Asn Glu Asp Val Gly Lys His Pro Ala Ser Asp Ser Glu

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145             150             155             160
Ile Glu Glu Leu Gln Lys Ser Pro Ala Ser Asp Ser Glu Thr Glu Asp
165
Ala Leu Lys Pro Gln Ile Ser Asp Ser Glu Ser Glu Glu Pro Pro Arg
180
His Gln Ala Ser Asp Ser Glu Asn Glu Glu Pro Pro Lys Pro Arg Met
195
Ser Asp Ser Glu Ser Glu Glu Leu Pro Lys Pro Gln Val Ser Asp Ser
210
Glu Ser Glu Glu Pro Pro Arg His Gln Ala Ser Asp Ser Glu Asn Glu
225
Glu Leu Pro Lys Pro Arg Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro
245
Arg His Gln Ala Ser Asp Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg
260
Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro Arg Asn Gln Ala Ser Asp
275
Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg Val Ser Asp Ser Glu Ser
290
Glu Gly Pro Gln Lys Gly Pro Ala Ser Asp Ser Glu Thr Glu Asp Ala
305
Ser Arg His Lys Gln Lys Pro Glu Ser Asp Asp Ser Asp Arg Glu
325
Asn Lys Gly Glu Asp Thr Glu Met Gln Asn Asp Ser Phe His Ser Asp
340
Ser His Met Asp Arg Lys Lys Phe His Ser Ser Asp Ser Glu Glu Glu
355
Glu His Lys Lys Gln Lys Met Asp Ser Asp Glu Asp Glu Lys Glu Gly
370
Glu Glu Glu Lys Val Ala Lys Arg Lys Ala Ala Val Leu Ser Asp Ser
385
Glu Asp Glu Glu Lys Ala Ser Ala Lys Lys Ser Arg Val Val Ser Asp
405
Ala Asp Asp Ser Asp Ser Asp Ala Val Ser Asp Lys Ser Gly Lys Arg
420
Glu Lys Thr Ile Ala Ser Asp Ser Glu Glu Glu Ala Gly Lys Glu Leu
435
Ser Asp Lys Lys Asn Glu Glu Lys Asp Leu Phe Gly Ser Asp Ser Glu
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<210> 3715

<211> 288

<212> DNA

<213> Homo sapiens

<400> 3715

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120

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 180
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<210> 3716

<211> 96

<212> PRT

<213> Homo sapiens

<400> 3716

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		20						25					30		
Gly	Lys	Ile	Arg	Ser	Tyr	Glu	Glu	His	Leu	Glu	Lys	His	Arg	Lys	Asp
		35						40					45		
Lys	Ala	His	Lys	Arg	Tyr	Leu	Leu	Met	Ser	Ile	Asp	Gln	Arg	Lys	Lys
		50						55			60				
Met	Leu	Lys	Asn	Leu	Arg	Asn	Thr	Asn	Tyr	Asp	Val	Phe	Glu	Lys	Ile
65					70					75				80	
Cys	Trp	Gly	Leu	Gly	Ile	Glu	Tyr	Thr	Phe	Pro	Pro	Leu	Tyr	Tyr	Arg
			85						90					95	

<210> 3717

<211> 1545

<212> DNA

<213> Homo sapiens

<400> 3717

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 240
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 300
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 480
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 660

gaagcagcgt gtgtcagtat tccacattta gatctgaaga atgtttctga tgggtataaa
 720
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 780
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 1020
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 1080
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<210> 3718

<211> 374

<212> PRT

<213> Homo sapiens

<400> 3718

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			20					25					30		
Cys	Leu	Glu	Arg	Glu	Glu	Tyr	Leu	Leu	Phe	Asp	Ser	Asp	Lys	Leu	Ser
		35				40					45				
His	Leu	Ile	Leu	Asp	Ser	Ser	Ser	Lys	Ile	Cys	Asp	Leu	Asn	Ala	Asn
	50			55						60					
Thr	Glu	Ser	Glu	Val	Pro	Gly	Gly	Gln	Ser	Val	Gly	Val	Gln	Gly	Glu
	65			70				75					80		
Ala	Ala	Cys	Val	Ser	Ile	Pro	His	Leu	Asp	Leu	Lys	Asn	Val	Ser	Asp
			85					90					95		
Gly	Asp	Lys	Trp	Glu	Glu	Pro	Phe	Pro	Ala	Phe	Lys	Ser	Trp	Gln	Glu
		100				105						110			
Asp	Ser	Glu	Ser	Gly	Glu	Ala	Gln	Leu	Ser	Pro	Gln	Ala	Gly	Arg	Met
		115				120					125				
Asn	His	His	Pro	Leu	Glu	Glu	Asp	Cys	Pro	Pro	Val	Leu	Ser	His	Arg

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Ser Leu Asp Phe Gly Gln Ser Gln Arg Phe Leu His Asp Pro Glu Lys
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Leu Asp Ser Ser Ser Lys Ala Leu Ser Phe Thr Arg Ile Arg Arg Ser
      165              170              175
Ser Phe Ser Ser Lys Asp Glu Lys Arg Glu Asp Arg Thr Pro Tyr Gln
      180              185              190
Leu Val Lys Lys Leu Gln Lys Lys Ile Arg Gln Phe Glu Glu Gln Phe
      195              200              205
Glu Arg Glu Arg Asn Ser Lys Pro Ser Tyr Ser Asp Ile Ala Ala Asn
      210              215              220
Pro Lys Val Leu Lys Trp Met Thr Glu Leu Thr Lys Leu Arg Lys Gln
      225              230              235              240
Ile Lys Asp Ala Lys His Lys Asn Ser Asp Gly Glu Phe Val Pro Gln
      245              250              255
Thr Arg Pro Arg Ser Asn Thr Leu Pro Lys Ser Phe Gly Ser Ser Leu
      260              265              270
Asp His Glu Asp Glu Glu Asn Glu Asp Glu Pro Lys Val Ile Gln Lys
      275              280              285
Glu Lys Lys Pro Ser Lys Glu Ala Thr Leu Glu Leu Ile Leu Lys Arg
      290              295              300
Leu Lys Glu Lys Arg Ile Glu Arg Cys Leu Pro Glu Asp Ile Lys Lys
      305              310              315              320
Met Thr Lys Asp His Leu Val Glu Glu Lys Ala Ser Leu Gln Lys Ser
      325              330              335
Leu Leu Tyr Tyr Glu Ser Gln His Gly Arg Pro Val Thr Lys Glu Glu
      340              345              350
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Met Leu Thr Arg Ala Ser
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<210> 3719

<211> 422

<212> DNA

<213> Homo sapiens

<400> 3719

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180
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240
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300
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422

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<210> 3720

<211> 122

<212> PRT

<213> Homo sapiens

<400> 3720

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Asn Gln Lys Lys Phe Glu Cys Asn Ser Arg Gln Pro Gly Cys Lys Asn
 35             40             45
Val Cys Phe Asp Asp Phe Phe Pro Ile Ser Gln Val Arg Leu Trp Ala
 50             55             60
Leu Gln Leu Ile Met Val Ser Thr Pro Ser Leu Val Val Leu His
 65             70             75             80
Val Ala Tyr His Glu Gly Arg Glu Lys Arg His Arg Lys Lys Leu Tyr
 85             90             95
Val Ser Pro Gly Thr Met Asp Gly Gly Leu Trp Tyr Ala Tyr Leu Ile
100             105             110
Ser Leu Ile Val Lys Thr Gly Phe Glu Thr
115             120

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<210> 3721

<211> 4728

<212> DNA

<213> Homo sapiens

<400> 3721

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720

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 gactaaaaat gtgtttataa taagatgtgg atatttcctt cagtagattg taaccataat
 4500
 ttaaatattt ttgttccaca ctgtttttta tatctgtcat gtacattgca ttttgatctg
 4560
 taactgcaca accctggggg ttgctgcaga gctatttctt tccatgtaaa gtatgggac
 4620
 catcttgctt ttgccttata taaagcctac agttatggaa gtgtggaaaa ctgtggcttc
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 4728

<210> 3722

<211> 1216

<212> PRT

<213> Homo sapiens

<400> 3722

Ser Glu Lys Glu Lys Glu Leu Glu Arg Leu Gln Lys Glu Glu Glu
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 20 25 30
 Ala Tyr Pro Phe Asn Ala Lys Gln Pro Thr Asp Met Ala Arg Arg Gln
 35 40 45
 Gln Lys Ile Ser Lys Gln Gln Leu Gln Thr Val Lys Asp Arg Phe Gln
 50 55 60
 Ala Phe Leu Asn Gly Glu Thr Gln Ile Met Ala Asp Glu Ala Phe Met
 65 70 75 80
 Asn Ala Val Gln Ser Tyr Tyr Glu Val Phe Leu Lys Ser Asp Arg Val
 85 90 95
 Ala Arg Met Val Gln Ser Gly Gly Cys Ser Ala Asn Asp Ser Arg Glu
 100 105 110
 Val Phe Lys Lys His Ile Glu Lys Arg Val Arg Ser Leu Pro Glu Ile
 115 120 125
 Asp Gly Leu Ser Lys Glu Thr Val Leu Ser Ser Trp Met Ala Lys Phe
 130 135 140
 Asp Ala Ile Tyr Arg Gly Glu Glu Asp Pro Arg Lys Gln Gln Ala Arg
 145 150 155 160
 Met Thr Ala Ser Ala Ala Ser Glu Leu Ile Leu Ser Lys Glu Gln Leu

					65											170								175
Tyr	Glu	Met	Phe	Gln	Asn	Ile	Leu	Gly	Ile	Lys	Lys	Phe	Glu	His	Gln									
			180					185																
Leu	Leu	Tyr	Asn	Ala	Cys	Gln	Leu	Asp	Asn	Pro	Asp	Glu	Gln	Ala	Ala									
		195						200				205												
Gln	Ile	Arg	Arg	Glu	Leu	Asp	Gly	Arg	Leu	Gln	Met	Ala	Asp	Gln	Ile									
		210				215					220													
Ala	Arg	Glu	Arg	Lys	Phe	Pro	Lys	Phe	Val	Ser	Lys	Glu	Met	Glu	Asn									
225					230					235														
Met	Tyr	Ile	Glu	Glu	Leu	Lys	Ser	Ser	Val	Asn	Leu	Leu	Met	Ala	Asn									
				245					250															
Leu	Glu	Ser	Met	Pro	Val	Ser	Lys	Gly	Gly	Glu	Phe	Lys	Leu	Gln	Lys									
		260						265				270												
Leu	Lys	Arg	Ser	His	Asn	Ala	Ser	Ile	Ile	Asp	Met	Gly	Glu	Glu	Ser									
		275					280					285												
Glu	Asn	Gln	Leu	Ser	Lys	Ser	Asp	Val	Val	Leu	Ser	Phe	Ser	Leu	Glu									
		290				295						300												
Val	Val	Ile	Met	Glu	Val	Gln	Gly	Leu	Lys	Ser	Leu	Ala	Pro	Asn	Arg									
305					310					315														
Ile	Val	Tyr	Cys	Thr	Met	Glu	Val	Glu	Gly	Gly	Glu	Lys	Leu	Gln	Thr									
				325					330					335										
Asp	Gln	Ala	Glu	Ala	Ser	Lys	Pro	Thr	Trp	Gly	Thr	Gln	Gly	Asp	Phe									
		340						345						350										
Ser	Thr	Thr	His	Ala	Leu	Pro	Ala	Val	Lys	Val	Lys	Leu	Phe	Thr	Glu									
		355					360					365												
Ser	Thr	Gly	Val	Leu	Ala	Leu	Glu	Asp	Lys	Glu	Leu	Gly	Arg	Val	Ile									
		370				375					380													
Leu	His	Pro	Thr	Pro	Asn	Ser	Pro	Lys	Gln	Ser	Glu	Trp	His	Lys	Met									
385				390						395					400									
Thr	Val	Ser	Lys	Asn	Cys	Pro	Asn	Gln	Asp	Leu	Lys	Ile	Lys	Leu	Ala									
				405				410						415										
Val	Arg	Met	Asp	Lys	Pro	Gln	Asn	Met	Lys	His	Ser	Gly	Tyr	Leu	Trp									

595					600					605					
Gly	Trp	Phe	Ser	Pro	Gly	Gln	Val	Phe	Val	Leu	Asp	Glu	Tyr	Cys	Ala
610					615					620					
Arg	Asn	Gly	Val	Arg	Gly	Cys	His	Arg	His	Leu	Cys	Tyr	Leu	Arg	Asp
625					630					635					640
Leu	Leu	Glu	Arg	Ala	Glu	Asn	Gly	Ala	Met	Ile	Asp	Pro	Thr	Leu	Leu
				645					650					655	
His	Tyr	Ser	Phe	Ala	Phe	Cys	Ala	Ser	His	Val	His	Gly	Asn	Arg	Pro
			660					665					670		
Asp	Gly	Ile	Gly	Thr	Val	Thr	Val	Glu	Glu	Lys	Glu	Arg	Phe	Glu	Glu
		675				680						685			
Ile	Lys	Glu	Arg	Leu	Arg	Val	Leu	Leu	Glu	Asn	Gln	Ile	Thr	His	Phe
690					695					700					
Arg	Tyr	Cys	Phe	Pro	Phe	Gly	Arg	Pro	Glu	Gly	Ala	Leu	Lys	Ala	Thr
705					710					715					720
Leu	Ser	Leu	Leu	Glu	Arg	Val	Leu	Met	Lys	Asp	Ile	Val	Thr	Pro	Val
				725					730					735	
Pro	Gln	Glu	Glu	Val	Lys	Thr	Val	Ile	Arg	Lys	Cys	Leu	Glu	Gln	Ala
				740				745					750		
Ala	Leu	Val	Asn	Tyr	Ser	Arg	Leu	Ser	Glu	Tyr	Ala	Lys	Ile	Glu	Glu
		755					760					765			
Asn	Gln	Lys	Asp	Ala	Glu	Asn	Val	Gly	Arg	Leu	Ile	Thr	Pro	Ala	Lys
770					775					780					
Lys	Leu	Glu	Asp	Thr	Ile	Arg	Leu	Ala	Glu	Leu	Val	Ile	Glu	Val	Leu
785					790					795					800
Gln	Gln	Asn	Glu	Glu	His	His	Ala	Glu	Pro	His	Val	Asp	Lys	Gly	Glu
				805					810					815	
Ala	Phe	Ala	Trp	Trp	Ser	Asp	Leu	Met	Val	Glu	His	Ala	Glu	Thr	Phe
			820					825					830		
Leu	Ser	Leu	Phe	Ala	Val	Asp	Met	Asp	Ala	Ala	Leu	Glu	Val	Gln	Pro
			835				840					845			
Pro	Asp	Thr	Trp	Asp	Ser	Phe	Pro	Leu	Phe	Gln	Leu	Leu	Asn	Asp	Phe
850					855					860					
Leu	Arg	Thr	Asp	Tyr	Asn	Leu	Cys	Asn	Gly	Lys	Phe	His	Lys	His	Leu
865					870					875					880
Gln	Asp	Leu	Phe	Ala	Pro	Leu	Val	Val	Arg	Tyr	Val	Asp	Leu	Met	Glu
				885					890					895	
Ser	Ser	Ile	Ala	Gln	Ser	Ile	His	Arg	Gly	Phe	Glu	Arg	Glu	Ser	Trp
			900					905					910		
Glu	Pro	Val	Asn	Asn	Gly	Ser	Gly	Thr	Ser	Glu	Asp	Leu	Phe	Trp	Lys
			915				920					925			
Leu	Asp	Ala	Leu	Gln	Thr	Phe	Ile	Arg	Asp	Leu	His	Trp	Pro	Glu	Glu
930					935					940					
Glu	Phe	Gly	Lys	His	Leu	Glu	Gln	Arg	Leu	Lys	Leu	Met	Ala	Ser	Asp
945					950					955					960
Met	Ile	Glu	Ser	Cys	Val	Lys	Arg	Thr	Arg	Ile	Ala	Phe	Glu	Val	Lys
				965					970				975		
Leu	Gln	Lys	Thr	Ser	Arg	Ser	Thr	Asp	Phe	Arg	Val	Pro	Gln	Ser	Ile
			980					985				990			
Cys	Thr	Met	Phe	Asn	Val	Met	Val	Asp	Ala	Lys	Ala	Gln	Ser	Thr	Lys
			995				1000					1005			
Leu	Cys	Ser	Met	Glu	Met	Gly	Gln	Glu	Phe	Ala	Lys	Met	Trp	His	Gln
			1010			1015					1020				
Tyr	His	Ser	Lys	Ile	Asp	Glu	Leu	Ile	Glu	Glu	Thr	Val	Lys	Glu	Met


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1025          1030          1035          1040
Ile Thr Leu Leu Val Ala Lys Phe Val Thr Ile Leu Glu Gly Val Leu
          1045          1050          1055
Ala Lys Leu Ser Arg Tyr Asp Glu Gly Thr Leu Phe Ser Ser Phe Leu
          1060          1065          1070
Ser Phe Thr Val Lys Ala Ala Ser Lys Tyr Val Asp Val Pro Lys Pro
          1075          1080          1085
Gly Met Asp Val Ala Asp Ala Tyr Val Thr Phe Val Arg His Ser Gln
          1090          1095          1100
Asp Val Leu Arg Asp Lys Val Asn Glu Glu Met Tyr Ile Glu Arg Leu
1105          1110          1115          1120
Phe Asp Gln Trp Tyr Asn Ser Ser Met Asn Val Ile Cys Thr Trp Leu
          1125          1130          1135
Thr Asp Arg Met Asp Leu Gln Leu His Ile Tyr Gln Leu Lys Thr Leu
          1140          1145          1150
Ile Arg Met Val Lys Lys Thr Tyr Arg Asp Phe Arg Leu Gln Gly Val
          1155          1160          1165
Leu Asp Ser Thr Leu Asn Ser Lys Thr Tyr Glu Thr Ile Arg Asn Arg
1170          1175          1180
Leu Thr Val Glu Glu Ala Thr Ala Ser Val Ser Glu Gly Gly Gly Leu
1185          1190          1195          1200
Gln Gly Ile Ser Met Lys Asp Ser Asp Glu Glu Asp Glu Glu Asp Asp
          1205          1210          1215

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<210> 3723

<211> 830

<212> DNA

<213> Homo sapiens

<400> 3723

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120
aaccccaacg agaagctgaa ggtgaacttt gggaccccag agttcctgtc acctgagggtg
180
gtgaattatg accaaatctc cgataagaca gacatgtgga gtatgggggt gatcacctac
240
atgtctgtga gggcctctc ccccttctg ggagatgatg acacagagac cctaaacaac
300
gttctatctg gcaactggta ctttgatgaa gagaccttgg aggcgctatc agacgaggcc
360
aaagactttg tctccaacct catcgtcaag gaccagaggg ccggatgaa cgctgccacg
420
tgtctgcgcc atccctggct caacaacctg gcggagaagg ccaaagcgtg taaccgacgc
480
cttaagtccc agatcttgct taagaaatc ctcattgaaga ggcgctggaa gaaaaacttc
540
attgctgtca gcgctgccaa ccgcttcaag aagatcagca gctcgggggc actgatggct
600
ctgggggtct gagccctggg cgcagctgaa gcctggacgc agccacacag tggccggggc
660
tgaagccaca cagcccagaa gccagaaaaa ggcagccaga tcccaggggc agcctcgtaa
720

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ggacaaggct gtgccaggct gggaggctcg gggctcccca cgcccccatg cagtgaccgc
 780
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 830

<210> 3724

<211> 203

<212> PRT

<213> Homo sapiens

<400> 3724

Ile Leu Leu Met His Lys Met Arg Val Leu His Leu Asp Leu Lys Pro
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 Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu Val Lys Ile Ile
 20 25 30
 Asp Phe Gly Leu Ala Arg Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val
 35 40 45
 Asn Phe Gly Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp
 50 55 60
 Gln Ile Ser Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr
 65 70 75
 Met Leu Leu Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu
 85 90 95
 Thr Leu Asn Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr
 100 105 110
 Phe Glu Ala Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile
 115 120 125
 Val Lys Asp Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His
 130 135 140
 Pro Trp Leu Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg
 145 150 155 160
 Leu Lys Ser Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp
 165 170 175
 Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg Phe Lys Lys Ile
 180 185 190
 Ser Ser Ser Gly Ala Leu Met Ala Leu Gly Val
 195 200

<210> 3725

<211> 1244

<212> DNA

<213> Homo sapiens

<400> 3725

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 120
 gaccatcttc acttttgttt tcaggccttt aaaattgtgc cctacaacac agagaccctt
 180
 gataaaatgc taaccgaatc cctgaagaac aatatccctg caagcggact gcacctcttt
 240
 ggaatcaacc agctggaaga agaagatatg atgacaaatc agagggatga agagctgccc
 300

accctgttgc attttgcctgc gaagtatgga ctgaagaacc tcaactgcctt gttgctcacc
 360
 tgcccaggag ccctgcaggc gtacagcgtg gccacaagc atggccacta ccccaacacc
 420
 atcgcgtgaga aacacggcctt cagggaacctg cggcagttca tcgacgagta tgtggaaacg
 480
 gtggacatgc tcaagagtca cattaaagag gaactgatgc acggggaggga ggctgatgct
 540
 gtgtacgagt ccatggccca cctttccaca gacctgctta tgaaatgctc gctcaacccc
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 ggctgtgacg aggatctcta tgagtccatg gctgcctttg tccagctgc cactgaagac
 660
 ctctatgttg aaatgcttca ggccagtaca tctaaccaca tccctggaga tggtttctct
 720
 cggggccacta aggactctat gatccgcaag tttttagaag gcaacagcat gggaatgacc
 780
 aatctggaga gagatcagtg ccatcttggt caggaagaag atgtttatca cacggtggat
 840
 gacgatgagg ccttttctgt ggacttgccc agcaggcccc ctgtcccagt gccagacca
 900
 gagaccactg ctctcggtgc tcaccagctg cctgacaacg aaccatacat ttttaaaggc
 960
 aagtatggca gggaatgatg tccaactggt tctttggagc ttctcaacag ggatttctgt
 1020
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 1080
 agccctaaga gacaggggtc atatcctggg gccagattct ggagctagaa taggagtaat
 1140
 gaccagatgc agtgcctggc ttcttggaag tatttacgca cagttgcaa ggaggtgaaa
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 1244

<210> 3726

<211> 325

<212> PRT

<213> Homo sapiens

<400> 3726

Xaa	Ile	His	Val	Ser	Gly	Lys	Asp	Ile	Thr	Arg	Lys	Pro	Glu	Ile	Ser
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Gly	His	Val	Ile	Ser	Ala	His	Gly	Leu	Ser	Val	Leu	Asn	Leu	Arg	Asp
			20				25						30		
Gly	Arg	Glu	Leu	Asp	Phe	Arg	Ser	Asp	His	Leu	His	Phe	Cys	Phe	Gln
		35					40					45			
Ala	Phe	Lys	Ile	Val	Pro	Tyr	Asn	Thr	Glu	Thr	Leu	Asp	Lys	Leu	Leu
		50				55				60					
Thr	Glu	Ser	Leu	Lys	Asn	Asn	Ile	Pro	Ala	Ser	Gly	Leu	His	Leu	Phe
					70				75					80	
Gly	Ile	Asn	Gln	Leu	Glu	Glu	Glu	Asp	Met	Met	Thr	Asn	Gln	Arg	Asp
			85					90						95	
Glu	Glu	Leu	Pro	Thr	Leu	Leu	His	Phe	Ala	Ala	Lys	Tyr	Gly	Leu	Lys
			100					105					110		
Asn	Leu	Thr	Ala	Leu	Leu	Leu	Thr	Cys	Pro	Gly	Ala	Leu	Gln	Ala	Tyr

```

      115              120              125
Ser Val Ala Asn Lys His Gly His Tyr Pro Asn Thr Ile Ala Glu Lys
130              135              140
His Gly Phe Arg Asp Leu Arg Gln Phe Ile Asp Glu Tyr Val Glu Thr
145              150              155              160
Val Asp Met Leu Lys Ser His Ile Lys Glu Glu Leu Met His Gly Glu
      165              170              175
Glu Ala Asp Ala Val Tyr Glu Ser Met Ala His Leu Ser Thr Asp Leu
      180              185              190
Leu Met Lys Cys Ser Leu Asn Pro Gly Cys Asp Glu Asp Leu Tyr Glu
      195              200              205
Ser Met Ala Ala Phe Val Pro Ala Ala Thr Glu Asp Leu Tyr Val Glu
      210              215              220
Met Leu Gln Ala Ser Thr Ser Asn Pro Ile Pro Gly Asp Gly Phe Ser
      225              230              235              240
Arg Ala Thr Lys Asp Ser Met Ile Arg Lys Phe Leu Glu Gly Asn Ser
      245              250              255
Met Gly Met Thr Asn Leu Glu Arg Asp Gln Cys His Leu Gly Gln Glu
      260              265              270
Glu Asp Val Tyr His Thr Val Asp Asp Asp Glu Ala Phe Ser Val Asp
      275              280              285
Leu Ala Ser Arg Pro Pro Val Pro Val Pro Arg Pro Glu Thr Thr Ala
      290              295              300
Pro Gly Ala His Gln Leu Pro Asp Asn Glu Pro Tyr Ile Phe Lys Gly
      305              310              315              320
Lys Tyr Gly Arg Glu
      325

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<210> 3727

<211> 630

<212> DNA

<213> Homo sapiens

<400> 3727

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120
ctcgaccccc ctgagaaaca agaaacaggc tgtcctcctt tgggtctgga gtccctcgga
180
gtttcagata gccggcttga ggcacacagc agccagtcct ttggtcttgg accacaccga
240
ggacggctca acattcagtc aggcctggag gacggcgatc tatatgatgg agcctgggtgt
300
gctgaggagc aggacgccga tccatgggtt cagggtggacg ctgggcaccc caccgccttc
360
tcgggtgttta tcacacaggg caggaactct gtctggaggt atgactgggt caccatcatac
420
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480
atggacgcag tatttctctg caattcagac ccagaaactc cagtgtctgaa cctcctgcgc
540
gagccccagg tggcccgctt cattcgctg ctgccccaga cctggctcca gggaggcgcg
600

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ccttgccctcc gggcagagat cctggcctgc
630

<210> 3728

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3728

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Arg Ile Arg Val Ile Lys Lys Lys Lys Val Ile Met Lys Lys Arg Lys
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Lys Leu Thr Leu Thr Arg Pro Thr Pro Leu Val Thr Ala Gly Pro Leu
      20             25             30
Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln Glu
      35             40             45
Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp Ser
 50             55             60
Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His Arg
 65             70             75             80
Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr Asp
      85             90             95
Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln Val
      100            105            110
Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly Arg
      115            120            125
Asn Ser Val Trp Arg Tyr Asp Trp Val Thr Ser Tyr Lys Val Gln Phe
      130            135            140
Ser Asn Asp Ser Arg Thr Trp Trp Gly Ser Arg Asn His Ser Ser Gly
      145            150            155            160
Met Asp Ala Val Phe Pro Ala Asn Ser Asp Pro Glu Thr Pro Val Leu
      165            170            175
Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe Ile Arg Leu Leu Pro
      180            185            190
Gln Thr Trp Leu Gln Gly Gly Ala Pro Cys Leu Arg Ala Glu Ile Leu
      195            200            205
Ala Cys
      210

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<210> 3729

<211> 1552

<212> DNA

<213> Homo sapiens

<400> 3729

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 120
atcaagttagt cagcagatgt caaacattt gtcccagat ttgcccgggt caatgtggca
 180
tggttagagt cctcagaagc atgtgtcttc cccagctctg cagccacata ctatccgttt
 240
gttcaggaac caccagtgc agagcagaaa atatatactg aagacatggc ctttggagct
 300

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tcaacttttc caccctcagta tttatcttct gagataaactc ttcattccata tgcctattct
 360
 ccttatcccc ttgactccac acagaatggt tactcagtgcc ctggctccca gtatctttat
 420
 aaccaaccca gttgttaccg aggttttcaa acagtgaagc atcgaaatga gaacacatgc
 480
 cctctccccc aagaaatgaa agctctgttt aagaagaaaa cctatgatga gaaaaaacg
 540
 tatgatcagc aaaagtttga cagtgaagg gctgatggaa ctatatcatc tgagataaaa
 600
 tcagctagag gttcacatca tttgtccatt tacgctgaga atagtttgaa atcagatggt
 660
 taccataagc gaacagacag gaaatccaga atcattgcaa aaaatgtatc tacctccaaa
 720
 cctgagtttg aatttaccac actggacttt cctgaactgc aagggtgcaga gaacaatatg
 780
 tcagagatac agaagcaacc caagtgggga cctgtccact ctgtctctac cgacattttc
 840
 cttctaagag aagtagtaaa accagctgca gtgttatcaa agggtgaaat agtggtgaaa
 900
 aataacccaa atgaatctgt aactgctaata gccgctacca attctccttc atgtacaaga
 960
 gagtttatctt ggacaccaat ggggttatggt gttcgacaga cattatctac agaactgtca
 1020
 gcagccctca aaaaatgttac ttctatgata aacttaaaga ccattgtctc atcagcagat
 1080
 cctaaaatgt ttagtatacc atcttctgaa gctttatctt cggatccttc ctacaacaaa
 1140
 gaaaaacaca ttattcatcc taccacaaaag tctaaagcat cacaaggtag tgaccttgaa
 1200
 caaaatgaag cctcaagaaa gaataagaaa aagaaagaaa aatctcatc aaaatatgaa
 1260
 gtccctgacag ttcaagagcc tccaaggatt gaagatgccg aggaatttcc caacctggca
 1320
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 1380
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 1440
 ggcacgtctga cagccctgga gaagaagcag cactctcagc atgcaaaagca gtcctccaaa
 1500
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 1552

<210> 3730

<211> 422

<212> PRT

<213> Homo sapiens

<400> 3730

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 20 25 30
 Gln Asn Val Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro

35					40					45					
Ser	Cys	Tyr	Arg	Gly	Phe	Gln	Thr	Val	Lys	His	Arg	Asn	Glu	Asn	Thr
50						55					60				
Cys	Pro	Leu	Pro	Gln	Glu	Met	Lys	Ala	Leu	Phe	Lys	Lys	Lys	Thr	Tyr
65						70				75				80	
Asp	Glu	Lys	Lys	Thr	Tyr	Asp	Gln	Gln	Lys	Phe	Asp	Ser	Glu	Arg	Ala
				85					90					95	
Asp	Gly	Thr	Ile	Ser	Ser	Glu	Ile	Lys	Ser	Ala	Arg	Gly	Ser	His	His
			100					105					110		
Leu	Ser	Ile	Tyr	Ala	Glu	Asn	Ser	Leu	Lys	Ser	Asp	Gly	Tyr	His	Lys
			115					120					125		
Arg	Thr	Asp	Arg	Lys	Ser	Arg	Ile	Ile	Ala	Lys	Asn	Val	Ser	Thr	Ser
			130			135					140				
Lys	Pro	Glu	Phe	Glu	Phe	Thr	Thr	Leu	Asp	Phe	Pro	Glu	Leu	Gln	Gly
145					150					155				160	
Ala	Glu	Asn	Asn	Met	Ser	Glu	Ile	Gln	Lys	Gln	Pro	Lys	Trp	Gly	Pro
				165					170					175	
Val	His	Ser	Val	Ser	Thr	Asp	Ile	Ser	Leu	Leu	Arg	Glu	Val	Val	Lys
			180					185					190		
Pro	Ala	Ala	Val	Leu	Ser	Lys	Gly	Glu	Ile	Val	Val	Lys	Asn	Asn	Pro
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Asn	Glu	Ser	Val	Thr	Ala	Asn	Ala	Ala	Thr	Asn	Ser	Pro	Ser	Cys	Thr
			210			215					220				
Arg	Glu	Leu	Ser	Trp	Thr	Pro	Met	Gly	Tyr	Val	Val	Arg	Gln	Thr	Leu
225					230					235				240	
Ser	Thr	Glu	Leu	Ser	Ala	Ala	Pro	Lys	Asn	Val	Thr	Ser	Met	Ile	Asn
				245				250						255	
Leu	Lys	Thr	Ile	Ala	Ser	Ser	Ala	Asp	Pro	Lys	Asn	Val	Ser	Ile	Pro
			260					265					270		
Ser	Ser	Glu	Ala	Leu	Ser	Ser	Asp	Pro	Ser	Tyr	Asn	Lys	Glu	Lys	His
			275				280					285			
Ile	Ile	His	Pro	Thr	Gln	Lys	Ser	Lys	Ala	Ser	Gln	Gly	Ser	Asp	Leu
			290			295					300				
Glu	Gln	Asn	Glu	Ala	Ser	Arg	Lys	Asn	Lys	Lys	Lys	Lys	Glu	Lys	Ser
305					310					315				320	
Thr	Ser	Lys	Tyr	Glu	Val	Leu	Thr	Val	Gln	Glu	Pro	Pro	Arg	Ile	Glu
				325					330					335	
Asp	Ala	Glu	Glu	Phe	Pro	Asn	Leu	Ala	Val	Ala	Ser	Glu	Arg	Arg	Asp
				340				345					350		
Arg	Ile	Glu	Thr	Pro	Lys	Phe	Gln	Ser	Lys	Gln	Gln	Pro	Gln	Asp	Asn
			355				360					365			
Phe	Lys	Asn	Asn	Val	Lys	Lys	Ser	Gln	Leu	Pro	Val	Gln	Leu	Asp	Leu
			370			375					380				
Gly	Gly	Met	Leu	Thr	Ala	Leu	Glu	Lys	Lys	Gln	His	Ser	Gln	His	Ala
385					390					395				400	
Lys	Gln	Ser	Ser	Lys	Pro	Val	Val	Val	Ser	Val	Gly	Ala	Val	Pro	Val
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<210> 3731

<211> 1704

<212> DNA

<213> Homo sapiens

<400> 3731

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720
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<210> 3732

<211> 281

<212> PRT

<213> Homo sapiens

<400> 3732

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		20						25					30		
Glu	Gly	Ile	Thr	Asp	Ala	Ser	Ser	Cys	Ala	Val	Leu	Leu	Pro	Ala	Ser
		35					40					45			
Leu	Phe	Val	Asn	Ser	His	Pro	Gly	Ile	Asp	Arg	Pro	Gly	Met	Leu	Cys
	50					55					60				
Ser	Phe	Arg	Ile	Pro	Gly	Ala	Trp	Ser	Cys	Ala	Trp	Ser	Leu	Asn	Ile
	65				70					75				80	
Gln	Ala	Asn	Asn	Cys	Phe	Ser	Thr	Gly	Leu	Ser	Arg	Arg	Val	Leu	Leu
		85							90					95	
Thr	Asn	Val	Val	Thr	Gly	His	Arg	Gln	Ser	Phe	Gly	Thr	Asn	Ser	Asp
		100						105					110		
Val	Leu	Ala	Gln	Gln	Phe	Ala	Leu	Met	Ala	Pro	Leu	Leu	Phe	Asn	Gly
		115					120						125		
Cys	Arg	Ser	Gly	Glu	Ile	Phe	Ala	Ile	Asp	Leu	Arg	Cys	Gly	Asn	Gln
		130				135				140					
Gly	Lys	Gly	Trp	Lys	Ala	Thr	Arg	Leu	Phe	His	Asp	Ser	Ala	Val	Thr
				150						155				160	
Ser	Val	Arg	Ile	Leu	Gln	Asp	Glu	Gln	Tyr	Leu	Met	Ala	Ser	Asp	Met
				165					170					175	
Ala	Gly	Lys	Ile	Lys	Leu	Trp	Asp	Leu	Arg	Thr	Thr	Lys	Cys	Val	Arg
			180					185					190		
Gln	Tyr	Glu	Gly	His	Val	Asn	Glu	Tyr	Ala	Tyr	Leu	Pro	Leu	His	Val
		195					200					205			
His	Glu	Glu	Glu	Gly	Ile	Leu	Val	Ala	Val	Gly	Gln	Asp	Cys	Tyr	Thr
		210				215					220				
Arg	Ile	Trp	Ser	Leu	His	Asp	Ala	Arg	Leu	Leu	Arg	Thr	Ile	Pro	Ser
				230						235				240	
Pro	Tyr	Pro	Ala	Ser	Lys	Ala	Asp	Ile	Pro	Ser	Val	Ala	Phe	Ser	Ser
				245					250					255	
Arg	Leu	Gly	Gly	Ser	Arg	Gly	Ala	Pro	Gly	Leu	Leu	Met	Ala	Val	Gly
		260						265					270		
Gln	Asp	Leu	Tyr	Cys	Tyr	Ser	Tyr	Ser							
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<210> 3733

<211> 515

<212> DNA

<213> Homo sapiens

<400> 3733

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 180
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<210> 3734

<211> 171

<212> PRT

<213> Homo sapiens

<400> 3734

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Val	Ser	Gly	Ser	Arg	Tyr	Arg	Arg	Gly	Arg	Arg	Arg	Gly	Arg	Leu	Lys
			20					25					30		
Gly	Lys	Asp	Pro	Gly	Ser	Ala	Pro	Ser	Ser	Val	Arg	Glu	Arg	Glu	Thr
		35					40					45			
Pro	Gly	Ala	Xaa	Pro	Cys	Leu	Pro	Arg	Arg	Gly	Trp	Cys	Val	Pro	Gly
		50				55					60				
Asp	Val	Arg	Ser	Ser	Pro	Pro	Leu	Pro	Gly	Trp	Cys	Ala	Leu	Ser	Asp
65					70				75					80	
Val	Arg	Ser	Arg	Gly	Arg	Ser	Cys	Pro	Ser	Ala	Pro	Lys	Ala	Ala	Gly
			85						90				95		
Gly	Leu	Arg	Ala	Trp	Gly	Arg	Gly	Ser	Gly	Ala	Ala	Arg	Ala	Pro	Ala
			100					105					110		
Pro	Ala	Pro	Ser	Pro	Ser	Ser	Gly	Xaa	Ser	Pro	Ser	Ser	Arg	Thr	Pro
			115				120					125			
Arg	Asp	Trp	Ser	Ala	Ser	Arg	Cys	Trp	Thr	Trp	Ser	Gly	Ala	Ala	Thr
		130				135					140				
Ala	Pro	Thr	Pro	Phe	Ser	Pro	Ala	Gln	Gln	Pro	Pro	Ser	Ser	His	Asp
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Gly	Leu	Ser	Leu	Asp	Pro	Ser	Gln	Leu	Glu	Pro					
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<210> 3735

<211> 2512

<212> DNA

<213> Homo sapiens

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120
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180
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240
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300
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360
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420
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480
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660
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1560

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<210> 3736

<211> 155

<212> PRT

<213> Homo sapiens

<400> 3736

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			20					25					30		
Lys	Asp	Glu	Leu	Arg	Lys	Leu	Asn	Thr	Met	Pro	Ala	Ala	Glu	Ala	Asn
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Glu	Ile	Glu	Asp	Val	Trp	His	Leu	Asp	Leu	Ser	Ser	Arg	Trp	Gln	Leu
	50					55				60					
Tyr	Arg	Leu	Trp	Leu	Gln	Leu	Tyr	Gln	Ala	Asp	Thr	Pro	Pro	Gly	Lys
65					70					75				80	
Ile	Leu	Ser	Tyr	Glu	Arg	Gln	Tyr	Arg	Thr	Ser	Ala	Glu	Arg	Met	Ala
			85					90						95	
Glu	Leu	Arg	Leu	Gln	Glu	Asp	Leu	His	Ile	Leu	Lys	Asp	Ala	Gln	Val
			100					105					110		
Val	Gly	Met	Thr	Thr	Thr	Gly	Ala	Ala	Lys	Tyr	Arg	Gln	Ile	Leu	Gln

	115		120		125										
Lys	Val	Glu	Pro	Arg	Ile	Val	Ile	Val	Glu	Glu	Ala	Ala	Glu	Val	Leu
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Glu	Ala	His	Thr	Ile	Ala	Thr	Leu	Ser	Lys	Ala					
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<210> 3737

<211> 1046

<212> DNA

<213> Homo sapiens

<400> 3737

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<210> 3738

<211> 348

<212> PRT

<213> Homo sapiens

<400> 3738

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 35 40 45
 Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg
 50 55 60
 Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala
 65 70 75 80
 Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Gly Ala Leu
 85 90 95
 Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe
 100 105 110
 His Gly Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu
 115 120 125
 Gln Glu Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr
 130 135 140
 Leu Tyr Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe
 145 150 155 160
 Arg Asp Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile
 165 170 175
 Ser Ser Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg
 180 185 190
 Leu Leu Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe
 195 200 205
 Arg Asp Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu
 210 215 220
 Ser Ala Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr
 225 230 235 240
 Leu Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro
 245 250 255
 Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro
 260 265 270
 Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala
 275 280 285
 Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro
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 Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys
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<210> 3739

<211> 1252

<212> DNA

<213> Homo sapiens

<400> 3739

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 420
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 1140
 agccccgcgc tcgctcagaa gctcgggcag cctcgcgacc ctcacctacc cctcccaata
 1200
 tcgcgcgtgt ctcaaccgcc gccagcccca tagcctcgcg ccagctggat cc
 1252

<210> 3740

<211> 139

<212> PRT

<213> Homo sapiens

<400> 3740

Met	Gly	Lys	Phe	Leu	His	Gln	Gly	Leu	Gly	Glu	Ser	Thr	Gly	Ser	Pro
1				5				10					15		
Gly	Gln	Trp	Glu	Ser	Ala	Ala	Pro	Pro	Val	Trp	Arg	Pro	Arg	Ala	His
			20					25					30		
Ser	Thr	Glu	Ala	Pro	Gly	His	Pro	Gln	Glu	Asp	Gly	Lys	Gly	Gln	Leu
		35				40					45				
Ala	Gly	Glu	Ser	Pro	Gly	His	Arg	Glu	Pro	Ser	Pro	Gly	Ser	Lys	Gln

```

      50              55              60
Asp Leu Pro Ser Asp Cys Leu Arg Asn Ala Gly Trp Thr Ser Arg Asn
65              70              75              80
Phe Pro Phe Thr Gly Gln Pro Ala Ala Ala Pro Pro Arg Leu Gly Pro
      85              90              95
Ala Pro Gly Ala Ala Asp Arg Pro Ser Arg Val Pro Lys Ser Pro Ala
      100              105              110
Leu Ala Gln Lys Leu Gly Gln Pro Arg Asp Pro His Leu Pro Leu Pro
      115              120              125
Ile Ser Pro Leu Ser Gln Pro Pro Ser Pro
      130              135

```

<210> 3741

<211> 562

<212> DNA

<213> Homo sapiens

<400> 3741

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cagacagcaa gcgacggccc agctcctcaa ggccacctcc gacctcgcg ggggtggggca
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gtcgtgtcca ctgtggggat ccacgtcctg actaaccttg tgttctaga aatccctcac
120
cggcagatcg gtgcctcctg aatccccccc aaaattccca ctgggaatgt gttcctgaaa
180
gagctgcccc ggcttgagaa agcctctttt cagaccaaac ttcgtattca aagctcaaaa
240
agaactgcac acaattagga cagtcataca agatgctgcc cctaactctg ccacaatctg
300
cgagaaggga ggcggggctt ccgagggcaa agtgcccctg ggaagggatc cgcagggaac
360
agcttttga aa ggaccacagc cccagccac gaggggagca agcacgagcc ggggagagag
420
ctctgcgctc gcacacggga ttcattctccg ccgcctctgc ccgtttccag caacacggag
480
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540
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562

```

<210> 3742

<211> 138

<212> PRT

<213> Homo sapiens

<400> 3742

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Met Gly Trp Arg Asn Cys Phe Arg Leu Ala Pro Cys Cys Trp Lys Arg
1      5      10      15
Ala Glu Ala Ala Glu Met Asn Pro Val Cys Glu Arg Arg Ala Leu Ser
      20      25      30
Pro Ala Arg Ala Cys Ser Pro Arg Gly Trp Gly Leu Trp Ser Phe Gln
      35      40      45
Ser Cys Ser Leu Arg Ile Pro Ser Gln Gly His Phe Ala Leu Gly Ser
      50      55      60
Pro Ala Ser Leu Leu Ala Asp Cys Gly Arg Ile Arg Gly Ser Ile Leu

```



```

65              70              75              80
Tyr Asp Cys Pro Asn Cys Val Gln Phe Phe Leu Ser Phe Glu Tyr Glu
              85              90              95
Val Trp Ser Glu Lys Arg Leu Ser Gln Ala Trp Ala Ala Leu Ser Gly
              100              105              110
Thr His Ser Gln Trp Glu Phe Trp Val Gly Phe Arg Arg His Arg Ser
              115              120              125
Ala Gly Glu Gly Phe Leu Gly Thr Gln Gly
              130              135

```

<210> 3743

<211> 468

<212> DNA

<213> Homo sapiens

<400> 3743

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nntcatgagc cttcttacaa gtcctcat ttt ggcaaggcgc tgacaatggc ggaggctgaa
60
ggcaatgcgca gctgcacagt cagtctagg ggtgccaata tggcagagac ccacaaagcc
120
atgatcctgc aactcaatcc cagtgagaac tgcacctgga caatagaaag accagaaaaac
180
aaaagcatca gaattatctt ttcctatgtc cagcttgatc cagatggaag ctgtgaaagt
240
gaaaacatta aagctcttga cggaacctcc agcaatgggc ctctgctagg gcaagtctgc
300
agtaaaaaacg actatgttcc tgtatttgaa tcatcatcca gtacattgac gtttcaata
360
gttactgact cagcaagaat tcaaagaact gtctttgtgt tctagtagtt cttatttcct
420
aacatcttta ttccaaagtg tggcggttac ctggatccct ggaaggat
468

```

<210> 3744

<211> 134

<212> PRT

<213> Homo sapiens

<400> 3744

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Xaa His Glu Pro Ser Tyr Lys Leu His Phe Gly Lys Ala Leu Thr Met
1              5              10              15
Ala Glu Ala Glu Gly Asn Ala Ser Cys Thr Val Ser Leu Gly Gly Ala
              20              25              30
Asn Met Ala Glu Thr His Lys Ala Met Ile Leu Gln Leu Asn Pro Ser
              35              40              45
Glu Asn Cys Thr Trp Thr Ile Glu Arg Pro Glu Asn Lys Ser Ile Arg
              50              55              60
Ile Ile Phe Ser Tyr Val Gln Leu Asp Pro Asp Gly Ser Cys Glu Ser
65              70              75              80
Glu Asn Ile Lys Val Phe Asp Gly Thr Ser Ser Asn Gly Pro Leu Leu
              85              90              95
Gly Gln Val Cys Ser Lys Asn Asp Tyr Val Pro Val Phe Glu Ser Ser
              100              105              110
Ser Ser Thr Leu Thr Phe Gln Ile Val Thr Asp Ser Ala Arg Ile Gln

```

115
Arg Thr Val Phe Val Phe
130

120

125

<210> 3745
<211> 345
<212> DNA
<213> Homo sapiens

<400> 3745
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gacgctgtgg gagaggaaaa cagccacatg tgggctggct gcttggagga gacacatgag
120
ccgtgaacac gtctcccccg gccgctccct ggttccatgc gtgctcgtct tgggcaccac
180
gagaacacag ccatgcagcc ccgatcctg cagccacagc caggcctcgg cctggctcgga
240
tgacgcatct gctccggacg cctctcgtg tcgggtgccag gcctgccagg ccaagccccg
300
attctcaggg gcggcaggag gtgggaggca cgtttgggag gatcc
345

<210> 3746
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3746
Met Ala Gly Trp Cys Val Tyr Gly Thr Leu Trp Glu Arg Lys Thr Ala
1 5 10 15
Thr Cys Gly Leu Ala Ala Trp Arg Arg His Met Ser Arg Glu His Val
20 25 30
Ser Pro Gly Arg Ser Leu Val Pro Cys Val Leu Val Leu Gly Thr Thr
35 40 45
Arg Thr Gln Pro Cys Ser Pro Arg Ser Cys Ser His Ser His Gly Ile
50 55 60
Ala Trp Ser Asp Ala Ala Ser Ala Pro Asp Ala Ser Arg Cys Arg Cys
65 70 75 80
Gln Ala Cys Gln Ala Lys Pro Arg Phe Ser Gly Ala Ala Gly Gly Gly
85 90 95
Arg His Val Trp Ala Asp
100

<210> 3747
<211> 800
<212> DNA
<213> Homo sapiens

<400> 3747
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60
cgcgccggac cctgggatgc tcttcggcgc catcccgctg cgctacgcca tactgggtgag
120

aagggggcgc gcccgccac tttctgctg agcccgac cctctctggt ggtctctct
 180
 ggggcgcccc tgccaatccc cgcttcccc tcccgagat gcagatgcgc ttcgatggac
 240
 gcctgggctt ccccgggga ttcgtggaca cgcaggacag aagcctagag gacgggctga
 300
 accgcgagct gcgcgaggag ctgggcgaag cggctgccgc tttccgctg gagcgactg
 360
 actaccgcag ctcccacgtc ggggtcaggg ccacgcgttg tggcccaact ctatgccaa
 420
 cgtctgacgc tcgaggagct gtggctgtg gaggccggcg caacacgcgc caaggaccac
 480
 gggctggagg tgggaccagc ctgggactct gtccttttc caatttctc ttctcccaa
 540
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 600
 tctccacgc tttcttggtg gagttgggat cgtgatcctc tatactctga attagtactg
 660
 ccaacctggg cttttctgaa aggtcttttc caccctttac caggagagat cctttctaga
 720
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 780
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 800

<210> 3748

<211> 138

<212> PRT

<213> Homo sapiens

<400> 3748

Met	Gln	Met	Arg	Phe	Asp	Gly	Arg	Leu	Gly	Phe	Pro	Gly	Gly	Phe	Val
1				5					10					15	
Asp	Thr	Gln	Asp	Arg	Ser	Leu	Glu	Asp	Gly	Leu	Asn	Arg	Glu	Leu	Arg
			20					25					30		
Glu	Glu	Leu	Gly	Glu	Ala	Ala	Ala	Ala	Phe	Arg	Val	Glu	Arg	Thr	Asp
		35				40						45			
Tyr	Arg	Ser	Ser	His	Val	Gly	Val	Arg	Ala	Thr	Arg	Cys	Gly	Pro	Leu
	50				55				60						
Leu	Cys	Gln	Ala	Ser	Asp	Ala	Arg	Gly	Ala	Val	Gly	Cys	Gly	Gly	Arg
65				70					75					80	
Arg	Asn	Thr	Arg	Gln	Gly	Pro	Arg	Ala	Gly	Gly	Gly	Thr	Ser	Leu	Gly
			85					90						95	
Leu	Cys	Pro	Phe	Pro	Asn	Phe	Leu	Phe	Ser	Gln	Ser	Phe	Leu	Ser	Pro
		100					105						110		
Lys	Lys	Ala	Ser	Leu	Glu	Lys	Ser	Leu	Cys	Pro	Ser	Asp	Leu	Ala	Leu
		115				120						125			
Ser	Pro	Ala	Phe	Leu	Val	Glu	Leu	Gly	Ser						
	130					135									

<210> 3749

<211> 648

<212> DNA

<213> Homo sapiens

<400> 3749

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 120
 ggctactcca tgcctcggga gggatcgaca agcaagcaga tgccccccag tgatgctgaa
 180
 ggtgacccgc tgatgaacat gctgatgagg ctgcaggagg cagccaacta ctccagcccc
 240
 cagagctatg acagcgactc caacagcaac agccatcacg atgacatctt ggactcctct
 300
 ttggagctca ctctgtgaca ggggcccgga gccacgccc ctctcttctt cctcacgcga
 360
 ttccacctgc atccccaca tcacctgaa gatgacttcc tgagccagcc ccagccaca
 420
 gccttagagc tgcgggaaca ccgagacccc ccgtccttca gcctcgacct ggggtcaggc
 480
 atccccggcc agctgcctgc ggaccgcttc ctccacagc gagaactgca ctaccttctg
 540
 ttgtacttta attattgttt tgccttgttg ctgtgacctc cctaagacac tgaagatact
 600
 tctcgggaaa ggatcatcgc cgttgaaatg aaaaaaaaaa aaaaaaaaa
 648

<210> 3750

<211> 105

<212> PRT

<213> Homo sapiens

<400> 3750

Arg	Ala	Pro	Trp	Glu	Asp	Pro	Ala	Lys	Trp	Val	Met	Asp	Thr	Tyr	Pro
1				5					10					15	
Trp	Ala	Ala	Ser	Pro	Gln	Gln	His	Glu	Trp	Pro	Pro	Leu	Leu	Gln	Leu
			20					25					30		
Arg	Pro	Glu	Asp	Val	Gly	Phe	Asp	Gly	Tyr	Ser	Met	Pro	Arg	Glu	Gly
		35				40					45				
Ser	Thr	Ser	Lys	Gln	Met	Pro	Pro	Ser	Asp	Ala	Glu	Gly	Asp	Pro	Leu
	50				55				60						
Met	Asn	Met	Leu	Met	Arg	Leu	Gln	Glu	Ala	Ala	Asn	Tyr	Ser	Ser	Pro
65					70				75					80	
Gln	Ser	Tyr	Asp	Ser	Asp	Ser	Asn	Ser	Asn	Ser	His	His	Asp	Asp	Ile
			85				90						95		
Leu	Asp	Ser	Ser	Leu	Glu	Ser	Thr	Leu							
			100					105							

<210> 3751

<211> 554

<212> DNA

<213> Homo sapiens

<400> 3751

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 120
 acgcaggggc agagtccgga gccgcggacc cgcgaggat tctactacg tggaccacca
 180
 gggccagctt ttcttgatg attccaaaat gaagaatttc atcactgtct tcaaagaccc
 240
 gcagttctcg gtcaccttct tctccgcct gagacccaac cgcagcgggc gctacgaggc
 300
 cgttttcccc ttctctcgc cctgcggcag agagcgcaac ttctgctgt gcgaggaccg
 360
 gccggtggtc ttacgcacc tgctgaccgc ggaccacggg cctccgcgc tctcctactg
 420
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 480
 caacggggcg ctgtaccacc cggcgccgga gcgtgcgggc ggcgtgggccc tgggtgcgc
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 554

<210> 3752

<211> 66

<212> PRT

<213> Homo sapiens

<400> 3752

Ala	Arg	Leu	Ser	Ala	Leu	Ala	Arg	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Arg
1			5					10				15			
Pro	His	His	Gly	Pro	Gly	Pro	Ala	Ala	Ala	Arg	Gly	Ser	Val	Ala	Pro
			20					25				30			
Ser	Gly	Ala	Lys	Gly	Val	Ser	Tyr	Thr	Gln	Gly	Gln	Ser	Pro	Glu	Pro
			35				40					45			
Arg	Thr	Arg	Glu	Val	Phe	Leu	Leu	Arg	Gly	Pro	Pro	Gly	Pro	Ala	Phe
			50			55					60				
Pro	Gly														
65															

<210> 3753

<211> 1426

<212> DNA

<213> Homo sapiens

<400> 3753

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 120
 gcttaggcctc cggagatcgg gccatctggg ctctgaaagc aaattagttt tccaactcat
 180
 gtctggctcc ggogttaccc agacgcctgg aaggtccttc ctgcagtctg atcaccattt
 240
 ttctgtctgc actgaccaat cagctccctt tggccttcaa cctcgggaat gatggattag
 300
 gggagtctag aaatggacga agccctagaa acgcagctga agacgagcag aggacgcttc
 360

tcggctacag aatccctccc caccttggag ctcttatctc aggtggacat ggactgcagg
 420
 gtccacatgc gaccatcgg cctgacgtgg gtgctgcaac tgacctggc atggatcctg
 480
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 540
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 600
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 660
 gaatgcgaat ccttctgga acacctccaa cgtgcccttc gcagtcgctt ccgctgcgg
 720
 ctattggggg tacgccaggc acagccgctc tgcgaggagc tctgccaggc ctggttcgcc
 780
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 840
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 900
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 960
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 1080
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 1200
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 1320
 aaaaagtcca tgtccacctg agataagagc tgttggtctg attggggggg ccacatgcga
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 1426

<210> 3754

<211> 261

<212> PRT

<213> Homo sapiens

<400> 3754

Met Asp Glu Ala Leu Glu Thr Gln Leu Lys Thr Ser Arg Gly Arg Phe
 1 5 10 15
 Ser Ala Thr Glu Ser Leu Pro Thr Leu Glu Leu Leu Ser Gln Val Asp
 20 25 30
 Met Asp Cys Arg Val His Met Arg Pro Ile Gly Leu Thr Trp Val Leu
 35 40 45
 Gln Leu Thr Leu Ala Trp Ile Leu Leu Glu Ala Cys Gly Gly Ser Arg
 50 55 60
 Pro Leu Gln Ala Arg Ser Gln Gln His His Gly Leu Ala Ala Asp Leu
 65 70 75 80
 Gly Lys Gly Lys Leu His Leu Ala Gly Pro Cys Cys Pro Ser Glu Met

```

      85              90              95
Asp Thr Thr Glu Thr Ser Gly Pro Gly Asn His Pro Glu Arg Cys Gly
      100              105              110
Val Pro Ser Pro Glu Cys Glu Ser Phe Leu Glu His Leu Gln Arg Ala
      115              120              125
Leu Arg Ser Arg Phe Arg Leu Arg Leu Leu Gly Val Arg Gln Ala Gln
      130              135              140
Pro Leu Cys Glu Glu Leu Cys Gln Ala Trp Phe Ala Asn Cys Glu Asp
      145              150              155              160
Asp Ile Thr Cys Gly Pro Thr Trp Leu Pro Leu Ser Glu Lys Arg Gly
      165              170              175
Cys Glu Pro Ser Cys Leu Thr Tyr Gly Gln Thr Phe Ala Asp Gly Thr
      180              185              190
Asp Leu Cys Arg Ser Ala Leu Gly His Ala Leu Pro Val Ala Ala Pro
      195              200              205
Gly Ala Arg His Cys Phe Asn Ile Ser Ile Ser Ala Val Pro Arg Pro
      210              215              220
Arg Pro Gly Arg Arg Gly Arg Glu Ala Pro Ser Arg Arg Ser Arg Ser
      225              230              235              240
Pro Arg Thr Ser Ile Leu Asp Ala Ala Gly Ser Gly Ser Gly Ser Gly
      245              250              255
Ser Gly Ser Gly Pro
      260

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<210> 3755

<211> 3149

<212> DNA

<213> Homo sapiens

<400> 3755

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120
aacaatacct cgataaccac gccaaactctt agtcccagcc agcagccgct tccgacagaa
180
ctgaatgtaa cttcaccgag taaagaggag tgtgggccat gcacagacac agtcctatgc
240
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300
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360
tctaaacaga agagtcgacg tcgggtgcttc cagtccaaaa ccaaactgga gctgggtgacg
420
cagggaattgg gatcgtgtcg ctgcggttat gtgttctgta tgttacatcg cctccccgag
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660
gacaaaagtc gccagacacc ttgtactggg cagcgctcag actgcagcca gtccgttttc
720

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tttcttttagc cagccatcct ggtactgtag tttaggggtt gatgggtggt gaaattgatt
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1020
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2280
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 2760
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 2880
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 3149

<210> 3756

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3756

Met	Asn	Leu	Cys	Ser	Lys	Cys	Phe	Ala	Asp	Phe	Gln	Lys	Lys	Gln	Pro
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Asp	Asp	Asp	Ser	Ala	Pro	Ser	Thr	Ser	Asn	Ser	Gln	Ser	Asp	Leu	Phe
			20					25					30		
Ser	Glu	Glu	Thr	Thr	Ser	Asp	Asn	Asn	Asn	Thr	Ser	Ile	Thr	Thr	Pro
			35				40					45			
Thr	Leu	Ser	Pro	Ser	Gln	Gln	Pro	Leu	Pro	Thr	Glu	Leu	Asn	Val	Thr
			50			55					60				
Ser	Pro	Ser	Lys	Glu	Glu	Cys	Gly	Pro	Cys	Thr	Asp	Thr	Ala	His	Val
65				70					75					80	
Ser	Leu	Ile	Thr	Pro	Thr	Lys	Arg	Ser	Cys	Gly	Thr	Asp	Ser	Gln	Ser
			85						90					95	
Glu	Asn	Glu	Ala	Ser	Pro	Val	Lys	Arg	Pro	Arg	Leu	Leu	Glu	Asn	Thr
			100				105						110		
Glu	Arg	Ser	Glu	Glu	Thr	Ser	Arg	Ser	Lys	Gln	Lys	Ser	Arg	Arg	Arg
			115			120					125				
Cys	Phe	Gln	Cys	Gln	Thr	Lys	Leu	Glu	Leu	Val	Gln	Gln	Glu	Leu	Gly
			130			135					140				
Ser	Cys	Arg	Cys	Gly	Tyr	Val	Phe	Cys	Met	Leu	His	Arg	Leu	Pro	Glu

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145                      150                      155                      160
Gln His Asp Cys Thr Phe Asp His Met Gly Arg Gly Arg Glu Glu Ala
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Ile Met Lys Met Val Lys Leu Asp Arg Lys Val Gly Arg Ser Cys Gln
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Arg Ile Gly Glu Gly Cys Ser
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<210> 3757

<211> 1046

<212> DNA

<213> Homo sapiens

<400> 3757

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120
ccgggectca gggtcgacaa catccaggga gatgcagtta aagacttgat gcttcgcttt
180
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240
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360
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480
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720
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780
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<210> 3758

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3758

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20      25      30
Gly Lys Ser Ser Gly Leu Leu Thr Ser His Thr Thr Asp Ser Leu Gln Leu
35      40      45
Trp Phe Val Arg Leu Ala Leu Leu Val Lys Leu Gly Leu Phe Gln Asn
50      55      60
Ala Glu Met Glu Phe Glu Pro Phe Gly Asn Leu Asp Gln Pro Asp Leu
65      70      75      80
Tyr Ser Glu Tyr Tyr Pro His Val Tyr Pro Gly Arg Arg Gly Ser Met
85      90      95
Val Pro Phe Ser Met Arg Ile Leu His Ala Glu Leu Gln Gln Tyr Leu
100     105     110
Gly Asn Pro Gln Glu Ser Leu Asp Arg Leu His Lys Val Lys Thr Val
115     120     125
Cys Ser Lys Val Gly Gly Ala Val Ile Leu Pro Cys His Gly Glu Asn
130     135     140
Met Pro Ser Thr Pro Ser Pro Gln Asp Met Pro Val Leu Phe Pro Ala
145     150     155     160
Arg Pro Ala Pro Cys Thr Ile Ala Ala Ser Ala Phe Arg Arg Leu Gly
165     170     175
Asp Pro Gly Leu Cys Gly Leu Val Val Ala Leu Ala Glu Ile Phe
180     185     190
Phe Arg Asp Gly Lys Ser Phe
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<210> 3759

<211> 830

<212> DNA

<213> Homo sapiens

<400> 3759

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120
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180
gaacaagcat tgtgttttca gagaaaaaga aacctgaac attgtccttg tggggagaag
240
cgggactggg aagagtgcga ccgggaactc tatcctgggg agcctcgtct tcacctctcg
300
gtcccgggcc cagccagtca ccaagaccag ccagagtggc aggaggacat gggacggaca
360
ggaggtgggt gttgtggaca ccttccttc aaccagatgc tggatgtcaa aggacccatc
420
ccggttaaaa gaggaggtca agcgcgtgtt gtccgtgtgt gaaaaagggg acacattttt
480
gtcctgggtg tccagctggg acgattcact gaagaggaca aaacagctgt ggcgaaactg
540

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gaggccatct ttggagcaga ctttacgaaa tacgcgatta tgctgttcac ccggaaggaa
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 gacctagggg cggggaattt ggaagacttc atgaagaact cagataacaa agcccttcgg
 660
 cgcattttaa aaaagtgggg ggggaggtt tgtgctttta acaacaaaga aacaggccag
 720
 gccaggaaa ccaggtgaa agctctttta acaagggtca atgatctgag aaaagaaagt
 780
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 830

<210> 3760

<211> 100

<212> PRT

<213> Homo sapiens

<400> 3760

Glu	His	Gly	Ala	Ser	Glu	Trp	Glu	Gln	Ala	Leu	Cys	Phe	Gln	Arg	Lys
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Arg	Asn	Pro	Glu	His	Cys	Pro	Cys	Gly	Glu	Lys	Arg	Asp	Trp	Glu	Glu
			20					25						30	
Cys	Asp	Arg	Glu	Leu	Tyr	Pro	Gly	Glu	Pro	Arg	Leu	His	Leu	Ser	Ala
			35					40					45		
Pro	Gly	Pro	Ala	Ser	His	Gln	Asp	Gln	Pro	Glu	Trp	Gln	Glu	Asp	Met
			50				55					60			
Gly	Arg	Thr	Gly	Gly	Gly	Gly	Cys	Gly	His	Pro	Ser	Phe	Asn	Gln	Met
65					70					75				80	
Leu	Asp	Val	Lys	Gly	Pro	Ile	Pro	Val	Lys	Arg	Gly	Gly	Gln	Ala	Leu
				85					90					95	
Phe	Val	Leu	Leu												
			100												

<210> 3761

<211> 458

<212> DNA

<213> Homo sapiens

<400> 3761

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 120
 aaggaggagcc gcccgccgcg agcgggaggt ggcccccgcg gacaccccgcg cgccccgagg
 180
 cgaggcaccg ccgaaccccg atccctgctg gcaggaccag aggtgtgagg gtggggggcg
 240
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 300
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 458

<210> 3762
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 3762
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 20 25 30
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 Gly Gly Gly Pro Pro Gly His Pro Gly Ala Pro Arg Arg Gly Thr Pro
 50 55 60
 Glu Pro Arg Ser Leu Leu Ala Gly Pro Glu Val
 65 70 75

<210> 3763
 <211> 1340
 <212> DNA
 <213> Homo sapiens

<400> 3763
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 300
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 360
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 420
 cagacatttg ctttgcttga gatagttcac tgtttaattg gaattgtacc tacttctgtg
 480
 attgtgactg gggccaagt gagctcaaga atctttatgg tgtggctcat tactcacagt
 540
 ataaaaccaa tccagaatga agagagtgtg gtgctttttc tggtcgcgtg gactgtgaca
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 660
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 720
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 780
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 840
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 960
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 1340

<210> 3764

<211> 288

<212> PRT

<213> Homo sapiens

<400> 3764

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			20					25					30		
Ser	Pro	Arg	Cys	Ala	Ala	Thr	Met	Ala	Ser	Ser	Asp	Glu	Asp	Gly	Thr
		35				40					45				
Asn	Gly	Gly	Ala	Ser	Glu	Ala	Gly	Glu	Asp	Arg	Glu	Ala	Pro	Gly	Lys
	50				55					60					
Arg	Arg	Arg	Leu	Gly	Phe	Leu	Ala	Thr	Ala	Trp	Leu	Thr	Phe	Tyr	Asp
65					70				75					80	
Ile	Ala	Met	Thr	Ala	Gly	Trp	Leu	Val	Leu	Ala	Ile	Ala	Met	Val	Arg
			85					90					95		
Phe	Tyr	Met	Glu	Lys	Gly	Thr	His	Arg	Gly	Leu	Tyr	Lys	Ser	Ile	Gln
			100					105					110		
Lys	Thr	Leu	Lys	Phe	Phe	Gln	Thr	Phe	Ala	Leu	Leu	Glu	Ile	Val	His
	115					120						125			
Cys	Leu	Ile	Gly	Ile	Val	Pro	Thr	Ser	Val	Ile	Val	Thr	Gly	Val	Gln
	130					135					140				
Val	Ser	Ser	Arg	Ile	Phe	Met	Val	Trp	Leu	Ile	Thr	His	Ser	Ile	Lys
145				150					155					160	
Pro	Ile	Gln	Asn	Glu	Ser	Val	Val	Leu	Phe	Leu	Val	Ala	Trp	Thr	
			165					170					175		
Val	Thr	Glu	Ile	Thr	Arg	Tyr	Ser	Phe	Tyr	Thr	Phe	Ser	Leu	Leu	Asp
			180					185					190		
His	Leu	Pro	Tyr	Phe	Ile	Lys	Trp	Ala	Arg	Tyr	Asn	Phe	Phe	Ile	Ile
	195					200					205				
Leu	Tyr	Pro	Val	Gly	Val	Ala	Gly	Glu	Leu	Leu	Thr	Ile	Tyr	Ala	Ala
	210					215					220				
Leu	Pro	Tyr	Val	Lys	Lys	Thr	Gly	Met	Phe	Ser	Ile	Arg	Leu	Pro	Asn
225				230					235					240	
Lys	Tyr	Asn	Val	Ser	Phe	Asp	Tyr	Tyr	Tyr	Phe	Leu	Leu	Ile	Thr	Met

	245		250		255
Ala Ser Tyr	Ile Pro Leu Phe	Pro Gln Leu Tyr	Phe His Met	Leu Arg	
	260	265	270		
Gln Arg Arg	Lys Val Leu His	Gly Glu Val Ile	Val Glu Lys	Asp Asp	
275	280		285		

<210> 3765

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 3765

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120
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360
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1200
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1260

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<210> 3766

<211> 464

<212> PRT

<213> Homo sapiens

<400> 3766

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          20          25          30
Arg Arg Arg Arg Gly Pro Ile Gly Arg Val Asn Met Asp Leu Glu Asn
          35          40          45
Lys Val Lys Lys Met Gly Leu Gly His Glu Gln Gly Phe Gly Ala Pro
          50          55          60
Cys Leu Lys Cys Lys Glu Lys Cys Glu Gly Phe Glu Leu His Phe Trp
          65          70          75          80
Arg Lys Ile Cys Arg Asn Cys Lys Cys Gly Gln Glu Glu His Asp Val
          85          90          95
Leu Leu Ser Asn Glu Glu Asp Arg Lys Val Gly Lys Leu Phe Glu Asp
          100          105          110
Thr Lys Tyr Thr Thr Leu Ile Ala Lys Leu Lys Ser Asp Gly Ile Pro
          115          120          125
Met Tyr Lys Arg Asn Val Met Ile Leu Thr Asn Pro Val Ala Ala Lys
          130          135          140
Lys Asn Val Ser Ile Asn Thr Val Thr Tyr Glu Trp Ala Pro Pro Val
          145          150          155          160
Gln Asn Gln Ala Leu Ala Arg Gln Tyr Met Gln Met Leu Pro Lys Glu
          165          170          175
Lys Gln Pro Val Ala Gly Ser Glu Gly Ala Gln Tyr Arg Lys Lys Gln
          180          185          190
Leu Ala Lys Gln Leu Pro Ala His Asp Gln Asp Pro Ser Lys Cys His
          195          200          205
Glu Leu Ser Pro Arg Glu Val Lys Glu Met Glu Gln Phe Val Lys Lys
          210          215          220
Tyr Lys Ser Glu Ala Leu Gly Val Gly Asp Val Lys Leu Pro Cys Glu
          225          230          235          240
Met Asp Ala Gln Gly Pro Lys Gln Met Asn Ile Pro Gly Gly Asp Arg
          245          250          255
Ser Thr Pro Ala Ala Val Gly Ala Met Glu Asp Lys Ser Ala Glu His
          260          265          270
Lys Arg Thr Gln Tyr Ser Cys Tyr Cys Cys Lys Leu Ser Met Lys Glu
          275          280          285
Gly Asp Pro Ala Ile Tyr Ala Glu Arg Ala Gly Tyr Asp Lys Leu Trp
          290          295          300
His Pro Ala Cys Phe Val Cys Ser Thr Cys His Glu Leu Leu Val Asp
          305          310          315          320
Met Ile Tyr Phe Trp Lys Asn Glu Lys Leu Tyr Cys Gly Arg His Tyr
          325          330          335
Cys Asp Ser Glu Lys Pro Arg Cys Ala Gly Cys Asp Glu Leu Ile Phe
          340          345          350
Ser Asn Glu Tyr Thr Gln Ala Glu Asn Gln Asn Trp His Leu Lys His
          355          360          365
Phe Cys Cys Phe Asp Cys Asp Ser Ile Leu Ala Gly Glu Ile Tyr Val
          370          375          380
Met Val Asn Asp Lys Pro Val Cys Lys Pro Cys Tyr Val Lys Asn His

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385		390		395		400									
Ala	Val	Val	Cys	Gln	Gly	Cys	His	Asn	Ala	Ile	Asp	Pro	Glu	Val	Gln
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Arg	Val	Thr	Tyr	Asn	Asn	Phe	Ser	Trp	His	Ala	Ser	Thr	Glu	Cys	Phe
			420					425						430	
Leu	Cys	Ser	Cys	Cys	Ser	Lys	Cys	Leu	Ile	Gly	Gln	Lys	Phe	Met	Pro
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Val	Glu	Gly	Met	Val	Phe	Cys	Ser	Val	Glu	Cys	Lys	Lys	Arg	Met	Ser
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<210> 3767

<211> 2439

<212> DNA

<213> Homo sapiens

<400> 3767

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120
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<211> 379

<212> PRT

<213> Homo sapiens

<400> 3768

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<211> 1931

<212> DNA

<213> Homo sapiens

<400> 3769

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<210> 3770

<211> 447

<212> PRT

<213> Homo sapiens

<400> 3770

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Val	Lys	Thr	Asp	Trp	Asn	Glu	Glu	Cys	Lys	Ser	Pro	Lys	Lys	Gly	Arg
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Pro Val Thr Ala Glu Phe Ser Ser Val Ser Gly Cys Pro Lys Ser		365
	370	375
Ala Ser Tyr Ser Leu Glu Ser Thr Asp Val Lys Ser Leu Ala Ala Gly		380
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Val Thr Lys Gln Ser Thr Ser Cys Pro Ala Leu Pro Pro Arg Ala Pro		395
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<210> 3771

<211> 1514

<212> DNA

<213> Homo sapiens

<400> 3771

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<211> 280

<212> PRT

<213> Homo sapiens

<400> 3772

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<211> 678

<212> PRT

<213> Homo sapiens

<400> 3774

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 580 585 590
 Gly Asn Ala Asp Phe Ser Asp Met Arg Leu Leu Asp Gly Asp Asp Gly
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 Pro Leu Arg Cys Pro Arg Gly Glu Pro Ala Leu Arg Asp Ile Val Gln
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 Phe Val Pro Phe Arg Glu Leu Lys Asn Ala Ser Pro Ala Ala Leu Ala
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 Lys Cys Val Leu Ala Glu Val Pro Lys Gln Val Val Glu Tyr Tyr Ser
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<210> 3775

<211> 549

<212> DNA

<213> Homo sapiens

<400> 3775

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<210> 3776

<211> 183

<212> PRT

<213> Homo sapiens

<400> 3776

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Pro	Met	Glu	Gln	Asn	Val	Ala	Glu	Leu	Leu	Gln	Phe	Leu	Leu	Val	Lys
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Asp	Gln	Ser	Lys	Tyr	Pro	Ile	Arg	Glu	Ser	Glu	Met	Arg	Glu	Tyr	Ile
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Val	Lys	Glu	Tyr	Arg	Asn	Gln	Phe	Pro	Glu	Ile	Leu	Arg	Arg	Ala	Ala
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Glu	Ala	His	Thr	Tyr	Ile	Leu	Leu	Asn	Lys	Leu	Gly	Pro	Val	Pro	Phe
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<210> 3777

<211> 4915

<212> DNA

<213> Homo sapiens

<400> 3777

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<210> 3778
 <211> 1049
 <212> PRT
 <213> Homo sapiens

<400> 3778

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 20          25          30
Glu Lys Arg Asn Lys Ile Glu Glu Ala Pro Glu Ala Thr Pro Gln Pro
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Ser Gln Pro Gly Pro Ser Ser Pro Ile Ser Leu Ser Ala Glu Glu Glu
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Asn Ala Glu Gly Glu Val Ser Arg Ala Asn Thr Pro Asp Ser Asp Ile
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Thr Glu Lys Thr Glu Asp Ser Ser Val Pro Glu Thr Pro Asp Asn Glu
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Arg Lys Ala Ser Ile Ser Tyr Phe Lys Asn Gln Arg Gly Ile Gln Tyr
100          105          110
Ile Asp Leu Ser Ser Asp Ser Glu Asp Val Val Ser Pro Asn Cys Ser
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Asn Thr Val Gln Glu Lys Thr Phe Asn Lys Asp Thr Val Ile Ile Val
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Ser Glu Pro Ser Glu Asp Glu Glu Ser Gln Gly Leu Pro Thr Met Ala
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Arg Arg Asn Asp Asp Ile Ser Glu Leu Glu Asp Leu Ser Glu Leu Glu
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Asp Leu Lys Asp Ala Lys Leu Gln Thr Leu Lys Glu Leu Phe Pro Gln
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Arg Ser Asp Asn Asp Leu Leu Lys Leu Ile Glu Ser Thr Ser Thr Met
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Asp Gly Ala Ile Ala Ala Leu Leu Met Phe Gly Asp Ala Gly Gly
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Gly Pro Arg Lys Arg Lys Leu Ser Ser Ser Ser Glu Pro Tyr Glu Glu
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Asp Glu Phe Asn Asp Asp Gln Ser Ile Lys Lys Thr Arg Leu Asp His
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Gln Glu Ser Ile Val Leu Lys Leu Gln Lys Glu Phe Pro Asn Phe Asp
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Lys Gln Glu Leu Arg Glu Val Leu Lys Glu His Glu Trp Met Tyr Thr
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Glu Ala Leu Glu Ser Leu Lys Val Phe Ala Glu Asp Gln Asp Met Gln
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Ser Gln Asn Tyr Pro Lys Asn Ala Thr Lys Thr Lys Leu Lys Gln Lys
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Phe Thr Lys Met Ser Lys Thr Asn Gly Leu Ser Glu Asp Leu Ile Trp					
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Met Gly Leu Gly Lys Thr Ile Gln Ala Ile Ala Phe Leu Ala Tyr Leu					
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Tyr Gln Glu Gly Asn Asn Gly Pro His Leu Ile Val Val Pro Ala Ser					
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Thr Asp Phe Glu Leu His Val Leu Cys Lys Gln Tyr Arg His Ile Asn
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Val Leu Phe Ser Gln Phe Thr Met Met Leu Asp Ile Leu Glu Val Leu
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Leu Lys His His Gln His Arg Tyr Leu Arg Leu Asp Gly Lys Thr Gln
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Tyr Asn Asp Lys Gln Ala Glu Asp Arg Cys His Arg Val Gly Gln Thr
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Lys Glu Val Leu Val Ile Lys Leu Ile Ser Gln Gly Thr Ile Glu Glu
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Ser Met Leu Lys Ile Asn Gln Gln Lys Leu Lys Leu Glu Gln Asp Met
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<210> 3779

<211> 1853

<212> DNA

<213> Homo sapiens

<400> 3779

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<210> 3780

<211> 530

<212> PRT

<213> Homo sapiens

<400> 3780

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Met Glu Lys Arg Glu Glu Ile Ile Ile Lys Lys Glu Val Ser Pro Glu			
	65	70	75
Val Val Arg Ser Lys Leu Ser Pro Ser Pro Ser Leu Arg Lys Ser Ser			
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Ser Arg His His Ser Ser Ser Ser Gln Ser Gly Ser Ser Ile Gln Arg			
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Arg Thr Leu Thr Pro Pro Leu Arg Arg Ser Ala Ser Pro Tyr Pro Ser			
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His Ser Leu Ser Ser Pro Gln Arg Lys Gln Ser Pro Pro Arg His Arg			
	260	265	270
Ser Pro Met Arg Glu Lys Gly Arg His Asp His Glu Arg Thr Ser Gln			
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Ser His Asp Arg Arg His Glu Gly Arg Glu Asp Thr Arg Gly Lys Arg			
	290	295	300
Asp Arg Glu Lys Asp Ser Arg Glu Glu Arg Glu Tyr Glu Gln Asp Gln			
	305	310	315
Ser Ser Ser Arg Asp His Arg Asp Asp Arg Glu Pro Arg Asp Gly Arg			
	325	330	335
Asp Arg Arg Asp Ala Arg Asp Thr Arg Asp Arg Arg Glu Leu Arg Asp			
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Ser Arg Asp Met Arg Asp Ser Arg Glu Met Arg Asp Tyr Ser Arg Asp			
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Thr Lys Glu Ser Arg Asp Pro Arg Asp Ser Arg Ser Thr Arg Asp Ala			
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His Asp Tyr Arg Asp Arg Glu Gly Arg Asp Thr His Arg Lys Glu Asp			
	385	390	395
Thr Tyr Pro Glu Glu Ser Arg Ser Tyr Gly Arg Asn His Leu Arg Glu			
	405	410	415
Glu Ser Ser Arg Thr Glu Ile Arg Asn Glu Ser Arg Asn Glu Ser Arg			
	420	425	430
Ser Glu Ile Arg Asn Asp Arg Met Gly Arg Ser Arg Gly Arg Val Pro			

	435		440		445	
Glu	Leu	Pro	Glu	Lys	Gly	Ser
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	465		470		475	
Ser	Tyr	Pro	Glu	Arg	Arg	Asp
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<210> 3781

<211> 1364

<212> DNA

<213> Homo sapiens

<400> 3781

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<210> 3782

<211> 112

<212> PRT

<213> Homo sapiens

<400> 3782

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Ile	Phe	Ser	Lys	Gln	Ser	Trp	Ala	Leu	Thr	Pro	Leu	Glu	Arg	Gly	Arg
			85					90					95		
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<210> 3783

<211> 4137

<212> DNA

<213> Homo sapiens

<400> 3783

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<210> 3784

<211> 804

<212> PRT

<213> Homo sapiens

<400> 3784

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		20						25					30		
Leu	Leu	Glu	Arg	Val	Glu	Glu	Pro	Val	Leu	Gln	Asn	Gln	Ile	Arg	Glu
		35					40					45			
His	Val	Ile	Ala	Ile	Glu	Asp	Ala	Phe	Val	Asn	Ser	Gln	Glu	Trp	Thr
		50				55				60					
Leu	Ser	Arg	Ser	Val	Pro	Glu	Leu	Lys	Val	Gly	Ile	Val	Gly	Asn	Leu
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Ala	Ser	Gly	Lys	Ser	Ala	Leu	Val	His	Arg	Tyr	Leu	Thr	Gly	Thr	Tyr
			85					90						95	
Val	Gln	Glu	Glu	Ser	Pro	Glu	Gly	Gly	Arg	Phe	Lys	Lys	Glu	Ile	Val
		100					105						110		
Val	Asp	Gly	Gln	Ser	Tyr	Leu	Leu	Leu	Ile	Arg	Asp	Glu	Gly	Gly	Pro
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Pro	Glu	Ala	Gln	Phe	Ala	Met	Trp	Val	Asp	Ala	Val	Ile	Phe	Val	Phe
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Ser	Leu	Glu	Asp	Glu	Ile	Ser	Phe	Gln	Thr	Val	Tyr	His	Tyr	Tyr	Ser
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<211> 1901

<212> DNA

<213> Homo sapiens

<400> 3785

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 1800
 actggataga cgtaaaggag gcattttcag ggagcagacc cccttgggag aggctagcag
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<210> 3786

<211> 168

<212> PRT

<213> Homo sapiens

<400> 3786

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Val	Trp	Glu	Gly	Gln	Leu	Gln	Ser	Leu	Val	Leu	Ser	Glu	Tyr	Ala	Ser
			20					25					30		
Thr	Glu	Met	Ser	Leu	His	Ala	Leu	Tyr	Met	His	Gln	Leu	His	Lys	Gln
		35				40						45			
Gln	Ala	Gln	Ala	Glu	Pro	Glu	Arg	His	Val	Trp	His	Arg	Arg	Glu	Ser
		50				55				60					
Asp	Glu	Ser	Gly	Glu	Ser	Ala	Pro	Asp	Glu	Gly	Gly	Glu	Gly	Ala	Arg
65					70				75					80	
Ala	Pro	Gln	Ser	Ile	Pro	Arg	Ser	Ala	Ser	Tyr	Pro	Cys	Ala	Ala	Pro
				85				90					95		
Arg	Pro	Gly	Ala	Pro	Glu	Thr	Thr	Ala	Leu	His	Gly	Gly	Phe	Gln	Arg

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          100              105              110
Arg Tyr Gly Gly Ile Thr Asp Pro Gly Thr Val Pro Arg Val Pro Ser
          115              120              125
His Phe Ser Arg Leu Pro Leu Gly Gly Trp Ala Glu Asp Gly Gln Ser
          130              135              140
Ala Ser Arg His Pro Glu Pro Val Pro Glu Glu Gly Ser Glu Asp Glu
          145              150              155              160
Leu Pro Pro Gln Val His Lys Val
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<210> 3787

<211> 717

<212> DNA

<213> Homo sapiens

<400> 3787

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420
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<210> 3788

<211> 113

<212> PRT

<213> Homo sapiens

<400> 3788

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Met Leu Gln Asn Thr Ala Ser Ile Asn Thr Glu Tyr Thr Glu Ser Leu
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Cys Ala Ser Ile Lys Leu Arg His Gly Ser Arg Ala Ala Pro Pro Gly
          20          25          30
Pro Trp Gly Ala Lys Cys Ser Trp Arg Gln Val Ala Lys Gly Glu His
          35          40          45
Leu Gly Gln Thr Pro Gly Phe Ser Ser Arg Leu Pro His Leu Pro Ala

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50		55		60											
Ser	Leu	Leu	Ser	Trp	Leu	Ser	Pro	Ser	Leu	Leu	Val	Cys	Asn	Lys	Gly
65			70						75						80
Ala	Ala	Val	Ile	Thr	His	Glu	Gln	Cys	Leu	Ala	Gln	Ser	Gly	Arg	Ser
			85						90						95
Ala	Val	Leu	Val	His	Met	Glu	Glu	Pro	Lys	Gln	Ala	Pro	Cys	Thr	Val
			100						105						110
Leu															

<210> 3789

<211> 4341

<212> DNA

<213> Homo sapiens

<400> 3789

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120
caggacagct ggaaagacat ggagccccag ctggcagaga tgattaagca gttccagagc
180
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240
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480
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1080
cagaccacca ggagcctgga cagacgctgg aggaacattt gtgccatgac catggagcgg
1140

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4341

<210> 3790

<211> 1092

<212> PRT

<213> Homo sapiens

<400> 3790

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Glu Thr Trp Asp Gln Cys Glu Lys Lys Ile Lys Glu Leu Lys Ser Arg
 20          25          30
Leu Gln Val Leu Lys Ala Gln Ser Glu Asp Pro Leu Pro Glu Leu His
 35          40          45
Glu Asp Leu His Asn Glu Lys Glu Leu Ile Lys Glu Leu Glu Gln Ser
 50          55          60
Leu Ala Ser Trp Thr Gln Asn Leu Lys Glu Leu Gln Thr Met Lys Ala
 65          70          75          80
Asp Leu Thr Arg His Val Leu Val Glu Asp Val Met Val Leu Lys Glu
 85          90          95
Gln Ile Glu His Leu His Arg Gln Trp Glu Asp Leu Cys Leu Arg Val
100          105          110
Ala Ile Arg Lys Gln Glu Ile Glu Asp Arg Leu Asn Thr Trp Val Val
115          120          125
Phe Asn Glu Lys Asn Lys Glu Leu Cys Ala Trp Leu Val Gln Met Glu
130          135          140
Asn Lys Val Leu Gln Thr Val Asp Ile Ser Ile Glu Glu Met Ile Glu
145          150          155          160
Lys Leu Gln Lys Asp Cys Met Glu Glu Ile Asn Leu Phe Ser Glu Asn
165          170          175
Lys Leu Gln Leu Lys Gln Met Gly Asp Gln Leu Ile Lys Ala Ser Asn
180          185          190
Lys Ser Arg Ala Ala Glu Ile Asp Asp Lys Leu Asn Lys Ile Asn Asp
195          200          205
Arg Trp Gln His Leu Phe Asp Val Ile Gly Ser Arg Val Lys Lys Leu
210          215          220
Lys Glu Thr Phe Ala Phe Ile Gln Gln Leu Asp Lys Asn Met Ser Asn
225          230          235          240
Leu Arg Thr Trp Leu Ala Arg Ile Glu Ser Glu Leu Ser Lys Pro Val
245          250          255
Val Tyr Asp Val Cys Asp Asp Gln Glu Ile Gln Lys Arg Leu Ala Glu
260          265          270
Gln Gln Asp Leu Gln Arg Asp Ile Glu Gln His Ser Ala Gly Val Glu
275          280          285
Ser Val Phe Asn Ile Cys Asp Val Leu Leu His Asp Ser Asp Ala Cys
290          295          300
Ala Asn Glu Thr Glu Cys Asp Ser Ile Gln Gln Thr Thr Arg Ser Leu
305          310          315          320
Asp Arg Arg Trp Arg Asn Ile Cys Ala Met Ser Met Glu Arg Arg Met
325          330          335
Lys Ile Glu Glu Thr Trp Arg Leu Trp Gln Lys Phe Leu Asp Asp Tyr
340          345          350
Ser Arg Phe Glu Asp Trp Leu Lys Ser Ala Glu Arg Thr Ala Ala Cys
355          360          365
Pro Asn Ser Ser Glu Val Leu Tyr Thr Ser Ala Lys Glu Glu Leu Lys

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370		375		380
Arg Phe Glu Ala Phe	Gln Arg Gln Ile His	Glu Arg Leu Thr Gln Leu		
385	390	395		400
Glu Leu Ile Asn Lys	Gln Tyr Arg Arg	Leu Ala Arg Glu Asn Arg Thr		
	405	410		415
Asp Thr Ala Ser Arg	Leu Lys Gln Met Val His	Glu Gly Asn Gln Arg		
	420	425		430
Trp Asp Asn Leu Gln Arg Arg	Val Thr Ala Val	Leu Arg Arg Leu Arg		
	435	440		445
His Phe Thr Asn Gln Arg Glu	Glu Phe Glu Gly Thr Arg	Glu Ser Ile		
	450	455		460
Leu Val Trp Leu Thr	Glu Met Asp Leu Gln Leu Thr	Asn Val Glu His		
	465	470		475
Phe Ser Glu Ser Asp Ala Asp	Asp Lys Met Arg	Gln Leu Asn Gly Phe		
	485	490		495
Gln Gln Glu Ile Thr	Leu Asn Thr Asn Lys	Ile Asp Gln Leu Ile Val		
	500	505		510
Phe Gly Glu Gln Leu Ile Gln	Lys Ser Glu Pro Leu Asp Ala Val Leu			
	515	520		525
Ile Glu Asp Glu Leu Glu Glu	Leu His Arg Tyr Cys Gln Glu Val Phe			
	530	535		540
Gly Arg Val Ser Arg Phe His	Arg Arg Leu Thr Ser Cys Thr Pro Gly			
	545	550		555
Leu Glu Asp Glu Lys Glu Ala	Ser Glu Asn Glu Thr Asp Met Glu Asp			
	565	570		575
Pro Arg Glu Ile Gln Thr Asp	Ser Trp Arg Lys Arg Gly Glu Ser Glu			
	580	585		590
Glu Pro Ser Ser Pro Gln Ser	Leu Cys His Leu Val Ala Pro Gly His			
	595	600		605
Glu Arg Ser Gly Cys Glu Thr	Pro Val Ser Val Asp Ser Ile Pro Leu			
	610	615		620
Glu Trp Asp His Thr Gly Asp	Val Gly Gly Ser Ser His Glu Glu			
	625	630		635
Asp Glu Glu Gly Pro Tyr Tyr	Ser Ala Leu Ser Gly Lys Ser Ile Ser			
	645	650		655
Asp Gly His Ser Trp His Val	Pro Asp Ser Pro Ser Cys Pro Glu His			
	660	665		670
His Tyr Lys Gln Met Glu Gly	Asp Arg Asn Val Pro Pro Val Pro Pro			
	675	680		685
Ala Ser Ser Thr Pro Tyr Lys	Pro Pro Tyr Gly Lys Leu Leu Leu Pro			
	690	695		700
Pro Gly Thr Asp Gly Gly Lys	Glu Gly Pro Arg Val Leu Asn Gly Asn			
	705	710		715
Pro Gln Gln Glu Asp Gly Gly	Leu Ala Gly Ile Thr Glu Gln Gln Ser			
	725	730		735
Gly Ala Phe Asp Arg Trp Glu	Met Ile Gln Ala Gln Glu Leu His Asn			
	740	745		750
Lys Leu Lys Ile Lys Gln Asn	Leu Gln Leu Asn Ser Asp Ile Ser			
	755	760		765
Ala Ile Thr Thr Trp Leu Lys	Lys Thr Glu Ala Glu Leu Glu Met Leu			
	770	775		780
Lys Met Ala Lys Pro Pro Ser	Asp Ile Gln Glu Ile Glu Leu Arg Val			
	785	790		795
Lys Arg Leu Gln Glu Ile Leu	Lys Ala Phe Asp Thr Tyr Lys Ala Leu			

805 810 815
 Val Val Ser Val Asn Val Ser Ser Lys Glu Phe Leu Gln Thr Glu Ser
 820 825 830
 Pro Glu Ser Thr Glu Leu Gln Ser Arg Leu Arg Gln Leu Ser Leu Leu
 835 840 845
 Trp Glu Ala Ala Gln Gly Ala Val Asp Ser Trp Arg Gly Leu Arg
 850 855 860
 Gln Ser Leu Met Gln Cys Gln Asp Phe His Gln Leu Ser Gln Asn Leu
 865 870 875 880
 Leu Leu Trp Leu Ala Ser Ala Lys Asn Arg Arg Gln Lys Ala His Val
 885 890 895
 Thr Asp Pro Lys Ala Asp Pro Arg Ala Leu Leu Glu Cys Arg Arg Glu
 900 905 910
 Leu Met Gln Leu Glu Lys Glu Leu Val Glu Arg Gln Pro Gln Val Asp
 915 920 925
 Met Leu Gln Glu Ile Ser Asn Ser Leu Leu Ile Lys Gly His Gly Glu
 930 935 940
 Asp Cys Ile Glu Ala Glu Glu Lys Val His Val Ile Glu Lys Lys Leu
 945 950 955 960
 Lys Gln Leu Arg Glu Gln Val Ser Gln Asp Leu Met Ala Leu Gln Gly
 965 970 975
 Thr Gln Asn Pro Ala Ser Pro Leu Pro Ser Phe Asp Glu Val Asp Ser
 980 985 990
 Gly Asp Gln Pro Pro Ala Thr Ser Val Pro Ala Pro Arg Ala Lys Gln
 995 1000 1005
 Phe Arg Ala Val Arg Thr Thr Glu Gly Glu Glu Glu Thr Glu Ser Arg
 1010 1015 1020
 Val Pro Gly Ser Thr Arg Pro Gln Arg Ser Phe Leu Ser Arg Val Val
 1025 1030 1035 1040
 Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu Leu Leu Leu Leu
 1045 1050 1055
 Ala Cys Leu Leu Pro Ser Ser Glu Glu Asp Tyr Ser Cys Thr Gln Ala
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<210> 3791

<211> 1011

<212> DNA

<213> Homo sapiens

<400> 3791

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<210> 3792

<211> 288

<212> PRT

<213> Homo sapiens

<400> 3792

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      20             25             30
Ala Leu Ser Met Gly Gly Lys Val Pro Val Ser Glu Gly Leu Glu His
      35             40             45
Ser Asp Leu Pro Asp Gly Thr Gly Glu Phe Leu Asp Ala Trp Leu Met
      50             55             60
Leu Val Glu Lys Met Val Asn Pro Thr Thr Val Leu Glu Ser Pro His
      65             70             75             80
Ser Leu Pro Ala Lys Leu Pro Gly Gly Val Gln Asn Phe Pro Gln Phe
      85             90             95
Ser Ala Leu Arg Phe Leu Val Val Thr Gln Lys Ala Ala Phe Thr Cys
      100            105            110
Ile Lys Asn Leu Trp Asn Arg Lys Pro Leu Lys Val Tyr Gly Gly Arg
      115            120            125
Met Ala Glu Ser Met Leu Ala Ile Leu Cys His Ile Leu Arg Gly Glu
      130            135            140
Pro Val Ile Arg Glu Arg Leu Ser Lys Glu Lys Glu Gly Ser Arg Gly
      145            150            155            160
Glu Glu Asp Thr Gly Gln Glu Glu Gly Gly Ser Arg Arg Glu Pro Gln
      165            170            175
Val Asn Gln Gln Gln Leu Gln Gln Leu Met Asp Met Gly Phe Thr Arg

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Glu His Ala Met Glu Ala Leu Leu Asn Thr Ser Thr Met Glu Gln Ala
      195              200              205
Thr Glu Tyr Leu Leu Thr His Pro Pro Pro Ile Met Gly Gly Val Val
      210              215              220
Arg Asp Leu Ser Met Ser Glu Glu Asp Gln Met Met Arg Ala Ile Ala
      225              230              235              240
Met Ser Leu Gly Gln Asp Ile Pro Met Asp Gln Arg Ala Glu Ser Pro
      245              250              255
Glu Glu Val Ala Cys Arg Lys Glu Glu Glu Arg Lys Ala Arg Glu
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Lys Gln Glu Glu Glu Glu Ala Lys Cys Leu Lys Lys Val Gln Gly Cys
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<210> 3793

<211> 360

<212> DNA

<213> Homo sapiens

<400> 3793

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<210> 3794

<211> 96

<212> PRT

<213> Homo sapiens

<400> 3794

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      20      25      30
Phe Val Pro Gly Arg Asn Asn Ser Phe Phe Phe Ser Trp Arg Gln Cys
      35      40      45
Phe Thr Leu Val Ala Gln Ala Gly Gly Gln Trp Arg Asp Leu Ser Ser
      50      55      60
Leu Gln Pro Pro Pro Phe Gly Leu Lys Arg Phe Ser Cys Leu Ser Leu
      65      70      75      80
Pro Ser Ser Trp Asp Tyr Arg His Ala Ser Pro Cys Thr Met Pro Asp
      85      90      95

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<210> 3795

<211> 1341

<212> DNA

<213> Homo sapiens

<400> 3795

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120
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180
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240
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300
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<210> 3796

<211> 294

<212> PRT

<213> Homo sapiens

<400> 3796

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          20           25           30
Pro Asn Gln Leu Tyr Tyr Glu Gly Leu Gln Ala Cys Ala Asp Val
          35           40           45
Val Asp Arg Glu Arg Phe Cys Arg Trp Ala Gly Leu Pro Arg Gln Gly
          50           55           60
Phe Pro Ile Ile Phe His Gly Val Met Gly Lys Asp Glu Arg Glu Gly
          65           70           75
Asn Ser Pro Ser Phe Phe Asn Pro Glu Glu Ala Ala Thr Val Thr Ser
          85           90           95
Tyr Leu Lys Leu Leu Ala Pro Ser Ser Lys Lys Gly Lys Ala Arg
          100          105          110
Leu Ser Pro Arg Ser Val Gly Val Ile Ser Pro Tyr Arg Lys Gln Val
          115          120          125
Glu Lys Ile Arg Tyr Cys Ile Thr Lys Leu Asp Arg Glu Leu Arg Gly
          130          135          140
Leu Asp Asp Ile Lys Asp Leu Lys Val Gly Ser Val Glu Glu Phe Gln
          145          150          155
Gly Gln Glu Arg Ser Val Ile Leu Ile Ser Thr Val Arg Ser Ser Gln
          165          170          175
Ser Phe Val Gln Leu Asp Leu Asp Phe Asn Leu Gly Phe Leu Lys Asn
          180          185          190
Pro Lys Arg Phe Asn Val Ala Val Thr Arg Ala Lys Ala Leu Leu Ile
          195          200          205
Ile Val Gly Asn Pro Leu Leu Leu Gly His Asp Pro Asp Trp Lys Val
          210          215          220
Phe Leu Glu Phe Cys Lys Glu Asn Gly Gly Tyr Thr Gly Cys Pro Phe
          225          230          235
Pro Ala Lys Leu Asp Leu Gln Gln Gly Gln Asn Leu Leu Gln Gly Leu
          245          250          255
Ser Lys Leu Ser Pro Ser Thr Ser Gly Pro His Ser His Asp Tyr Leu
          260          265          270
Pro Gln Glu Arg Glu Gly Glu Gly Gly Leu Ser Leu Gln Val Glu Pro
          275          280          285
Glu Trp Arg Asn Glu Leu
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<210> 3797

<211> 1970

<212> DNA

<213> Homo sapiens

<400> 3797

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ggggtgttcg tcgctacga cttcgaggcc gacgccact ggtggtcaga gaggacgcac
180

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aagaacttga gcgacatgga gaacgaattc tactatcgct acccaagctt ccaggacgtg
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 1970

<210> 3798

<211> 473

<212> PRT

<213> Homo sapiens

<400> 3798

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Val	Ile	Leu	Phe	Gly	Val	Phe	Val	Arg	Tyr	Asp	Phe	Glu	Ala	Asp	Ala
		20						25					30		
His	Trp	Trp	Ser	Glu	Arg	Thr	His	Lys	Asn	Leu	Ser	Asp	Met	Glu	Asn
		35						40				45			
Glu	Phe	Tyr	Tyr	Arg	Tyr	Pro	Ser	Phe	Gln	Asp	Val	His	Val	Met	Val
	50					55					60				
Phe	Val	Gly	Phe	Gly	Phe	Leu	Met	Thr	Phe	Leu	Gln	Arg	Tyr	Gly	Phe
65					70					75				80	
Ser	Ala	Val	Gly	Phe	Asn	Phe	Leu	Leu	Ala	Ala	Phe	Gly	Ile	Gln	Trp
			85					90						95	
Ala	Leu	Leu	Met	Gln	Gly	Trp	Phe	His	Phe	Leu	Gln	Asp	Arg	Tyr	Ile
			100					105						110	
Val	Val	Gly	Val	Glu	Asn	Leu	Ile	Asn	Ala	Asp	Phe	Cys	Val	Ala	Ser
		115				120						125			
Val	Cys	Val	Ala	Phe	Gly	Ala	Val	Leu	Gly	Lys	Val	Ser	Pro	Ile	Gln
		130				135					140				
Leu	Leu	Ile	Met	Thr	Phe	Phe	Gln	Val	Thr	Leu	Phe	Ala	Val	Asn	Glu
145					150					155				160	
Phe	Ile	Leu	Leu	Asn	Leu	Leu	Lys	Val	Lys	Asp	Ala	Gly	Gly	Ser	Met
			165						170					175	
Thr	Ile	His	Thr	Phe	Gly	Ala	Tyr	Phe	Gly	Leu	Thr	Val	Thr	Arg	Ile
		180						185					190		
Leu	Tyr	Arg	Arg	Asn	Leu	Glu	Gln	Ser	Lys	Glu	Arg	Gln	Asn	Ser	Val
		195					200					205			
Tyr	Gln	Ser	Asp	Leu	Phe	Ala	Met	Ile	Gly	Thr	Leu	Phe	Leu	Trp	Met
		210				215					220				
Tyr	Trp	Pro	Ser	Phe	Asn	Ser	Ala	Ile	Ser	Tyr	His	Gly	Asp	Ser	Gln
225					230					235				240	
His	Arg	Ala	Ala	Ile	Asn	Thr	Tyr	Cys	Ser	Leu	Ala	Ala	Cys	Val	Leu
			245							250				255	
Thr	Ser	Val	Ala	Ile	Ser	Ser	Ala	Leu	His	Lys	Lys	Gly	Lys	Leu	Asp
			260				265						270		
Met	Val	His	Ile	Gln	Asn	Ala	Thr	Leu	Ala	Gly	Gly	Val	Ala	Val	Gly
		275					280						285		
Thr	Ala	Ala	Glu	Met	Met	Leu	Met	Pro	Tyr	Gly	Ala	Leu	Ile	Ile	Gly
		290				295					300				
Phe	Val	Cys	Gly	Ile	Ile	Ser	Thr	Leu	Gly	Phe	Val	Tyr	Leu	Thr	Pro
305					310					315				320	
Phe	Leu	Glu	Ser	Arg	Leu	His	Ile	Gln	Asp	Thr	Cys	Gly	Ile	Asn	Asn

```

          325          330          335
Leu His Gly Ile Pro Gly Ile Ile Gly Gly Ile Val Gly Ala Val Thr
          340          345          350
Ala Ala Ser Ala Ser Leu Glu Val Tyr Gly Lys Glu Gly Leu Val His
          355          360          365
Ser Phe Asp Phe Gln Gly Phe Asn Gly Asp Trp Thr Ala Arg Thr Gln
          370          375          380
Gly Lys Phe Gln Ile Tyr Gly Leu Leu Val Thr Leu Ala Met Ala Leu
          385          390          395          400
Met Gly Gly Ile Ile Val Gly Leu Ile Leu Arg Leu Pro Phe Trp Gly
          405          410          415
Gln Pro Ser Asp Glu Asn Cys Phe Glu Asp Ala Val Tyr Trp Glu Met
          420          425          430
Pro Glu Gly Asn Ser Thr Val Tyr Ile Pro Glu Asp Pro Thr Phe Lys
          435          440          445
Pro Ser Gly Pro Ser Val Pro Ser Val Pro Met Val Ser Pro Leu Pro
          450          455          460
Met Ala Ser Ser Val Pro Leu Val Pro
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<210> 3799

<211> 210

<212> DNA

<213> Homo sapiens

<400> 3799

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210

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<210> 3800

<211> 70

<212> PRT

<213> Homo sapiens

<400> 3800

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20          25          30
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
35          40          45
Ser Ser Ser Ser Ser Ser Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr
50          55          60
Lys Asp Lys Arg Arg Lys
65          70

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<210> 3801

<211> 4070

<212> DNA

<213> Homo sapiens

<400> 3801

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360
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<210> 3802

<211> 476

<212> PRT

<213> Homo sapiens

<400> 3802

Met	Ala	Ile	Lys	Phe	Leu	Glu	Val	Ile	Lys	Pro	Phe	Cys	Val	Ile	Leu
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Pro	Glu	Ile	Gln	Lys	Pro	Glu	Arg	Lys	Ile	Gln	Phe	Lys	Glu	Lys	Val
		20						25					30		
Leu	Trp	Thr	Ala	Ile	Thr	Leu	Phe	Ile	Phe	Leu	Val	Cys	Cys	Gln	Ile
		35					40					45			
Pro	Leu	Phe	Gly	Ile	Met	Ser	Ser	Asp	Ser	Ala	Asp	Pro	Phe	Tyr	Trp
	50				55					60					
Met	Arg	Val	Ile	Leu	Ala	Ser	Asn	Arg	Gly	Thr	Leu	Met	Glu	Leu	Gly
	65				70					75				80	
Ile	Ser	Pro	Ile	Val	Thr	Ser	Gly	Leu	Ile	Met	Gln	Leu	Leu	Ala	Gly
			85						90					95	
Ala	Lys	Ile	Ile	Glu	Val	Gly	Asp	Thr	Pro	Lys	Asp	Arg	Ala	Leu	Phe
		100					105						110		
Asn	Gly	Ala	Gln	Lys	Leu	Phe	Gly	Met	Ile	Ile	Thr	Ile	Gly	Gln	Ser

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Ile Val Tyr Val Met Thr Gly Met Tyr Gly Asp Pro Ser Glu Met Gly
  130              135              140
Ala Gly Ile Cys Leu Leu Ile Ile Ile Gln Leu Phe Val Ala Gly Leu
145              150              155
Ile Val Leu Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly
      165              170              175
Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val
      180              185              190
Trp Lys Ala Phe Ser Pro Thr Thr Ile Asn Thr Gly Arg Gly Thr Glu
      195              200              205
Phe Glu Gly Ala Val Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr
  210              215              220
Asp Lys Val Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro
225              230              235
Asn Leu Met Asn Leu Ile Ala Thr Ile Phe Val Phe Ala Val Val Ile
      245              250              255
Tyr Phe Gln Gly Phe Arg Val Asp Leu Pro Ile Lys Ser Ala Arg Tyr
      260              265              270
Arg Gly Gln Tyr Asn Thr Tyr Pro Ile Lys Leu Phe Tyr Thr Ser Asn
  275              280              285
Ile Pro Ile Ile Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile
      290              295              300
Ser Gln Met Leu Ser Ala Arg Phe Ser Gly Asn Phe Leu Val Asn Leu
305              310              315
Leu Gly Gln Trp Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr
      325              330              335
Pro Val Gly Gly Leu Cys Tyr Tyr Leu Ser Pro Pro Glu Ser Phe Gly
      340              345              350
Ser Val Leu Glu Asp Pro Val His Ala Val Val Tyr Ile Val Phe Met
  355              360              365
Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr Trp Ile Glu Val Ser Gly
      370              375              380
Ser Ser Ala Lys Asp Val Ala Lys Gln Leu Lys Glu Gln Gln Met Val
385              390              395
Met Arg Gly His Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr
      405              410              415
Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser
      420              425              430
Val Leu Ala Asp Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu
      435              440              445
Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu
      450              455              460
Gln Ser Glu Val Gly Ser Met Gly Ala Leu Leu Phe
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<210> 3803

<211> 345

<212> DNA

<213> Homo sapiens

<400> 3803

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 120
 aaatatgccc acttgagtga tgagcttcac gtattaattg aagtgtttgc tccacctggg
 180
 gaagcttatt cacgtatgag tcatgcattg gaagagatta aaaaattcct ggttctcgac
 240
 tacaatgatg aaattcgtca ggaacaacta cgtgaattat cttacttaaa tggctcagag
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 345

<210> 3804

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3804

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 20 25 30
 Glu Leu Arg Lys Ser Gly Glu Ala Lys Tyr Ala His Leu Ser Asp Glu
 35 40 45
 Leu His Val Leu Ile Glu Val Phe Ala Pro Pro Gly Glu Ala Tyr Ser
 50 55 60
 Arg Met Ser His Ala Leu Glu Glu Ile Lys Lys Phe Leu Val Pro Asp
 65 70 75 80
 Tyr Asn Asp Glu Ile Arg Gln Glu Gln Leu Arg Glu Leu Ser Tyr Leu
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 Asn Gly Ser Glu Asp Ser Gly Arg Gly Arg Gly Ile Arg Gly Arg Gly
 100 105 110
 Ile Arg Ile
 115

<210> 3805

<211> 1923

<212> DNA

<213> Homo sapiens

<400> 3805

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 aagagcccgct tgcctaccag atgccaggcc ctgtgcttcc tctctgccttt gaggtttttg
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1923

<210> 3806

<211> 280

<212> PRT

<213> Homo sapiens

<400> 3806

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Pro Leu Arg Phe Trp Leu Val Ile Asn Gln Glu Gly Asn Met Val Thr
 35           40           45
Ala Arg Gln Glu Pro Arg Leu Val Leu Ile Ser Leu Thr Cys Asp Gly
 50           55           60
Asp Thr Leu Thr Leu Ser Ala Ala Tyr Thr Lys Asp Leu Leu Leu Pro
 65           70           75           80
Ile Lys Thr Pro Thr Thr Asn Ala Val His Lys Cys Arg Val His Gly
 85           90           95
Leu Glu Ile Glu Gly Arg Asp Cys Gly Glu Ala Ala Ala Gln Trp Ile
100           105           110
Thr Ser Phe Leu Lys Ser Gln Pro Tyr Arg Leu Val His Phe Glu Pro
115           120           125
His Met Arg Pro Arg Arg Pro His Gln Ile Ala Asp Leu Phe Arg Pro
130           135           140
Lys Asp Gln Ile Ala Tyr Ser Asp Thr Ser Pro Phe Leu Ile Leu Ser
145           150           155           160
Glu Ala Ser Leu Ala Asp Leu Asn Ser Arg Leu Glu Lys Lys Val Lys
165           170           175
Ala Thr Asn Phe Arg Pro Asn Ile Val Ile Ser Gly Cys Asp Val Tyr
180           185           190
Ala Glu Asp Ser Trp Asp Glu Leu Leu Ile Gly Asp Val Glu Leu Lys
195           200           205
Arg Val Met Ala Cys Ser Arg Cys Ile Leu Thr Thr Val Asp Pro Asp
210           215           220
Thr Gly Val Met Ser Arg Lys Glu Pro Leu Glu Thr Leu Lys Ser Tyr
225           230           235           240
Arg Gln Cys Asp Pro Ser Glu Arg Lys Leu Tyr Gly Lys Ser Pro Leu
245           250           255
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<210> 3807

<211> 372

<212> DNA

<213> Homo sapiens

<400> 3807

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180

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<210> 3808

<211> 85

<212> PRT

<213> Homo sapiens

<400> 3808

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35 40 45
Ser Tyr His Pro Ala Pro Ser Gly Arg Gly Ser Ala Pro Ser Pro Arg
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Gly Gln Phe Ala Ala
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<210> 3809

<211> 1221

<212> DNA

<213> Homo sapiens

<400> 3809

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480
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540
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600

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 720
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 840
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 1080
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<210> 3810

<211> 97

<212> PRT

<213> Homo sapiens

<400> 3810

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Ser	Trp	Arg	Ala	Ser	Ser	Asn	Cys	Ser	Arg	Ala	Glu	Pro	Ile	Lys	Glu
		20					25					30			
Phe	Ser	Arg	Lys	Val	Gly	Arg	Pro	Thr	Pro	Ser	Arg	Arg	Val	Tyr	
	35					40					45				
Arg	Gly	Thr	Arg	Thr	Arg	Pro	Ser	Thr	Ser	Pro	Trp	Ser	Leu	Ala	
	50				55					60					
Arg	Val	Ala	Pro	Ala	Ser	Thr	Ala	Asn	Ser	Ser	Ser	Ser	Asp	Ala	
65				70					75				80		
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Arg

<210> 3811

<211> 296

<212> DNA

<213> Homo sapiens

<400> 3811

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 120

acaccacgcc agatatctgg gcagcagggga catctgacct ggggtgcttg ctggcagcac
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 296

<210> 3812

<211> 94

<212> PRT

<213> Homo sapiens

<400> 3812

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Pro	Val	Leu	Lys	Ala	Gln	Asn	Cys	Arg	Pro	Ser	Gly	Arg	Pro	Val	Leu
			20				25						30		
Pro	Tyr	Gln	Arg	Thr	Pro	Arg	Gln	Ile	Ser	Gly	Gln	Gln	Gly	His	Leu
		35				40					45				
Thr	Trp	Gly	Ala	Cys	Trp	Gln	His	Cys	Leu	Asp	Ser	Arg	Ala	Ser	Leu
	50				55					60					
Gly	Pro	Pro	Pro	Asn	Pro	Ala	Arg	Glu	Arg	Leu	Lys	Ala	Cys	Pro	Pro
65				70				75					80		
Cys	Trp	Ala	Trp	Val	Gly	Arg	Ser	Gly	Thr	Gly	Pro	Ser	Arg		
			85					90							

<210> 3813

<211> 1419

<212> DNA

<213> Homo sapiens

<400> 3813

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 180
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<210> 3814

<211> 294

<212> PRT

<213> Homo sapiens

<400> 3814

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 35 40 45
 Leu His Thr Phe Asp Leu Leu Gly Phe Gly Arg Ser Ser Arg Pro Ala
 50 55 60
 Phe Pro Arg Asp Pro Glu Gly Ala Glu Asp Glu Phe Val Thr Ser Ile
 65 70 75 80
 Glu Thr Trp Arg Glu Thr Met Gly Ile Pro Ser Met Ile Leu Leu Gly
 85 90 95
 His Ser Leu Gly Gly Phe Leu Ala Thr Ser Tyr Ser Ile Lys Tyr Pro
 100 105 110
 Asp Arg Val Lys His Leu Ile Leu Val Asp Pro Trp Gly Phe Pro Leu
 115 120 125
 Arg Pro Thr Asn Pro Ser Glu Ile Arg Ala Pro Pro Ala Trp Val Lys
 130 135 140
 Ala Val Ala Ser Val Leu Gly Arg Ser Asn Pro Leu Ala Val Leu Arg
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[illegible]

<210> 3815

<211> 3669

<212> DNA

<213> Homo sapiens

<400> 3815

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840					
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<212> PRT

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<400> 3816

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<211> 419

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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Ile Arg Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile
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Thr Cys Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Asp Leu Leu
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<213> Homo sapiens

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Gln Asn Trp His Leu Lys	His Phe Cys Cys Phe Asp Cys Asp Ser Ile	
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<212> DNA

<213> Homo sapiens

<400> 3821

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Glu	Gln	Ala	His	Arg	Gln	Arg	Ala	Ala	Leu	Glu	Trp	Asp	Val	Gly	Arg
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<211> 5713<212> DNA

<213> Homo sapiens

<400> 3829

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<211> 444

<212> PRT

<213> Homo sapiens

<400> 3830

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 Val Glu Ser Val Tyr Thr Thr Phe Arg Asp Arg Glu Ile Met Phe His

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Glu Asn Thr Pro Phe Val Pro Asp Met Ile Ala Ser Asn Phe Leu His
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Ala Tyr Ile Val Val Gln Val Glu Thr Pro Gly Thr Glu Thr Pro Ser
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Tyr Lys Val Ser Val Thr Ala Arg Glu Asp Val Pro Thr Phe Gly Pro
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Pro Leu Pro Ser Pro Pro Val Phe Gln Lys Gly Pro Glu Phe Arg Glu
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Asp Lys Phe Ala Lys Leu Glu Asp Arg Thr Arg Ala Ala Leu Leu Asp
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Glu Ser Phe Lys Arg Ala Ile Arg Val Arg Ser His Ser Met Glu Thr
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<211> 726

<212> DNA

<213> Homo sapiens

<400> 3831

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<210> 3832

<211> 107

<212> PRT

<213> Homo sapiens

<400> 3832

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35           40           45
Ser Thr Asn Ser His Ile Asp Arg Ile Asn Phe Ser Val Lys Met Val
50           55           60
Ser Ser Ile Leu Gln Ile Pro Lys Leu Ser Tyr Leu Gly Leu Gly Asp
65           70           75           80
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<210> 3833

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<211> 361

<212> PRT

<213> Homo sapiens

<400> 3834

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Val	Ser	Ala	Leu	Val	Gly	Phe	Ala	Thr	Glu	Pro	Gln	Phe	Leu	Gly	Arg
			260				265						270		
Ala	Ala	Ala	Val	Ser	Ala	Glu	Gly	Lys	Ala	Val	Gln	Thr	Ala	Ile	Leu
		275				280							285		
Gly	Gly	Ala	Met	Ser	Val	Val	Ser	Ala	Cys	Val	Leu	Leu	Thr	Gln	Cys

290		295		300
Leu Arg Asp	Leu Ala Gln His Pro Asp Gly Gly Ala Lys Met Ser Asp			
305	310	315	320	
His Arg Glu Arg	Leu Arg Asn Ser Ala Cys Ala Val Ser Glu Gly Cys			
	325	330	335	
Thr Leu Leu Ser	Gln Ala Leu Arg Glu Arg Ser Ser Pro Arg Thr Leu			
	340	345	350	
Pro Pro Val Asn	Ser Asn Ser Val Asn			
355	360			

<210> 3835

<211> 2366

<212> DNA

<213> Homo sapiens

<400> 3835

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 420
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 480
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 540
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 780
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 840
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 1140

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 1680
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 1920
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 1980
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 2040
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 2160
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 2220
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<210> 3836

<211> 479

<212> PRT

<213> Homo sapiens

<400> 3836

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 Gly Gly Ile Glu Gln Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr

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      35              40              45
Ala Arg Ala Gly Gly Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr
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Phe Phe Leu Phe Val Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu
  65              70              75
Val Leu Phe Met Val Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn
      85              90              95
Leu Gln Ala Thr Glu Arg Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu
      100              105              110
Gly Leu Thr Ala Ser Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr
      115              120              125
Thr Arg Ala Lys Asp Ala Ile Met Gln Met Trp Leu Asn Ala Arg Arg
      130              135              140
Asp Leu Asp Arg Ile Asn Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg
      145              150              155
Val Ile Tyr Thr Asn Asn Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser
      165              170              175
Glu Lys Gln Cys Arg Asp Gln Phe Lys Asp Met Asn Lys Ser Cys Asp
      180              185              190
Ala Leu Leu Phe Met Leu Asn Gln Lys Val Lys Thr Leu Glu Val Glu
      195              200              205
Ile Ala Lys Glu Lys Thr Ile Cys Thr Lys Asp Lys Glu Ser Val Leu
      210              215              220
Leu Asn Lys Arg Val Ala Glu Glu Gln Leu Val Glu Cys Val Lys Thr
      225              230              235
Arg Glu Leu Gln His Gln Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln
      245              250              255
Lys Val Gln Ala Leu Cys Leu Pro Leu Asp Lys Asp Lys Phe Glu Met
      260              265              270
Asp Leu Arg Asn Leu Trp Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp
      275              280              285
Asn Leu Gly Tyr Asn Leu Tyr His Pro Leu Gly Ser Glu Leu Ala Ser
      290              295              300
Ile Arg Arg Ala Cys Asp His Met Pro Ser Leu Met Ser Ser Lys Val
      305              310              315
Glu Glu Leu Ala Arg Ser Leu Arg Ala Asp Ile Glu Arg Val Ala Arg
      325              330              335
Glu Asn Ser Asp Leu Gln Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu
      340              345              350
Arg Ala Ser Gln Glu Ala Lys Gln Lys Val Glu Lys Glu Ala Gln Ala
      355              360              365
Arg Glu Ala Lys Leu Gln Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala
      370              375              380
Leu Glu Glu Lys Ala Val Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys
      385              390              395
Glu Leu Glu Glu Lys Lys Arg Glu Ala Glu Gln Leu Arg Met Glu Leu
      405              410              415
Ala Ile Arg Asn Ser Ala Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln
      420              425              430
Pro Met Met Pro Val Ser Arg Pro Met Gly Pro Val Pro Asn Pro Gln
      435              440              445
Pro Ile Asp Pro Ala Ser Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu
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Ser Gln Arg Pro Pro Ala Gly Ile Pro Val Ala Pro Ser Ser Gly

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465

470

475

<210> 3837

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 3837

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 120
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 180
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 240
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 300
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 360
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 480
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 540
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 720
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 1980
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 2084

<210> 3838

<211> 468

<212> PRT

<213> Homo sapiens

<400> 3838

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 20 25 30
 Ser His Leu Pro Pro Glu His Ser Asp Val Val Ile Val Gly Gly Gly
 35 40 45
 Val Leu Gly Leu Ser Val Ala Tyr Trp Leu Lys Lys Leu Glu Ser Arg
 50 55 60
 Arg Gly Ala Ile Arg Val Leu Val Val Glu Arg Asp His Thr Tyr Ser
 65 70 75 80
 Gln Ala Ser Thr Gly Leu Ser Val Gly Gly Ile Cys Gln Gln Phe Ser
 85 90 95
 Leu Pro Glu Asn Ile Gln Leu Ser Leu Phe Ser Ala Ser Phe Leu Arg
 100 105 110
 Asn Ile Asn Glu Tyr Leu Ala Val Val Asp Ala Pro Pro Leu Asp Leu
 115 120 125
 Arg Phe Asn Pro Ser Gly Tyr Leu Leu Ala Ser Glu Lys Asp Ala
 130 135 140
 Ala Ala Met Glu Ser Asn Val Lys Val Gln Arg Gln Glu Gly Ala Lys
 145 150 155 160
 Val Ser Leu Met Ser Pro Asp Gln Leu Arg Asn Lys Phe Pro Trp Ile
 165 170 175
 Asn Thr Glu Gly Val Ala Leu Ala Ser Tyr Gly Met Glu Asp Glu Gly

180 185 190
 Trp Phe Asp Pro Trp Cys Leu Leu Gln Gly Leu Arg Arg Lys Val Gln
 195 200 205
 Ser Leu Gly Val Leu Phe Cys Gln Gly Glu Val Thr Arg Phe Val Ser
 210 215 220
 Ser Ser Gln Arg Met Leu Thr Thr Asp Asp Lys Ala Val Val Leu Lys
 225 230 235 240
 Arg Ile His Glu Val His Val Lys Met Asp Arg Ser Leu Glu Tyr Gln
 245 250 255
 Pro Val Glu Cys Ala Ile Val Ile Asn Ala Ala Gly Ala Trp Ser Ala
 260 265 270
 Gln Ile Ala Ala Leu Ala Gly Val Gly Glu Gly Pro Pro Gly Thr Leu
 275 280 285
 Gln Gly Thr Lys Leu Pro Val Glu Pro Arg Lys Arg Tyr Val Tyr Val
 290 295 300
 Trp His Cys Pro Gln Gly Pro Gly Leu Glu Thr Pro Leu Val Ala Asp
 305 310 315 320
 Thr Ser Gly Ala Tyr Phe Arg Arg Glu Gly Leu Gly Ser Asn Tyr Leu
 325 330 335
 Gly Gly Arg Ser Pro Thr Glu Gln Glu Glu Pro Asp Pro Ala Asn Leu
 340 345 350
 Glu Val Asp His Asp Phe Phe Gln Asp Lys Val Trp Pro His Leu Ala
 355 360 365
 Leu Arg Val Pro Ala Phe Glu Thr Leu Lys Cys Phe Val His Pro Gln
 370 375 380
 Val Gln Ser Ala Trp Ala Gly Tyr Tyr Asp Tyr Asn Thr Phe Asp Gln
 385 390 395 400
 Asn Gly Val Val Gly Pro His Pro Leu Val Val Asn Met Tyr Phe Ala
 405 410 415
 Thr Gly Phe Ser Gly His Gly Leu Gln Gln Ala Pro Gly Ile Gly Arg
 420 425 430
 Ala Val Ala Glu Met Val Leu Lys Gly Arg Phe Gln Thr Ile Asp Leu
 435 440 445
 Ser Pro Phe Leu Phe Thr Arg Phe Tyr Leu Gly Glu Lys Ile Gln Glu
 450 455 460
 Asn Asn Ile Ile
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<210> 3839

<211> 758

<212> DNA

<213> Homo sapiens

<400> 3839

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 120
 gtctctttca cttattttcca gggagacatt gggctcagtag tggatgaaca cttctcaaga
 180
 gctttggggc aagccatcac cttccatcca gaatctgcca tttcaaaaag caagatgggg
 240
 ctaaccccc tatggcgaga cagtcagct ctctcaagcc agcggaatag tttccaact
 300

tccttttggg ccagctctta ccagccccc cctgcacctt gtttggggg agttcatcct
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 420
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 660
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<210> 3840

<211> 252

<212> PRT

<213> Homo sapiens

<400> 3840

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			20					25				30			
Met	Glu	Tyr	Leu	Asn	Ser	Arg	Cys	Val	Leu	Phe	Thr	Tyr	Phe	Gln	Gly
		35					40				45				
Asp	Ile	Gly	Ser	Val	Val	Asp	Glu	His	Phe	Ser	Arg	Ala	Leu	Gly	Gln
	50					55				60					
Ala	Ile	Thr	Leu	His	Pro	Glu	Ser	Ala	Ile	Ser	Lys	Ser	Lys	Met	Gly
	65				70				75					80	
Leu	Thr	Pro	Leu	Trp	Arg	Asp	Ser	Ser	Ala	Leu	Ser	Ser	Gln	Arg	Asn
			85					90					95		
Ser	Phe	Pro	Thr	Ser	Phe	Trp	Thr	Ser	Ser	Tyr	Gln	Pro	Pro	Pro	Ala
			100				105						110		
Pro	Cys	Leu	Gly	Gly	Val	His	Pro	Asp	Phe	Gln	Val	Thr	Gly	Pro	Pro
		115					120				125				
Gly	Thr	Phe	Ser	Ala	Ala	Asp	Pro	Ser	Pro	Trp	Pro	Gly	His	Asn	Leu
	130				135						140				
His	Gln	Thr	Gly	Pro	Ala	Pro	Pro	Pro	Ala	Val	Ser	Glu	Ser	Trp	Pro
	145				150				155					160	
Tyr	Pro	Leu	Thr	Ser	Gln	Val	Ser	Pro	Ser	Tyr	Ser	His	Met	His	Asp
			165					170					175		
Val	Tyr	Met	Arg	His	His	His	Pro	His	Ala	His	Met	His	His	Arg	His
			180					185					190		
Arg	His	His	His	His	His	His	His	Pro	Ala	Gly	Ser	Ala	Leu	Asp	
		195					200				205				
Pro	Ser	Tyr	Gly	Pro	Leu	Leu	Met	Pro	Ser	Val	His	Ala	Ala	Arg	Ile
	210				215						220				
Pro	Ala	Pro	Gln	Cys	Asp	Ile	Thr	Lys	Thr	Glu	Pro	Thr	Thr	Val	Thr
	225				230					235				240	
Ser	Ala	Thr	Ser	Ala	Trp	Ala	Gly	Ala	Phe	His	Gly				

245

250

<210> 3841

<211> 367

<212> DNA

<213> Homo sapiens

<400> 3841

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 120
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 180
 gtgacgcact caaaaggcta tgagaatggt acaaacagggt tgagcctccc gaagccaatc
 240
 ttgaagagcg aaaagaacaa gcctctggac ccagagatgc agtgctctgct gctctcagat
 300
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 cgggccg
 367

<210> 3842

<211> 122

<212> PRT

<213> Homo sapiens

<400> 3842

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Ala	Gly	Tyr	Trp	Val	Ser	Thr	Cys	Trp	Gly	Leu	Ser	Phe	Val	Val	Pro
			20					25					30		
Gly	Ala	Ile	Val	Ala	Ala	Met	Gly	Ile	Val	Cys	Phe	Leu	Phe	Leu	Ile
			35				40					45			
Glu	His	Pro	Asn	Asp	Val	Arg	Cys	Ser	Ser	Thr	Leu	Val	Thr	His	Ser
	50				55					60					
Lys	Gly	Tyr	Glu	Asn	Gly	Thr	Asn	Arg	Leu	Ser	Leu	Pro	Lys	Pro	Ile
	65			70				75						80	
Leu	Lys	Ser	Glu	Lys	Asn	Lys	Pro	Leu	Asp	Pro	Glu	Met	Gln	Cys	Leu
			85					90					95		
Leu	Leu	Ser	Asp	Gly	Lys	Gly	Ser	Ile	His	Pro	Asn	His	Val	Val	Ile
			100					105					110		
Leu	Pro	Gly	Asp	Gly	Gly	Ser	Gly	Pro	Ala						
			115				120								

<210> 3843

<211> 712

<212> DNA

<213> Homo sapiens

<400> 3843

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 120
 tcccgcaagc gctcgaggag tcgcagccgg tccccggggac gggggtcggg aaagagaaag
 180
 aagaagagca ggaagacac ctcgaggaac tgctcggcct ccacatccca aggtcgcaag
 240
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 300
 cagaaggccc ggaggagaac aagatccagc tcctcctcct cttcttccag ttcttctagc
 360
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 420
 aagtacaagg acaagaggag gaagaagaag aagaagagga agaagctgaa gaagaagggc
 480
 aaggagaagg cggaagcaca gcaggcagag catcatccgc aagggtgtgg accctgagac
 540
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 712

<210> 3844

<211> 143

<212> PRT

<213> Homo sapiens

<400> 3844

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 35 40 45
 Ala Pro Gly Ala Glu Ala Ser Pro Ser Pro Cys Ile Thr Glu Arg Ser
 50 55 60
 Lys Gln Lys Ala Arg Arg Arg Thr Arg Ser Ser Ser Ser Ser Ser Ser
 65 70 75 80
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 85 90 95
 Ser Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr Lys Asp Lys Arg Arg
 100 105 110
 Lys Lys Lys Lys Lys Arg Lys Lys Leu Lys Lys Lys Gly Lys Glu Lys
 115 120 125
 Ala Glu Ala Gln Gln Ala Glu His His Pro Gln Gly Gly Gly Pro
 130 135 140

<210> 3845

<211> 2302

<212> DNA

<213> Homo sapiens

<400> 3845

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120
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180
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420
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<210> 3846

<211> 197

<212> PRT

<213> Homo sapiens

<400> 3846

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			20					25					30		
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			35				40				45				
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Gln	Arg	Ala	Ala	Ser	Arg	Ala	Gly	Cys	Gly	His	Arg	Gln	Leu	Gln	Arg
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Ala	Pro	Ala	Pro	Gly	Leu	Arg	Gln	His	Pro	Cys	Gly	Ser	Gly	Thr	Glu
			115				120					125			
Gly	Leu	Arg	Gly	Gly	His	Leu	Ser	Glu	Thr	Val	Cys	Ala	His	Ala	Glu
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Arg	Thr	Gln	Ala	Pro	Leu	Gln	Ser	Ala	Leu	Gly	Gln	Pro	Ala	Pro	Arg
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Pro	His	Thr	Leu	Gln	Arg	His	Leu	Gly	Pro	His	Ala	Thr	Gly	His	Gly
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<210> 3847
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 3847
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<211> 120

<212> PRT

<213> Homo sapiens

<400> 3848

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			20					25					30		
Asn	Met	Asn	Thr	Leu	Tyr	Pro	Asp	Ala	Thr	Pro	Glu	Glu	Leu	Gln	Ala
			35				40					45			
Met	Asp	Asn	Val	Cys	Ile	Ile	Cys	Arg	Glu	Glu	Met	Val	Thr	Gly	Ala
			50			55					60				
Lys	Arg	Leu	Pro	Cys	Asn	His	Ile	Phe	His	Thr	Arg	Trp	Glu	Gly	Pro
			65			70				75				80	
Trp	Gly	Ala	Cys	Pro	Ala	Gly	Pro	Arg	Pro	Gln	Lys	Ala	Gly	Pro	Lys
			85					90					95		
Gly	Pro	Ala	Asp	Leu	Cys	Leu	Ala	Leu	Thr	Arg	Ser	Cys	Leu	Arg	Ser
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<210> 3849

<211> 1139

<212> DNA

<213> Homo sapiens

<400> 3849

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<210> 3850

<211> 257

<212> PRT

<213> Homo sapiens

<400> 3850

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 35 40 45
 Ala Ala Arg Gly Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp
 50 55 60
 Asp Asp Pro Pro Pro Ser Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro
 65 70 75 80
 Gly Ile Glu Lys Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu
 85 90 95
 Met Ala Asn Lys Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met
 100 105 110
 Lys Lys Ile Val Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg
 115 120 125
 Ile Ile Ala Leu Ser Val Lys Ile Arg Ser Tyr Glu Glu His Leu Glu
 130 135 140
 Lys His Arg Lys Asp Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile
 145 150 155 160
 Asp Gln Arg Lys Lys Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp
 165 170 175
 Val Phe Glu Lys Ile Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro

	180		185		190									
Pro	Leu	Tyr	Arg	Arg	Ala	His	Arg	Arg	Phe	Val	Thr	Lys	Lys	Ala
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Leu	Cys	Ile	Arg	Val	Phe	Gln	Glu	Thr	Gln	Lys	Leu	Lys	Lys	Arg
	210				215						220			
Arg	Ala	Leu	Lys	Ala	Ala	Ala	Ala	Gln	Lys	Gln	Ala	Lys	Arg	Arg
	225			230				235					240	
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<210> 3851

<211> 1183

<212> DNA

<213> Homo sapiens

<400> 3851

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<210> 3852
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 3852
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 35 40 45
 Leu Gln Gly Gln Val Gln Arg Thr Glu Val Ala Arg Gly Arg Leu Glu
 50 55 60
 Lys Arg Asn Ser Asp Leu Leu Leu Leu Val Asp Thr His Lys Lys Gln
 65 70 75 80
 Ile Asp Gln Lys Glu Ala Asp Tyr Gly Arg Leu Ser Ser Arg Leu Gln
 85 90 95
 Ala Arg Glu Gly Leu Gly Lys Arg Cys Glu Asp Asp Lys Val Lys Leu
 100 105 110
 Gln Asn Asn Ile Ser Tyr Gln Met Ala Asp Ile His His Leu Lys Glu
 115 120 125
 Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp Gln Leu
 130 135 140
 Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu Glu Tyr
 145 150 155 160
 Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala Gln His
 165 170 175
 Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu Gln Lys
 180 185 190
 Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu Asp Ile
 195 200 205
 Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu Asn Val
 210 215 220
 Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His Gly Lys
 225 230 235 240
 Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile Glu Glu
 245 250 255
 Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg Lys Pro
 260 265 270
 Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser His Leu
 275 280 285
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<210> 3853
 <211> 375
 <212> DNA
 <213> Homo sapiens

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<210> 3854
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 3854
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 35 40 45
 Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile
 50 55 60
 Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser
 65 70 75 80
 Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser
 85 90 95
 Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln His
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 Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser
 115 120 125

<210> 3855
 <211> 1377
 <212> DNA
 <213> Homo sapiens

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<210> 3856

<211> 330

<212> PRT

<213> Homo sapiens

<400> 3856

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Tyr Val Gly Asp Gly Phe Ser Cys Ser Gly Asn Leu Leu Gln Val Leu
      85              90              95
Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr Glu Val Leu Ala Tyr
      100              105              110
Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu Glu His Leu Thr Asp
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Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln Asn Ser Gly Leu Gly
      130              135              140
Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu His His Leu Ala Asn
      145              150              155              160
Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Xaa Pro Ala
      165              170              175
Asn Glu Gly Gly Lys Gln Ala Ala His His Cys Gln Pro Gly Pro Thr
      180              185              190
Xaa Gln Pro Thr Glu Thr Arg Phe Val Asp Gly Arg Ala Ile Leu Gln
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Trp Asp Ile Phe Ala Ser Asn Gly Ile Ile His Val Ile Ser Arg Pro
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His Phe Glu Ser Glu Glu Asp Ile Asn Val Ala Ala Leu Gly Lys Gln
      275              280              285
Gln Pro Glu Asn Ile Ser Asn Pro Leu Tyr Glu Ser Thr Thr Ser Ala
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<210> 3857

<211> 797

<212> DNA

<213> Homo sapiens

<400> 3857

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 300

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 420
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 480
 aatcgccctt tgccctctcg tcggagcact cctcggagaa cgggagcttg cgctcttcca
 540
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 660
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 797

<210> 3858

<211> 76

<212> PRT

<213> Homo sapiens

<400> 3858

Xaa	Arg	Ala	Thr	Thr	Arg	Thr	Ala	Ser	Gly	Ala	Arg	Ser	Trp	Ala	Trp
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Ala	Thr	Arg	Ala	Ala	Pro	Cys	Pro	Thr	Ser	Cys	Arg	Ala	Trp	Cys	Ser
			20					25					30		
Ala	Pro	Cys	Ser	Thr	Ser	Ala	Arg	Pro	Ser	Thr	Arg	Ser	Trp	Ala	Arg
		35					40				45				
Ser	Ile	Ser	Ala	Ala	Thr	Trp	Pro	Arg	Pro	Arg	Ala	Thr	Gly	Thr	Leu
	50					55				60					
Ala	Thr	Lys	Thr	Arg	Trp	Pro	Ala	Ser	Arg	Thr	Ala				
65				70						75					

<210> 3859

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 3859

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 120
 tttgaagctc ggagtaaaac tgcttgcaag caccctcgga agtgcagtgt ggaacatcat
 180
 acatttttta gaatgcaga aaatgaatcc aattcactgt caagaaaact cagcaagttt
 240
 ggatccatac gttataagca ccgctacagt ggcaggacag ctttgcaaat gagccgagat
 300
 ctttctatcc agcttccccg gcctgatcag aatgtgacaa gaagtogaag caagacttac
 360

cctaagcgaa tagcacaaac acagccagct gaatcaaaca ccatcagtag gataactgca
 420
 aacatggaaa atggagaaaa tgaaggaaca attaaaatta ttgcaccttc accagtaaaa
 480
 agctttaaga aagcaaaaga tgaatatagc cctgataccc aaagaagcaa atctcatgca
 540
 ccgtgggaag aaaatggccc ccagagtggga ctctacaatt ctcccagtga tcgactaag
 600
 tcgccaagt tcctctacac gcgtgcgga aacccctcct gtggaagtga caatgattct
 660
 gtacagcctg tgaggaggag gaaagcccat aacagtgggt aagattcaga tcttaagcaa
 720
 aggaggagg caggttcacg ctgtaacacc agcagtggta gtgaatcaga aaattctaat
 780
 agagaacacc ggaataagag aaacagaata cggcaggaga atgatatggg tgattcagcg
 840
 cctcagtggt aagctgtatt aaggagacaa aaggaaaaaa accaagccga cccaacaac
 900
 aggcgatcca gacacagatc tcgttcgaga agccccgata tccaagcaaa agaaggtta
 960
 tggaaagcaca ttcaaaaaga acttgtggat ccatccggat tgtccgaaga acaattaaaa
 1020
 gagattccat acactaaaa agagtggatg ccttccagaa tcttctcacc aaagcttat
 1080
 tagtgcttga cacaaggtga cccaatccgc atcaggcatt ctcatcgc acgaagttac
 1140
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 1200
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 1260
 ggggatgcta cagttcatca gagaagaaat ggttctaaag atagcctgat ggaagaaaaa
 1320
 cctcagacat ctacaacaa cctggctgga aaacacacag caaaaacaat aaaactata
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 1440
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 1449

<210> 3860

<211> 348

<212> PRT

<213> Homo sapiens

<400> 3860

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Lys	Val	His	Phe	Lys	Glu	Thr	Gln	Phe	Glu	Leu	Arg	Val	Leu	Gly	Lys
		20						25				30			
Asp	Cys	Asn	Glu	Thr	Ser	Phe	Phe	Phe	Glu	Ala	Arg	Ser	Lys	Thr	Ala
		35				40						45			
Cys	Lys	His	Leu	Trp	Lys	Cys	Ser	Val	Glu	His	His	Thr	Phe	Phe	Arg
		50			55					60					
Met	Pro	Glu	Asn	Glu	Ser	Asn	Ser	Leu	Ser	Arg	Lys	Leu	Ser	Lys	Phe


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65          70          75          80
Gly Ser Ile Arg Tyr Lys His Arg Tyr Ser Gly Arg Thr Ala Leu Gln
      85          90
Met Ser Arg Asp Leu Ser Ile Gln Leu Pro Arg Pro Asp Gln Asn Val
      100          105          110
Thr Arg Ser Arg Ser Lys Thr Tyr Pro Lys Arg Ile Ala Gln Thr Gln
      115          120          125
Pro Ala Glu Ser Asn Thr Ile Ser Arg Ile Thr Ala Asn Met Glu Asn
      130          135          140
Gly Glu Asn Glu Gly Thr Ile Lys Ile Ile Ala Pro Ser Pro Val Lys
145          150          155          160
Ser Phe Lys Lys Ala Lys Asn Glu Asn Ser Pro Asp Thr Gln Arg Ser
      165          170          175
Lys Ser His Ala Pro Trp Glu Glu Asn Gly Pro Gln Ser Gly Leu Tyr
      180          185          190
Asn Ser Pro Ser Asp Arg Thr Lys Ser Pro Lys Phe Pro Tyr Thr Arg
      195          200          205
Arg Arg Asn Pro Ser Cys Gly Ser Asp Asn Asp Ser Val Gln Pro Val
      210          215          220
Arg Arg Arg Lys Ala His Asn Ser Gly Glu Asp Ser Asp Leu Lys Gln
      225          230          235          240
Arg Arg Arg Ser Arg Ser Arg Cys Asn Thr Ser Ser Gly Ser Glu Ser
      245          250          255
Glu Asn Ser Asn Arg Glu His Arg Lys Lys Arg Asn Arg Ile Arg Gln
      260          265          270
Glu Asn Asp Met Val Asp Ser Ala Pro Gln Trp Glu Ala Val Leu Arg
      275          280          285
Arg Gln Lys Glu Lys Asn Gln Ala Asp Pro Asn Asn Arg Arg Ser Arg
      290          295          300
His Arg Ser Arg Ser Arg Ser Pro Asp Ile Gln Ala Lys Glu Glu Leu
      305          310          315          320
Trp Lys His Ile Gln Lys Glu Leu Val Asp Pro Ser Gly Leu Ser Glu
      325          330          335
Glu Gln Leu Lys Glu Ile Pro Tyr Thr Lys Ile Glu
      340          345

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<210> 3861

<211> 748

<212> DNA

<213> Homo sapiens

<400> 3861

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gccaccatgt cgaggagacaa acttctgagc gaactcggtt ataagctggg ccgcacaatt
120
ggagaggggca gctactccaa ggtgaagggt gccacatcca agaagtacaa gggtagcgtg
180
gccatcaagg tggtaggaccg gcggcgagcg ccccggaact tcgtcaacaa gttcctgccg
240
cgagagctgt ccatactgcg gggcgtagca caccgcaca tcgtgcacgt ctctcagttc
300
atcgaggtgt gcaacgggaa actgtacatc gtgatggaag cggccgccac cgacctgctg
360

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caagccgtgc agcgcacgg gcgcacccc ggagttcagg cgcgcgacct ctttcgcag
 420
 atcgccggcg ccgtgcgcta cctgcacgat catcacctgg tgcaccgcga cctcaagtgc
 480
 gaaaaagtcg tgctgagccc ggacgagcgc cgcgtcaagc tcaccgactt cggttcggc
 540
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 600
 acccgagtca tgcattttct gagcacctac tgtctgccag gccccagagc tcatggcgaa
 660
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 720
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 748

<210> 3862

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3862

Met	Ser	Gly	Asp	Lys	Leu	Leu	Ser	Glu	Leu	Gly	Tyr	Lys	Leu	Gly	Arg
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Thr	Ile	Gly	Glu	Gly	Ser	Tyr	Ser	Lys	Val	Lys	Val	Ala	Thr	Ser	Lys
			20					25				30			
Lys	Tyr	Lys	Gly	Thr	Val	Ala	Ile	Lys	Val	Val	Asp	Arg	Arg	Arg	Ala
			35				40				45				
Pro	Pro	Asp	Phe	Val	Asn	Lys	Phe	Leu	Pro	Arg	Glu	Leu	Ser	Ile	Leu
			50			55				60					
Arg	Gly	Val	Arg	His	Pro	His	Ile	Val	His	Val	Phe	Glu	Phe	Ile	Glu
65				70				75				80			
Val	Cys	Asn	Gly	Lys	Leu	Tyr	Ile	Val	Met	Glu	Ala	Ala	Ala	Thr	Asp
			85					90				95			
Leu	Leu	Gln	Ala	Val	Gln	Arg	Asn	Gly	Arg	Ile	Pro	Gly	Val	Gln	Ala
			100				105					110			
Arg	Asp	Leu	Phe	Ala	Gln	Ile	Ala	Gly	Ala	Val	Arg	Tyr	Leu	His	Asp
			115				120					125			
His	His	Leu	Val	His	Arg	Asp	Leu	Lys	Cys	Glu	Asn	Val	Leu	Leu	Ser
			130			135				140					
Pro	Asp	Glu	Arg	Arg	Val	Lys	Leu	Thr	Asp	Phe	Gly	Phe	Gly	Arg	Gln
145				150				155				160			
Ala	His	Gly	Tyr	Pro	Asp	Leu	Ser	Thr	Thr	Tyr	Cys	Gly	Ser	Ala	Val
			165					170				175			
Arg	Val	Thr	Arg	Val	Met	His	Phe	Leu	Ser	Thr	Tyr	Cys	Leu	Pro	Gly
			180					185				190			
Pro	Arg	Ala	His	Gly	Glu	Glu	Thr	Trp	Ala	His	Pro	Cys	Arg	Lys	Arg
			195				200					205			

Asp Asn
 210

<210> 3863

<211> 341

<212> DNA

<213> Homo sapiens

<400> 3863

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 120
 agttttgtct tcagttggga ctctgggaaa aaaactgtgt ggctgatctc cagcagggttc
 180
 ttctgggtga ggctccccga gaaccatctg gccatgggct ggcagccgag ttctcgcagt
 240
 gtccaggctg acggtacatt ccaggctagc cctcctatca taatcgaatc tgagtagatt
 300
 tttatcaatc gcttgggaca agccattgaa ttttcggaga g
 341

<210> 3864

<211> 108

<212> PRT

<213> Homo sapiens

<400> 3864

Met	Ala	Cys	Pro	Lys	Arg	Leu	Ile	Lys	Ile	Tyr	Ser	Asp	Ser	Ile	Met
1				5					10					15	
Ile	Gly	Trp	Leu	Ala	Trp	Asn	Val	Pro	Ser	Ala	Trp	Thr	Leu	Arg	Glu
			20					25					30		
Leu	Gly	Cys	Gln	Pro	Met	Ala	Arg	Trp	Phe	Ser	Gly	Ser	Leu	Asp	Gln
			35				40					45			
Lys	Asn	Leu	Val	Glu	Ile	Ser	His	Thr	Val	Phe	Phe	Pro	Glu	Ser	Gln
	50					55				60					
Leu	Arg	Ala	Lys	Leu	Lys	Cys	Pro	Gly	Gly	Ser	Cys	Thr	Pro	Gly	Leu
65				70					75					80	
Lys	Lys	Ile	Gly	Ser	Leu	Lys	Val	Ser	Cys	Glu	Glu	Phe	Leu	Leu	Met
			85					90					95		
Gly	Leu	Arg	Tyr	Gln	His	Leu	Asp	Pro	Pro	Ser	Arg				
			100					105							

<210> 3865

<211> 492

<212> DNA

<213> Homo sapiens

<400> 3865

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 120
 gagacctatg tgaagcccac ttaattttct gaaacttcac atcatgtacc ttcattgtaa
 180
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 240
 ttgtccacaa gggtttcagga taattaatac aaatgggttg ggccagccat cacacagcag
 300
 tctcctattt acttcactac aactacagct ttcattcttc attacattac tttttctgag
 360

tagtctgggt caaatagtac aaactgaata ttccttaacc aaaatgcttg gaagtaggcc
 420
 gggagcagcg gctcaccct gtaatcccag cattttggga ggccaaagca gacagatcac
 480
 tcaaggtcag ca
 492

<210> 3866
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 3866
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 Ser His Asn Phe Lys Phe Leu Val Arg Leu Cys Ser Gln Gly Phe Arg
 20 25 30
 Ile Ile Asn Thr Asn Gly Leu Gly Gln Pro Ser His Ser Ser Leu Leu
 35 40 45
 Phe Thr Ser Leu Gln Leu Gln Leu Ser Phe Phe Ile Thr Leu Leu Phe
 50 55 60
 Leu Ser Ser Leu Gly Gln Ile Val Gln Thr Glu Tyr Ser Leu Thr Lys
 65 70 75 80
 Met Leu Gly Ser Arg Pro Gly Ala Ala Ala His Pro Cys Asn Pro Ser
 85 90 95
 Ile Leu Gly Gly Gln Ser Arg Gln Ile Thr Gln Gly Gln
 100 105

<210> 3867
 <211> 1032
 <212> DNA
 <213> Homo sapiens

<400> 3867
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 60
 gacagcatc agactgagat cagggatctc caggaccagc tctcagaaat gcacgatgaa
 120
 ctggacagtg caaagcgatc ggaggacagg gagaaggagg ctctgattga ggagctctta
 180
 caggcaaaac aggatcttca agatctgctg attgccaaag aggagcaaga agacctcttg
 240
 agaaagcgag agcgtgaact caccgccctg aaggaggccc tgaaagaaga ggtttccagg
 300
 catgatcagg agatggacaa gctgaaggag caatatgatg ctgagttgca ggccctgagg
 360
 gagagtgtgg aagaagcaac caagaatgtc gaggtcttgg cgagcaggag caacacttca
 420
 gagcaagacc aggcggggac tgaatgcgc gtgaagcttc tgaggaggga gaatgagaag
 480
 ctgcagggaa gaagcgaaga gctggagcgg agagttgctc agcttcaaag gcagatcgag
 540
 gacctgaaag gcgatgaagc caaggcgaag gaaacgctga agaagtacga gggagaaaaa
 600

cgacagtttag agggaggccct tgtgcacgcc agaaaggaag aaaaagaagc tgtgtcagcc
 660
 agaagggccc tggagaatga actggaggct gctcagggaa atctgagtca gactaccag
 720
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 780
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 840
 cagaaggaga tggcagacat tgttgaggcc tcccgtaact caacctgga gctccagaac
 900
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 960
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 1020
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 1032

<210> 3868

<211> 344

<212> PRT

<213> Homo sapiens

<400> 3868

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Lys	Met	Glu	Arg	Glu	Gln	His	Gln	Thr	Glu	Ile	Arg	Asp	Leu	Gln	Asp
				20				25					30		
Gln	Leu	Ser	Glu	Met	His	Asp	Glu	Leu	Asp	Ser	Ala	Lys	Arg	Ser	Glu
		35					40					45			
Asp	Arg	Glu	Lys	Gly	Ala	Leu	Ile	Glu	Glu	Leu	Leu	Gln	Ala	Lys	Gln
				50		55					60				
Asp	Leu	Gln	Asp	Leu	Leu	Ile	Ala	Lys	Glu	Glu	Gln	Glu	Asp	Leu	Leu
65				70					75					80	
Arg	Lys	Arg	Glu	Arg	Glu	Leu	Thr	Ala	Leu	Lys	Gly	Ala	Leu	Lys	Glu
				85				90						95	
Glu	Val	Ser	Ser	His	Asp	Gln	Glu	Met	Asp	Lys	Leu	Lys	Glu	Gln	Tyr
				100				105					110		
Asp	Ala	Glu	Leu	Gln	Ala	Leu	Arg	Glu	Ser	Val	Glu	Glu	Ala	Thr	Lys
				115			120						125		
Asn	Val	Glu	Val	Leu	Ala	Ser	Arg	Ser	Asn	Thr	Ser	Glu	Gln	Asp	Gln
				130			135					140			
Ala	Gly	Thr	Glu	Met	Arg	Val	Lys	Leu	Leu	Gln	Glu	Glu	Asn	Glu	Lys
145				150						155				160	
Leu	Gln	Gly	Arg	Ser	Glu	Glu	Leu	Glu	Arg	Arg	Val	Ala	Gln	Leu	Gln
				165				170						175	
Arg	Gln	Ile	Glu	Asp	Leu	Lys	Gly	Asp	Glu	Ala	Lys	Ala	Lys	Glu	Thr
				180				185					190		
Leu	Lys	Lys	Tyr	Glu	Gly	Glu	Ile	Arg	Gln	Leu	Glu	Glu	Ala	Leu	Val
				195			200						205		
His	Ala	Arg	Lys	Glu	Glu	Lys	Glu	Ala	Val	Ser	Ala	Arg	Arg	Ala	Leu
				210			215					220			
Glu	Asn	Glu	Leu	Glu	Ala	Ala	Gln	Gly	Asn	Leu	Ser	Gln	Thr	Thr	Gln
225				230						235				240	
Glu	Gln	Lys	Gln	Leu	Ser	Glu	Lys	Leu	Lys	Glu	Glu	Ser	Glu	Gln	Lys

245										250					255				
Glu	Gln	Leu	Arg	Arg	Leu	Lys	Asn	Glu	Met	Glu	Asn	Glu	Arg	Trp	His				
260										265					270				
Leu	Gly	Lys	Thr	Ile	Glu	Lys	Leu	Gln	Lys	Glu	Met	Ala	Asp	Ile	Val				
275										280					285				
Glu	Ala	Ser	Arg	Thr	Ser	Thr	Leu	Glu	Leu	Gln	Asn	Gln	Leu	Asp	Glu				
290										295					300				
Tyr	Lys	Glu	Lys	Asn	Arg	Arg	Glu	Leu	Ala	Glu	Met	Gln	Arg	Gln	Leu				
305										310					315				
Lys	Glu	Lys	Thr	Leu	Glu	Ala	Glu	Lys	Ser	Arg	Leu	Thr	Ala	Met	Lys				
320										325					330				
Met	Gln	Asp	Glu	Met	Arg	Leu	Met												
340																			

<210> 3869

<211> 1226

<212> DNA

<213> Homo sapiens

<400> 3869

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120					
tgatgcacac	acattccaga	aatgcagagg	tatgctgctg	ccacggggta	gggggtcggg
180					
aggcgggcgt	gcctcatggc	cgcagaccgt	gccccagccc	gggcgtggca	ggtagctggc
240					
cactgataaa	tgccactggg	atcctaggag	aagctgggga	ccatgcgtga	ggtactgaag
300					
gggacatgat	tggtatggcat	cctgggcact	ttgtagcttg	tctgagggaa	aggcctctgc
360					
tgccatagaa	aagctggaca	catgtcaccc	tggggccctg	acatcctaaa	atgccccact
420					
gactaccagt	cactaggaga	aagggtctcg	gctatgccct	tcccagtgat	gcttgcccac
480					
gagtgactgg	tcacaggttg	gggacaggtt	tgtctccaaa	accgtaggcc	ttctttgtct
540					
ggccccctaa	agaggaccca	agatcaggaa	aactccccag	tttaaaaaaa	tatctgtcca
600					
ttctgtatata	aaatacctat	tattagctgg	agttgcacac	atgcaggacc	aggagagact
660					
gcctgaggtt	ctgcctggac	cgaaggaggc	ctcgctcaca	gcacctctgt	gaggggagct
720					
gtgctctctg	gaagtcaatt	ctcttggtga	ccgagctgac	acccccctca	cttggaagac
780					
acaggggactg	agcaggcggg	acctgtgctg	gagggagacc	ctcctgggtga	ggaactatgc
840					
ggggccttctg	ggcctcagca	gtctccagccc	actcctggcc	tggcaggcca	cctgcccacc
900					
cacccacccta	tctgcctctg	gcccccagtg	aagtcagaag	aggcaggagc	ccgcgaggct
960					
gtgagccctg	cgcaggtcgg	ctgacacgca	gctttctcatc	tgccctgggtg	tagagcgga
1020					

gctctcggca gcctgcacgg cccggctcag ggccttggtg agctcctcta ggtcgcacag
 1080
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 1200
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 1226

<210> 3870
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 3870
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 Ala Ile His His Gly Pro Leu Gln Tyr Leu Thr His Gly Pro Gln Leu
 20 25 30
 Leu Leu Gly Ser Gln Trp His Leu Ser Val Ala Ser Tyr Leu Pro Gly
 35 40 45
 Pro Gly Trp Gly Thr Val Cys Gly His Glu Ala Arg Pro Pro Pro Ala
 50 55 60
 Pro Leu Pro Arg Gly Ser Ile Pro Leu His Phe Trp Asn Val Cys
 65 70 75 80
 Ala Ser Met Met Phe Val Tyr Leu Arg His Leu Lys Ile Tyr Phe Arg
 85 90 95
 Tyr Glu Gly Lys
 100

<210> 3871
 <211> 473
 <212> DNA
 <213> Homo sapiens

<400> 3871
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 60
 tgcctcacat ttcccagtgc ttctctgca cccctccatt ggagtaaaaa ccacagtttg
 120
 tgggatgggt gagttgacag ctctgaatcc cagaaacctt aattttggct tatcttttga
 180
 taggctgagg gaaaatacaa agatgatcct gttgatctcc gccttgatat tgaacgtcgt
 240
 aaaaaacata aggagagaga tcttaaacga ggtaaatcga gagaatcagt ggattcccca
 300
 gactccagtc actcaaggga aaggtcagct gaaaaaacag agaaaactca taaaggatca
 360
 aagaaacaga agaaagacct ctgagagccg agacaagctg ggagcgaaag gagatttttc
 420
 cacaggaaag tcttcctttt ccattactcg agaggcacag gtcaatgtcc gga
 473

<210> 3872

<211> 66

<212> PRT

<213> Homo sapiens

<400> 3872

Ala Glu Gly Lys Tyr Lys Asp Asp Pro Val Asp Leu Arg Leu Asp Ile
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 Glu Arg Arg Lys Lys His Lys Glu Arg Asp Leu Lys Arg Gly Lys Ser
 20 25 30
 Arg Glu Ser Val Asp Ser Arg Asp Ser Ser His Ser Arg Glu Arg Ser
 35 40 45
 Ala Glu Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys Lys
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 Asp Leu
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<210> 3873

<211> 869

<212> DNA

<213> Homo sapiens

<400> 3873

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<210> 3874

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<400> 3874

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Leu Thr Ile Arg Gly Asn Thr Ala Leu His Glu Ala Val Ile Glu Lys
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<211> 2640

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<213> Homo sapiens

<400> 3875

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<210> 3876

<211> 824

<212> PRT

<213> Homo sapiens

<400> 3876

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 Pro Pro Lys Glu Glu Glu Leu Arg Ala Ala Val Glu Val Leu Arg Gly
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 His Gly Leu His Ser Val Leu Glu Glu Trp Phe Val Glu Val Leu Gln
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 Asn Asp Leu Gln Ala Asn Ile Ser Pro Glu Phe Trp Asn Ala Ile Ser
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 Gln Cys Glu Asn Ser Ala Asp Glu Pro Gln Cys Leu Leu Leu Leu Leu
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 Asp Ala Phe Gly Leu Leu Glu Ser Arg Leu Asp Pro Tyr Leu Arg Ser
 115 120 125
 Leu Glu Leu Leu Glu Lys Trp Thr Arg Leu Gly Leu Leu Met Gly Thr

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Tyr Gly Cys Phe Leu Arg Val Tyr Met Gln Ser Lys Arg Lys Gly Glu					
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Gly Gly Thr Asp Pro Glu Leu Glu Gly Glu Leu Asp Ser Arg Tyr Ala					
	195		200		205
Arg Arg Arg Tyr Tyr Arg Leu Leu Gln Ser Pro Leu Cys Ala Gly Cys					
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Ser Ser Asp Lys Gln Gln Cys Trp Cys Arg Gln Ala Leu Glu Gln Phe					
	225		230		240
His Gln Leu Ser Gln Val Leu His Arg Leu Ser Leu Leu Glu Arg Val					
	245		250		255
Ser Ala Glu Ala Val Thr Thr Thr Leu His Gln Val Thr Arg Glu Arg					
	260		265		270
Met Glu Asp Arg Cys Arg Gly Glu Tyr Glu Arg Ser Phe Leu Arg Glu					
	275		280		285
Phe His Arg Trp Ile Glu Arg Val Val Gly Trp Leu Gly Lys Val Phe					
	290		295		300
Leu Gln Asp Gly Pro Ala Arg Pro Ala Ser Pro Glu Ala Gly Asn Thr					
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Leu Arg Arg Trp Arg Cys His Val Gln Arg Phe Phe Tyr Arg Ile Tyr					
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Ala Ser Leu Arg Ile Glu Glu Leu Phe Ser Ile Val Arg Asp Phe Pro					
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Asp Leu Phe Ile Asn Glu Tyr Arg Ser Leu Leu Ala Asp Arg Leu Leu					
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His Gln Phe Ser Phe Ser Pro Glu Arg Glu Ile Arg Asn Val Glu Leu					
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Leu Lys Leu Arg Phe Gly Glu Ala Pro Met His Phe Cys Glu Val Met					
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Leu Lys Asp Met Ala Asp Ser Arg Arg Ile Asn Ala Asn Ile Arg Glu					

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 Thr Gly Pro Ala Leu Ala Glu Ile Asp Leu Gln Glu Leu Gln Gly Tyr
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<212> DNA

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<210> 3878

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<212> PRT

<213> Homo sapiens

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Gln Thr Thr Phe Glu Ser Gln Asp Arg Lys Ala Val Ser Pro Ser Ser
      50             55             60
Ser Glu Lys Arg Ser Lys Asn Pro Ile Ser Arg Pro Leu Glu Gly Lys
      65             70             75             80
Lys Ser Leu Ser Leu Ser Ala Lys Thr His Asn Ile Gly Phe Asp Lys
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Asp Ser Cys His Ser Thr Thr Lys Thr Glu Ala Ser Gln Glu Glu Arg
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Ser Asp Ser Ser Gly Leu Thr Ser Leu Lys Lys Ser Pro Lys Val Ser
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Ser Lys Asp Thr Arg Glu Ile Lys Thr Asp Phe Ser Leu Ser Ile Ser
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Asn Ser Ser Asp Val Ser Ala Lys Asp Lys His Ala Glu Asp Asn Glu
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Lys Arg Leu Ala Ala Leu Glu Ala Arg Gln Lys Ala Lys Glu Val Gln
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Lys Lys Leu Val His Asn Ala Leu Ala Asn Leu Asp Gly His Pro Glu

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Lys Glu Ser Met Gly Lys Thr Ser Gly Lys Leu Phe Asp Ser Ser Asp
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Pro Gln Phe Glu Gly Arg Ala Gly Gln Lys Leu Met Asp Leu Gln Ser
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Thr Asp Ser Glu Glu Glu Gln Glu Glu Val Asn Glu Lys Lys Thr Ala
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<212> DNA

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<210> 3880
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 <212> PRT
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 Thr Ala Leu Pro Ala Leu Glu Thr Ile Asn Leu Glu Glu Asn Glu Ile
 50 55 60
 Val Asp Val Pro Val Glu Lys Leu Ala Ala Met Pro Ala Leu Arg Ser
 65 70 75 80
 Ile Asn Leu Arg Phe Asn Pro Leu Asn Ala Glu Val Arg Val Ile Ala
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<211> 277

<212> PRT

<213> Homo sapiens

<400> 3882

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<212> DNA

<213> Homo sapiens

<400> 3883

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<212> PRT

<213> Homo sapiens

<400> 3884

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<211> 277

<212> PRT

<213> Homo sapiens

<400> 3886

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 65 70 75 80
 Thr Ala Ala Lys Phe Lys Leu Thr Arg His Gln Ala Val Thr Gly Ser
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<212> DNA

<213> Homo sapiens

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			145		150					155				160	
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Lys	Arg	Thr	Ile	Ile	Ala	Leu	Gly	His	Leu	Val	Met	Ser	Cys	Gly	Asn				
		195					200					205							
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Ala	Leu	Ser	Cys</																

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Gly	Asp	Phe	Leu	Lys	Thr	Leu	Glu	Asp	Pro	Asp	Leu	Asn	Val	Arg	Arg
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Val	Ala	Leu	Val	Thr	Phe	Asn	Ser	Ala	Ala	His	Asn	Lys	Pro	Ser	Leu

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          1045          1050          1055
Lys Val Arg Lys Glu Leu Ile Arg Glu Val Glu Met Gly Pro Phe Lys
          1060          1065          1070
His Thr Val Asp Asp Gly Leu Asp Ile Arg Lys Ala Ala Phe Glu Cys
          1075          1080          1085
Met Tyr Thr Leu Leu Asp Ser Cys Leu Asp Arg Leu Asp Ile Phe Glu
          1090          1095          1100
Phe Leu Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile Lys
1105          1110          1115          1120
Met Leu Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser
          1125          1130          1135
Ala Val Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr
          1140          1145          1150
Cys Thr Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys
          1155          1160          1165
Gln Asp Glu Leu Lys Arg Ser Ala Met Arg Ala Val Ala Ala Leu Leu
          1170          1175          1180
Thr Ile Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser
1185          1190          1195          1200
Gln Ile Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln
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<210> 3889

<211> 556

<212> DNA

<213> Homo sapiens

<400> 3889

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556

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<210> 3890

<211> 101
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Arg Lys Val Val Asp Pro Glu Thr Gly Arg Thr Arg Leu Ile Lys Gly
 50 55 60
 Asp Gly Glu Val Leu Glu Glu Ile Val Thr Lys Glu Arg His Arg Glu
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 Ala Gly Leu Leu Pro
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<210> 3891
 <211> 1687
 <212> DNA
 <213> Homo sapiens

<400> 3891
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 720
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 1020
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 1080
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 1140
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<210> 3892

<211> 179

<212> PRT

<213> Homo sapiens

<400> 3892

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		20						25					30		
Ser	Gly	Leu	Phe	Ala	Leu	Cys	Thr	Leu	Asp	Gly	Thr	Leu	Lys	Leu	Met
		35					40					45			
Glu	Glu	Met	Glu	Glu	Ala	Asp	Lys	Leu	Leu	Trp	Ser	Val	Gln	Val	Asp
		50				55					60				
His	Gln	Leu	Phe	Ala	Leu	Glu	Lys	Leu	Asp	Val	Thr	Gly	Asn	Gly	His
		65			70					75				80	
Glu	Glu	Val	Val	Ala	Cys	Ala	Trp	Asp	Gly	Gln	Thr	Tyr	Ile	Ile	Asp
			85					90					95		
His	Asn	Arg	Thr	Val	Val	Arg	Phe	Gln	Val	Asp	Glu	Asn	Ile	Arg	Ala
		100					105					110			
Phe	Cys	Ala	Gly	Leu	Tyr	Ala	Cys	Lys	Glu	Gly	Arg	Asn	Ser	Pro	Cys
		115					120					125			
Leu	Val	Tyr	Val	Thr	Phe	Asn	Gln	Lys	Ile	Tyr	Val	Tyr	Trp	Glu	Val

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<210> 3893

<211> 1591

<212> DNA

<213> Homo sapiens

<400> 3893

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<210> 3894

<211> 334

<212> PRT

<213> Homo sapiens

<400> 3894

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			20					25					30		
Gly	Glu	Ser	Phe	Val	Met	Tyr	Tyr	Lys	Ser	Lys	Glu	Asn	Cys	Val	Val
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Cys	Val	Cys	Ile	Thr	Met	Arg	Val	Pro	Arg	Asn	Pro	Thr	Ile	Gly	Asp
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Pro	Ala	Glu	Asp	Met	Pro	Phe	Thr	Glu	Ser	Gly	Met	Val	Pro	Asp	Ile
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Leu	Phe	Asn	Pro	His	Gly	Phe	Pro	Ser	Arg	Met	Thr	Ile	Gly	Met	Leu
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Ile	Glu	Ser	Met	Ala	Gly	Lys	Ser	Ala	Ala	Leu	His	Gly	Leu	Cys	His
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Asp	Ala	Thr	Pro	Phe	Ile	Phe	Ser	Glu	Glu	Asn	Ser	Ala	Leu	Glu	Tyr
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			165					170					175		
Arg	Leu	Tyr	Ser	Gly	Ile	Ser	Gly	Leu	Glu	Leu	Glu	Ala	Asp	Ile	Phe
			180				185						190		
Ile	Gly	Val	Val	Tyr	Tyr	Gln	Arg	Leu	Arg	His	Met	Val	Ser	Asp	Lys
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Phe	Gln	Val	Arg	Thr	Thr	Gly	Ala	Arg	Asp	Arg	Val	Thr	Asn	Gln	Pro
	210					215					220				
Ile	Gly	Gly	Arg	Asn	Val	Gln	Gly	Gly	Ile	Arg	Phe	Gly	Glu	Met	Glu
	225				230				235					240	
Arg	Asp	Ala	Leu	Leu	Ala	His	Gly	Thr	Ser	Phe	Leu	Leu	His	Asp	Arg
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[illegible]

<210> 3895

<211> 1227

<212> DNA

<213> Homo sapiens

<400> 3895

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180					
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300					
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360					
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420					
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480					
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660					
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780					
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1140					

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 1227

<210> 3896

<211> 346

<212> PRT

<213> Homo sapiens

<400> 3896

Lys	Thr	Leu	Arg	Val	Val	Tyr	Glu	Glu	Glu	Glu	Asp	Gly	Thr
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Leu	Lys	Gln	His	Lys	Glu	Ala	Lys	Arg	Phe	Glu	Ile	Ala	Arg
		20					25					30	
Pro	Glu	Asp	Thr	Pro	Glu	Asn	Thr	Val	Arg	Arg	Gln	Glu	Pro
		35				40					45		Ser
Ile	Glu	Ser	Thr	Ser	Pro	Ile	Ser	Arg	Thr	Asp	Glu	Ile	Arg
	50				55					60			Lys
Thr	Tyr	Arg	Thr	Leu	Asp	Ser	Leu	Glu	Gln	Thr	Ile	Lys	Gln
65				70					75				80
Asn	Thr	Ile	Ser	Glu	Met	Ser	Pro	Lys	Ala	Leu	Val	Asp	Thr
			85					90				95	
Ser	Ser	Asn	Arg	Asp	Ser	Val	Ala	Ser	Ser	Ser	His	Ile	Ala
		100					105					110	Glu
Ala	Ser	Pro	Arg	Pro	Leu	Leu	Val	Pro	Asp	Glu	Gly	Pro	Thr
	115					120					125		Ala
Glu	Pro	Pro	Thr	Ser	Ile	Pro	Ser	Ala	Ser	Arg	Lys	Gly	Ser
	130				135						140		Ser
Ala	Pro	Gln	Thr	Ser	Arg	Met	Pro	Val	Pro	Met	Ser	Ala	Lys
145				150					155				160
Pro	Gly	Thr	Leu	Asp	Lys	Pro	Gly	Lys	Gln	Ser	Lys	Leu	Gln
		165						170				175	Asp
Arg	Gln	Tyr	Arg	Gln	Ala	Asn	Gly	Ser	Ala	Lys	Lys	Ser	Gly
	180					185						190	Gly
Phe	Lys	Pro	Thr	Ser	Pro	Ser	Leu	Pro	Ala	Ser	Lys	Ile	Pro
	195					200						205	Ala
Ser	Pro	Ser	Ser	Gly	Lys	Ser	Ser	Ser	Leu	Pro	Ser	Ser	Ser
210				215						220			Gly
Ser	Ser	Asn	Leu	Pro	Asn	Pro	Pro	Ala	Thr	Lys	Pro	Ser	Ile
225				230						235			240
Asn	Pro	Leu	Ser	Pro	Gln	Thr	Gly	Pro	Pro	Ala	His	Ser	Ala
		245							250				255
Ile	Pro	Ser	Val	Ser	Asn	Gly	Ser	Leu	Lys	Phe	Gln	Ser	Leu
	260						265					270	Thr
Thr	Gly	Lys	Gly	His	His	Leu	Ser	Phe	Ser	Pro	Gln	Ser	Gln
	275					280					285		Asn
Arg	Ala	Pro	Pro	Pro	Leu	Ser	Phe	Ser	Ser	Ser	Pro	Pro	Ser
	290				295					300			Ala
Ser	Ser	Val	Ser	Leu	Asn	Gln	Gly	Ala	Lys	Gly	Thr	Arg	Thr
305				310						315			Ile
Thr	Pro	Ser	Leu	Thr	Ser	Tyr	Lys	Ala	Gln	Asn	Gly	Ser	Ser
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Ala	Thr	Pro	Ser	Thr	Ala	Lys	Glu	Thr	Ser				

340

<210> 3897
 <211> 366
 <212> DNA
 <213> Homo sapiens

345

<400> 3897
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 366

<210> 3898
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 3898
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 20 25 30
 His Pro Arg Phe Val His Glu Trp Lys Ala Met Leu Thr Ala Ala Gln
 35 40 45
 Cys Val Gln Asp Val Ser Glu Thr Pro Val Pro Leu Pro Val Pro Leu
 50 55 60
 Ser Val Pro Leu Ser Thr Ser Val Thr Ser Ser Leu Arg Gly Ser His
 65 70 75 80
 Pro Thr Leu Cys His Cys His Ile Phe Leu Cys Ala Gln Pro Leu Pro
 85 90 95
 Pro Pro Glu Thr Phe Leu Glu Ile Ser Lys Cys Asn Ser Arg Ser
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<210> 3899
 <211> 1092
 <212> DNA
 <213> Homo sapiens

<400> 3899
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accttccgga aaatggcggc tgccaggccc agcctggggc gagtctctccc aggatcctct
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 240
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 360
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 960
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 1080
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 1092

<210> 3900

<211> 249

<212> PRT

<213> Homo sapiens

<400> 3900

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 Pro Ser Glu Arg Arg Glu Val Arg Val Pro Pro Pro His Leu Gln Arg
 20 25 30
 Gly Arg Ser Gly Leu Glu Pro Gly Thr Phe Arg Lys Met Ala Ala Ala
 35 40 45
 Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser Val Leu Phe Leu
 50 55 60
 Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala Tyr Phe Pro Gln
 65 70 75 80
 Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala Arg Leu Leu Glu
 85 90 95
 Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly Leu Gly Pro Thr

```

          100                      105                      110
Val Pro Glu Leu Gly Thr Xaa Gly Pro Ser Ala Ala Gly Gln Asp Leu
          115                      120                      125
Leu Gln His Gly Ala Cys Leu Gln Gln Glu Leu Asp Ser Arg Pro Gln
          130                      135                      140
Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln Ala Cys Ile Leu
          145                      150                      155                      160
Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln Val His Val Val
          165                      170                      175
Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg Leu Val Ala Leu
          180                      185                      190
Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr Ser Glu Gly Leu
          195                      200                      205
Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln Phe Lys Glu Ile
          210                      215                      220
Gln Lys Leu Ile Lys Glu Pro Ala Pro Asp Ser Gly Leu Leu Gly Leu
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Phe Gln Gly Gln Asn Ser Leu Leu His
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<210> 3901

<211> 1287

<212> DNA

<213> Homo sapiens

<400> 3901

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240
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480
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540
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600
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720
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840

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<210> 3902

<211> 312

<212> PRT

<213> Homo sapiens

<400> 3902

Met Leu Leu Leu Val Leu Lys Leu Met Arg Asp His Val Pro Pro
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 20 25 30
 Trp Ala Ala Thr Thr Ala Arg Asn Ala Leu Val Val Ser Phe Ala Ala
 35 40 45
 Leu Val Ala Tyr Ser Phe Glu Val Thr Gly Tyr Gln Pro Phe Ile Leu
 50 55 60
 Thr Gly Glu Thr Ala Glu Gly Leu Pro Pro Val Arg Ile Pro Pro Phe
 65 70 75 80
 Ser Val Thr Thr Ala Asn Gly Thr Ile Ser Phe Thr Glu Met Val Gln
 85 90 95
 Asp Met Gly Ala Gly Leu Ala Val Val Pro Leu Met Gly Leu Leu Glu
 100 105 110
 Ser Ile Ala Val Ala Lys Ala Phe Ala Ser Gln Asn Asn Tyr Arg Ile
 115 120 125
 Asp Ala Asn Gln Glu Leu Leu Ala Ile Gly Leu Thr Asn Met Leu Gly
 130 135 140
 Ser Leu Val Ser Ser Tyr Pro Val Thr Gly Ser Phe Gly Arg Thr Ala
 145 150 155 160
 Val Asn Ala Gln Ser Gly Val Cys Thr Pro Ala Gly Gly Leu Val Thr
 165 170 175
 Gly Val Leu Val Leu Leu Ser Leu Asp Tyr Leu Thr Ser Leu Phe Tyr
 180 185 190
 Tyr Ile Pro Lys Ser Ala Leu Ala Ala Val Ile Ile Met Ala Val Ala
 195 200 205
 Pro Leu Phe Asp Thr Lys Ile Phe Arg Thr Leu Trp Arg Val Lys Arg
 210 215 220
 Leu Asp Leu Leu Pro Leu Cys Val Thr Phe Leu Leu Cys Phe Trp Glu
 225 230 235 240
 Val Gln Tyr Gly Ile Leu Ala Gly Ala Leu Val Ser Leu Leu Met Leu

```

                245                250                255
Leu His Ser Ala Ala Arg Pro Glu Thr Lys Val Ser Glu Gly Pro Val
                260                265                270
Leu Val Leu Gln Pro Ala Ser Gly Leu Ser Phe Pro Val Leu Cys Pro
                275                280                285
Pro Leu Pro Ala Val Gln Asp Pro Lys Thr Leu Ser Pro Thr Leu Ser
                290                295                300
Ser Pro Gln Gly Cys Arg His Leu
305                310

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<210> 3903

<211> 598

<212> DNA

<213> Homo sapiens

<400> 3903

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gccagtctgg cctcggtgcg ggcctttgcc actgcctttc tgagctctga gccacggttg
180
gacatcctca tccacaatgc cggatatcagt tcctgtggcc ggaccctga ggcgtttaac
240
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360
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598

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<210> 3904

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3904

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Ala Arg Arg Gly Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg
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20          25          30
Val Ile Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala
35          40          45
Phe Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
50          55          60
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe Asn
65          70          75          80
Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr His Leu

```



```

      85              90              95
Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val Val Val Val
100              105              110
Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe Lys Arg Leu Asp
115              120              125
Arg Pro Val Val Leu Ala Ala Gly Ala Ala Ala Tyr Ala Asp Thr Lys
130              135              140
Leu Ala Asn Val Leu Phe Ala Arg Glu Leu Ala Asn Gln Leu Glu Ala
145              150              155              160
Thr Gly Val Thr Cys Tyr Ala Ala His Pro Gly Pro Val Asn Ser Glu
165              170              175
Leu Phe Leu Arg His Val Pro Gly Trp Leu Arg Pro Leu Leu Arg Pro
180              185              190
Leu Ala Trp Leu Val Pro Arg
195

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<210> 3905

<211> 370

<212> DNA

<213> Homo sapiens

<400> 3905

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gccaccggcc agtttcgctg ccgcgtgccc ggcgcctact tcttctcctt caccgctggc
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370

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<210> 3906

<211> 123

<212> PRT

<213> Homo sapiens

<400> 3906

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Gly Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro
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20     25     30
Asn Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg
35     40     45
Val Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His
50     55     60
Lys Ser Pro Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala
65     70     75     80
Leu Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser

```

	85		90		95
Gln Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg					
	100		105		110
Leu His Gly Ala Pro Gln Tyr Ala Leu Gly Ala					
	115		120		

<210> 3907

<211> 4474

<212> DNA

<213> Homo sapiens

<400> 3907

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 120
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 420
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 Gln Pro Ala Glu Gly Leu Val Ala Asn Val Ile Thr Ala Gly Asp Tyr
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<213> Homo sapiens

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 <213> Homo sapiens
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 35 40 45
 Met Glu Glu Val Leu Leu Gly Leu Lys Asp Lys Glu Gly Tyr Thr
 50 55 60
 Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Gly Ile Leu
 65 70 75 80
 Ile Glu Leu Ala Met Arg Gly Arg Ile Tyr Leu Glu Pro Pro Thr Met
 85 90 95
 Arg Lys Lys Arg Leu Leu Asp Arg Lys Val Leu Leu Lys Ser Asp Ser
 100 105 110
 Pro Thr Gly Asp Val Leu Leu Asp Glu Thr Leu Lys His Ile Lys Ala
 115 120 125
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130 135 140
 Glu Thr Trp Asn Pro Phe Lys Leu
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 <210> 3919
 <211> 1278
 <212> DNA
 <213> Homo sapiens

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 360
 ctagcggcag acgcccggtc tgctcgtgcc tatcgagacg agctggattc cctgccccgag
 420
 aaggcgaacc gcgtggagag gctggagctg gagctgaccc gctgcaagga gaagctgcac
 480
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 900
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 960
 aaggagaacc accagctcag caagaagatt gaaaagtac aaaccagct ggagagagaa
 1020
 aagcagagca accaagatct ggagaccctc agtgaggagc tgatcagaga gaaggagcag
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 1278

<210> 3920

<211> 426

<212> PRT

<213> Homo sapiens

<400> 3920

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Arg Arg Leu Ile Asp Gln Arg Asp Glu Cys Thr Glu Leu Ile Val Asp
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Leu Thr Gln Glu Arg Asp Tyr Leu Gln Ala Gln His Pro Pro Ser Pro
 35           40           45
Ile Lys Ser Ser Ser Ala Asp Ser Thr Pro Ser Pro Thr Ser Ser Leu
 50           55           60
Ser Ser Glu Asp Lys Gln His Leu Ala Val Glu Leu Ala Asp Thr Lys
 65           70           75           80
Ala Arg Leu Arg Arg Val Arg Gln Glu Leu Glu Asp Lys Thr Glu Gln
 85           90           95
Leu Val Asp Thr Arg His Glu Val Asp Gln Leu Val Leu Glu Leu Gln
100          105          110
Lys Val Lys Gln Glu Asn Ile Gln Leu Ala Ala Asp Ala Arg Ser Ala
115          120          125
Arg Ala Tyr Arg Asp Glu Leu Asp Ser Leu Arg Glu Lys Ala Asn Arg
130          135          140
Val Glu Arg Leu Glu Leu Glu Leu Thr Arg Cys Lys Glu Lys Leu His
145          150          155          160
Asp Val Asp Phe Tyr Lys Ala Arg Met Glu Glu Leu Arg Glu Asp Asn
165          170          175
Ile Ile Leu Ile Glu Thr Lys Ala Met Leu Glu Glu Gln Leu Thr Ala
180          185          190
Ala Arg Ala Arg Gly Asp Lys Val His Glu Leu Glu Lys Glu Asn Leu
195          200          205
Gln Leu Lys Ser Lys Leu His Asp Leu Glu Leu Asp Arg Asp Thr Asp
210          215          220
Lys Lys Arg Ile Glu Glu Leu Leu Glu Glu Asn Met Val Leu Glu Ile
225          230          235          240
Ala Gln Lys Gln Ser Met Asn Glu Ser Ala His Leu Gly Trp Glu Leu
245          250          255
Glu Gln Leu Ser Lys Asn Ala Asp Leu Ser Asp Ala Ser Arg Lys Ser
260          265          270
Phe Val Phe Glu Leu Asn Glu Cys Ala Ser Ser Arg Ile Leu Lys Leu
275          280          285
Glu Lys Glu Asn Gln Ser Leu Gln Ser Thr Ile Gln Gly Leu Arg Asp
290          295          300
Ala Ser Leu Val Leu Glu Glu Ser Gly Leu Lys Cys Gly Glu Leu Glu
305          310          315          320
Lys Glu Asn His Gln Leu Ser Lys Lys Ile Glu Lys Leu Gln Thr Gln
325          330          335
Leu Glu Arg Glu Lys Gln Ser Asn Gln Asp Leu Glu Thr Leu Ser Glu
340          345          350
Glu Leu Ile Arg Glu Lys Glu Gln Leu Gln Ser Asp Met Glu Thr Leu
355          360          365
Lys Ala Asp Lys Ala Arg Gln Ile Lys Asp Leu Glu Gln Glu Lys Asp

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      370              375              380
His Leu Asn Arg Ala Met Trp Ser Leu Arg Glu Arg Ser Gln Val Ser
385              390              395              400
Ser Glu Ala Arg Met Lys Asp Val Glu Lys Glu Asn Lys Ala Leu His
      405              410              415
Gln Thr Val Thr Glu Ala Asn Gly Lys Leu
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<210> 3921
 <211> 413
 <212> DNA
 <213> Homo sapiens

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<400> 3921
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240
gaggggttcca gagaatgggc ctggcggttct gcaagcctgg caccctctct ggaatgctttt
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413

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<210> 3922
 <211> 126
 <212> PRT
 <213> Homo sapiens

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<400> 3922
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Arg Gln Pro Gly Pro Val Phe Val Gly Thr Arg Phe Gln Met Pro Leu
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Leu Leu Ala Ser Leu Val Thr Phe Ile His Ala Gly Pro Cys Phe Leu
35      40      45
Asp Ser Val Gly Pro Ile Pro Ala Pro Arg Gly Asp Gly Cys Cys Arg
50      55      60
Asp Val Gln Ala Val Glu Gly Ser Arg Glu Trp Ala Trp Arg Ser Ala
65      70      75      80
Ser Leu Ala Pro Leu Leu Asp Ala Phe Leu Gln Pro Leu Glu Leu Arg
      85      90      95
Gln Cys Ser Val Arg Met Ile Ile Gly Phe Pro Pro Gln Phe Leu Ala
100      105      110
His Ser Phe Val Ala Leu Val Thr Ala Phe Cys Asp Asn Ile
115      120      125

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<210> 3923
 <211> 820

<212> DNA

<213> Homo sapiens

<400> 3923

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 120
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 180
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 240
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 300
 ctctcaacta gaacaccatt agtcagatca aatgattta atgtcttcaa ttgttgcttt
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 gttttgagga ctccacccaa aacactgttt tggggtagca ctgaattaac tgtggtgatt
 420
 ttcatgggtc tgcttatata gggtttgtct aacttggcat ctggagtga ccctaacc
 480
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 cagggtttca gtggggtctc agtgcacttt ttattatcac tgcctgttc tgcctttgtt
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 660
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<210> 3924

<211> 250

<212> PRT

<213> Homo sapiens

<400> 3924

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 20 25 30
 Ser Glu Tyr Thr Gly Pro Thr Ser Ala Asp Leu Asp His Phe Pro Ser
 35 40 45
 Val Ser Gln Thr Lys Ala Glu Gln Asp Ser Asp Asn Lys Ser Ser Thr
 50 55 60
 Glu Ile Pro Leu Glu Thr Cys Cys Ser Ser Glu Leu Lys Gly Gly Gly
 65 70 75 80
 Ser Gly Thr Ser Leu Glu Arg Glu Gln Phe Glu Gly Leu Gly Ser Thr
 85 90 95
 Pro Asp Ala Lys Leu Asp Lys Thr Cys Ile Ser Arg Ala Met Lys Ile
 100 105 110
 Thr Thr Val Asn Ser Val Leu Pro Gln Asn Ser Val Leu Gly Gly Val

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      115              120              125
Leu Lys Thr Lys Gln Gln Leu Lys Thr Leu Asn His Phe Asp Leu Thr
   130              135              140
Asn Gly Val Leu Val Glu Ser Leu Ser Glu Glu Pro Leu Pro Ser Leu
  145              150              155              160
Arg Arg Gly Arg Lys Arg His Cys Lys Thr Lys His Leu Glu Gln Asn
      165              170              175
Gly Ser Leu Lys Lys Leu Arg Gln Thr Ser Gly Glu Val Gly Leu Ala
   180              185              190
Pro Thr Asp Pro Val Leu Arg Glu Met Glu Gln Lys Leu Gln Gln Glu
   195              200              205
Glu Glu Asp Arg Gln Leu Ala Leu Gln Leu Gln Arg Met Phe Asp Asn
   210              215              220
Glu Arg Arg Thr Val Ser Arg Arg Lys Gly Ser Val Asp Gln Tyr Leu
  225              230              235              240
Leu Arg Ser Ser Asn Met Ala Gly Gly Arg
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<210> 3925

<211> 3296

<212> DNA

<213> Homo sapiens

<400> 3925

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<210> 3926

<211> 683

<212> PRT

<213> Homo sapiens

<400> 3926

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 Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser
 35 40 45
 Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
 50 55 60
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu Val
 65 70 75 80
 Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly Tyr
 85 90 95
 Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val Ser
 100 105 110
 Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr Lys
 115 120 125
 Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro Glu
 130 135 140
 Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Ala Val
 145 150 155 160
 Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val Asn

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165      170      175
Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala Leu
180      185      190
Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys Val
195      200      205
Ile Ile Leu Met Asp Pro Phe Asp Asp Leu Lys Gln Arg Gly Glu
210      215      220
Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Asp
225      230      235
Lys Glu His Phe Arg Lys Pro Val Pro Ser Pro Glu Asp Leu Ser
245      250      255
Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met
260      265      270
Ile Thr His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys
275      280      285
Val Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
290      295      300
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val Tyr
305      310      315
Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu
325      330      335
Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val Pro
340      345      350
Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys Thr
355      360      365
Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val Ser Ser Lys Phe Lys
370      375      380
Glu Leu Gln Lys Gly Ile Ile Arg His Asp Ser Phe Trp Asp Lys Leu
385      390      395
Ile Phe Ala Lys Ile Gln Asp Ser Leu Gly Gly Arg Val Arg Val Ile
405      410      415
Val Thr Gly Ala Ala Pro Ile Ser Thr Pro Val Leu Thr Phe Phe Arg
420      425      430
Ala Ala Met Gly Cys Trp Val Phe Glu Ala Tyr Gly Gln Thr Glu Cys
435      440      445
Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly His
450      455      460
Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala
465      470      475
Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys
485      490      495
Gly Thr Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln
500      505      510
Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg
515      520      525
Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
530      535      540
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn
545      550      555
Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His Gly Glu
565      570      575
Ser Leu Arg Ser Ser Leu Val Gly Val Val Pro Asp Thr Asp Val
580      585      590
Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly Ser Phe Glu Glu

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	595					600						605			
Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile	Leu	Glu	Asp	Leu	Gln
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Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr	Phe	Glu	Gln	Val	Lys	Ala
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Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser	Ile	Glu	Asn	Gly	Leu	Leu	Thr
			645					650						655	
Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly	Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr
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	675					680									

<210> 3927

<211> 3197

<212> DNA

<213> Homo sapiens

<400> 3927

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<211> 180

<212> PRT

<213> Homo sapiens

<400> 3928

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 Ile Leu Gly Val Cys Pro Val Ser Pro Gly Ala Leu Ser Tyr Met Glu
 115 120 125
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<211> 470

<212> DNA

<213> Homo sapiens

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 <211> 293
 <212> PRT
 <213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 3933

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<210> 3934

<211> 130

<212> PRT

<213> Homo sapiens

<400> 3934

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 660
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 720
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 780
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 840
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 900
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 960
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<210> 3936
 <211> 265
 <212> PRT

<213> Homo sapiens

<400> 3936

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Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
 35           40           45
Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
 50           55           60
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
 65           70           75           80
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
 85           90           95
Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
100           105           110
Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
115           120           125
Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
130           135           140
Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
145           150           155           160
Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
165           170           175
Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Lys
180           185           190
Gln Pro Trp Leu Cys Leu Ala Trp Gly Gly Gly Gln Ala Val Asp Ile
195           200           205
Ala Val Trp Leu Leu Gly Met Val Gly Gly Thr Gly Ile Trp Ala Glu
210           215           220
Gly Gly Gly Asp Ser Leu Ser Arg Glu Gly Gly Trp Gly Gly Arg Ile
225           230           235           240
Gly Gly Phe Pro Arg Thr Gly Gly Arg Leu Pro Gly Ala Ser Tyr Gln
245           250           255
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<210> 3937

<211> 744

<212> DNA

<213> Homo sapiens

<400> 3937

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180
ctcagtcgca atgctggggc caggggctgg cgtgggctac gcgctcctcg ttatcgtgac
240
ccggggagag cggcggaagc aggaaatgct aaaggagatg ccactgcagg acccaaggag
300

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cagggaggag gcggccagga cccagcagct attgctggcc actctgcagg aggcagcgac
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 420
 gcgggagggt accgtgagac cggacttgcc tccgtgggcy cgggaccttg gcttggggcg
 480
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 540
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<210> 3938

<211> 154

<212> PRT

<213> Homo sapiens

<400> 3938

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Gly	His	Val	Leu	Leu	Ala	Glu	Asn	Ala	Asp	Leu	Ser	Arg	Asn	Ala	Gly
			20					25					30		
Arg	Arg	Gly	Trp	Arg	Gly	Leu	Arg	Ala	Pro	Arg	Tyr	Arg	Asp	Pro	Gly
		35					40					45			
Arg	Ala	Ala	Glu	Ala	Gly	Asn	Ala	Lys	Gly	Asp	Ala	Thr	Ala	Gly	Pro
		50				55				60					
Lys	Glu	Gln	Gly	Gly	Gly	Gly	Gln	Asp	Pro	Ala	Ala	Ile	Ala	Gly	His
65					70					75				80	
Ser	Ala	Gly	Gly	Ser	Asp	His	Ala	Gly	Glu	Arg	Gly	Leu	Xaa	Gly	Arg
			85						90					95	
Thr	Gly	Trp	Leu	Ala	Ala	Lys	Ala	Ala	Pro	Ala	Gly	Gly	His	Arg	Glu
			100					105					110		
Thr	Gly	Leu	Ala	Ser	Val	Gly	Ala	Gly	Pro	Trp	Leu	Gly	Arg	Arg	Asn
		115					120					125			
Pro	Arg	Gln	Pro	Phe	Ser	Phe	Val	Gly	Pro	Ala	Glu	Ser	Pro	Asp	Arg
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<210> 3939

<211> 490

<212> DNA

<213> Homo sapiens

<400> 3939

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 120

ctgaagactg tgaagaaaag ggcaacagac agcgaggag gaagagacag gctggagccc
 180
 ttcttgtaaa cgcaggtgac ctggtgcacg gctgatgggt gttaaatcgg aactecaggt
 240
 gataaccact gtctcttgga gcctgtgggt cggcctcctg ctctgctgca agggccctgc
 300
 tggctggcgg gggggcggtcc cggagcctcg acccttcacg ttttcaactcc gttttctgttc
 360
 taaggaaacc acgggtcgga ggtgtcagga ggaaggtagc agcgtcttga ctttccaccg
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 cctcacgcgt
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<210> 3940

<211> 62

<212> PRT

<213> Homo sapiens

<400> 3940

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Thr	Asp	Arg	Gln	Thr	Gly	Lys	Val	Arg	Trp	Lys	His	Thr	Glu	Asp	Glu
			20					25				30			
Arg	Asp	Arg	Gln	Trp	Glu	Ala	Glu	Leu	Lys	Thr	Val	Lys	Glu	Arg	Ala
		35				40					45				
Thr	Asp	Ser	Glu	Gly	Gly	Arg	Asp	Arg	Leu	Glu	Pro	Phe	Leu		
	50					55					60				

<210> 3941

<211> 2077

<212> DNA

<213> Homo sapiens

<400> 3941

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 120
 aggtggggccc tgccctgtgg ccaactgatgt gggaacctga ggtcacatca gtctgtggac
 180
 tcctggggtta ggtgaccctt ctgccttgag gtctgctgga cacctgggca tgggatccag
 240
 tagtctgag ctcactcttt tgcccatctc cagctgctcc taggggacgt ggctcaggcc
 300
 cgctcctggg gcaggggggt ggcggtggca tgaggtgggt tggggaggag gacgtgtctc
 360
 cacattgcag ctggcttctc cctgggctga acctccttgt gctttgagac tgacaggaag
 420
 agcagagttg cttcaggtag aggcctcgcc caggcccttg gggcaggata acagcagaga
 480
 actcaggtgc ctctctggcag agacaggagg acagatggca caggtgagca tccacacact
 540

ccattgccac aggggggtatg gcatggccca tgaccatca aagcttcagg gtcgggatac
600
aggagagggc ctcagaagag ggggaccaag ccctaggccc catacttccc agaaggagcc
660
ccaggcctgc aggggcatct gaaaggatgg agtcctggcc cagctgggccc tcagggggaca
720
gggagtcctcc ctcaagagag gctgcggctg acaaggggct ggagcccaca aggagggctgt
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1560
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1620
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1680
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1740
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1800
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1860
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1920
aggtgtcccc ccagcgtcca ggtgcctgcc ctgccctggg ctctccagg agaggggtgg
1980
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2040
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2077

<211> 89
 <212> PRT
 <213> Homo sapiens

<400> 3942
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 Gln Glu Arg Leu Arg Leu Thr Arg Gly Trp Ser Pro Gln Gly Gly Cys
 35 40 45
 Gly Ala Arg Ser Gln Ser Thr Pro Ser Ser Asp Thr Leu Pro Pro Ala
 50 55 60
 Leu Leu Gly Ser Pro Ala Ser Val Ser Gly Thr Gly Thr Asp Met
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 Ser Ser Ala Asn Ala His Ser Ala Leu
 85

<210> 3943
 <211> 1524
 <212> DNA
 <213> Homo sapiens

<400> 3943
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 120
 ggggaaccgc agccgcagga caggagcagc gcggaggagg aggaggagga ggatgagctg
 180
 gtggggctag cggactacgg agacggggccc gactcctccg acgccgatcc ggacagcggc
 240
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 300
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 360
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 420
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 480
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 540
 gacgcacagg atgactacat ggaggcttta acaagacttc acattactgt ttctaaagcc
 600
 tacaaggtta acccagacat gaattttgag gtttttattc ataaagtga tggctctgct
 660
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 720
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 780
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 840
 aattgctga acatctttat ctcaaattct ggaattgaaa aggcatttct atttgatgtg
 900

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 960
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 1020
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 1080
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 1140
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 1200
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 1260
 aagaaaaaga gagccacccc taatgggacc cctagagtgc tgctgtaggt gaggtttcag
 1320
 gaatgtcttt tgaatcaga ccttatccat gaggctgctg cgccatgttg cactaaagga
 1380
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 1500
 aaaaaaaaaa aaaaaaaaaa aaaa
 1524

<210> 3944

<211> 435

<212> PRT

<213> Homo sapiens

<400> 3944

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Arg	Leu	Gly	Pro	Thr	Pro	Gly	Pro	Pro	Pro	Ser	Pro	Gly	Arg	Pro	Ala
			20					25					30		
Val	Gly	Thr	Met	Ser	Gln	Val	Leu	Gly	Lys	Pro	Gln	Pro	Gln	Asp	Glu
			35				40				45				
Asp	Asp	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Leu	Val	Gly	Leu	Ala
	50				55						60				
Asp	Tyr	Gly	Asp	Gly	Pro	Asp	Ser	Ser	Asp	Ala	Asp	Pro	Asp	Ser	Gly
	65				70				75					80	
Thr	Glu	Glu	Gly	Val	Leu	Asp	Phe	Ser	Asp	Pro	Phe	Ser	Thr	Glu	Val
			85					90					95		
Lys	Pro	Arg	Ile	Leu	Leu	Met	Gly	Leu	Arg	Arg	Ser	Gly	Lys	Ser	Ser
			100				105						110		
Ile	Gln	Lys	Val	Val	Phe	His	Lys	Met	Ser	Pro	Asn	Glu	Thr	Leu	Phe
		115					120					125			
Leu	Glu	Ser	Thr	Asn	Lys	Ile	Cys	Arg	Glu	Asp	Val	Ser	Asn	Ser	Ser
			130			135					140				
Phe	Val	Asn	Phe	Gln	Ile	Trp	Asp	Phe	Pro	Gly	Gln	Ile	Asp	Phe	Phe
	145				150					155				160	
Asp	Pro	Thr	Phe	Asp	Tyr	Glu	Met	Ile	Phe	Arg	Gly	Thr	Gly	Ala	Leu
			165					170					175		
Ile	Phe	Val	Ile	Asp	Ala	Gln	Asp	Asp	Tyr	Met	Glu	Ala	Leu	Thr	Arg
			180				185						190		
Leu	His	Ile	Thr	Val	Ser	Lys	Ala	Tyr	Lys	Val	Asn	Pro	Asp	Met	Asn

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      195              200              205
Phe Glu Val Phe Ile His Lys Val Asp Gly Leu Ser Asp Asp His Lys
 210              215              220
Ile Glu Thr Gln Arg Asp Ile His Gln Arg Ala Asn Asp Asp Leu Ala
 225              230              235
Asp Ala Gly Leu Glu Lys Ile His Leu Ser Phe Tyr Leu Thr Ser Ile
      245              250              255
Tyr Asp His Ser Ile Phe Glu Ala Phe Ser Lys Val Val Gln Lys Leu
      260              265              270
Ile Pro Gln Leu Pro Thr Leu Glu Asn Leu Leu Asn Ile Phe Ile Ser
      275              280              285
Asn Ser Gly Ile Glu Lys Ala Phe Leu Phe Asp Val Val Ser Lys Ile
 290              295              300
Tyr Ile Ala Thr Asp Ser Thr Pro Val Asp Met Gln Thr Tyr Glu Leu
 305              310              315
Cys Cys Asp Met Ile Asp Val Val Ile Asp Ile Ser Cys Ile Tyr Gly
      325              330              335
Leu Lys Glu Asp Gly Ala Gly Thr Pro Tyr Asp Lys Glu Ser Thr Ala
      340              345              350
Ile Ile Lys Leu Asn Asn Thr Thr Val Leu Tyr Leu Lys Glu Val Thr
      355              360              365
Lys Phe Leu Ala Leu Val Cys Phe Val Arg Glu Glu Ser Phe Glu Arg
      370              375              380
Lys Gly Leu Ile Asp Tyr Asn Phe His Cys Phe Arg Lys Ala Ile His
 385              390              395
Glu Val Phe Glu Val Arg Met Lys Val Val Lys Ser Arg Lys Val Gln
      405              410              415
Asn Arg Leu Gln Lys Lys Lys Arg Ala Thr Pro Asn Gly Thr Pro Arg
      420              425              430
Val Leu Leu
      435

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<210> 3945

<211> 696

<212> DNA

<213> Homo sapiens

<400> 3945

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cgggcgcgcc cagcagtagc accgcccgcg cccgcccctg gacacttgta agtttcgatt
 180
tcgatttcc gcggaaccga gtcccgcgcc cggcgagagc cagcacagcc agcgcgccat
 240
ggcggaccgg gaggtgtgct gttcatcac caaaatcctg tgcgcccacg ggggcccgcg
 300
ggccctggag cgcgtgctcc aggagatcgc gctgtctgag ccgcagctct gtgaggtgct
 360
gcaggtggcc gggcccgacc gctttgtggt gttggagacc ggcggcgagg ccgggatcac
 420
ccgatcggtg gtggccacca ctcgagcccg ggtctgccgt cgcaagtact gccagagacc
 480

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ctgcgataac ctgcatctct gcaaaactcaa cttgctgggc cgggtgcaact attcgcagtc
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 600
 gaaaaatcac gaactctctg gactgaacaa agaggaatta gcagtgctcc tctccaaaag
 660
 tgatcctttt tttatgcccg agccctatgc agtctc
 696

<210> 3946
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 3946
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 Gly Ser Ser Gly Gly His His Arg Ser Gly Asp Pro Gly Leu Ala Ala
 20 25 30
 Gly Leu Gln His His Lys Ala Val Gly Pro Gly His Leu Gln His Leu
 35 40 45
 Thr Glu Leu Arg Leu Arg Gln Arg Asp Leu Leu Glu Gln Arg Val Gln
 50 55 60
 Gly His Ala Ala Pro Val Gly Ala Gln Asp Phe Gly Asp Glu Ala Ala
 65 70 75 80
 His Leu Arg Val Arg His Gly Ala Leu Ala Val Leu Ala Leu Pro Arg
 85 90 95
 Arg Gly Thr Arg Phe Arg Gly Asn Arg Lys Ser Lys Leu Thr Ser Val
 100 105 110
 Gln Gly Arg Ala Arg Ala Val Leu Leu Leu Gly Ala Pro Gly Val Ser
 115 120 125
 Glu Gly Ala Leu Ser Val Ala Val Ser Pro Ala Gln Arg Ser Thr Leu
 130 135 140
 Gly Ser Gln Val Lys Arg Leu Asp Leu Thr Asp Arg Val Leu Val Ala
 145 150 155 160
 Gly Leu Gln Pro Ala
 165

<210> 3947
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 3947
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 ctgcagggca tcatcgacga cttgggtgtg ctgacagcag aacccccaaa actgcctccc
 180
 gccagcgagc aggtaatcaa agacctaaag ggctcggact acagctggtc ctaccagacc
 240
 ccacccctcat caccagcag ctccagctcc cggaagtcca gcatgtgcag tgccccagc
 300

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 360
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<210> 3948

<211> 133

<212> PRT

<213> Homo sapiens

<400> 3948

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Phe	Cys	Thr	Phe	Ile	Thr	Phe	Leu	Gln	Pro	Val	Val	Asn	Gly	Glu	Leu
			20					25					30		
Thr	Met	Leu	Gly	Glu	Ile	Thr	His	Leu	Gln	Gly	Ile	Ile	Asp	Asp	Leu
			35				40					45			
Val	Val	Leu	Thr	Ala	Glu	Pro	His	Lys	Leu	Pro	Pro	Ala	Ser	Glu	Gln
			50			55					60				
Val	Ile	Lys	Asp	Leu	Lys	Gly	Ser	Asp	Tyr	Ser	Trp	Ser	Tyr	Gln	Thr
65				70				75						80	
Pro	Pro	Ser	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Lys	Ser	Ser	Met	Cys
			85					90					95		
Ser	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ala	Lys	Gly	Gly	Ser	Pro	Met	
			100				105						110		
Ala	Trp	Gly	Cys	Pro	Asn	Ile	Leu	Thr	Gln	Phe	His	Leu	Ser	Leu	Pro
			115				120					125			
Gln	Pro	Gly	Ala	Ala											
			130												

<210> 3949

<211> 1462

<212> DNA

<213> Homo sapiens

<400> 3949

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 120
 ccaccatctt tctggctgca agagtcagggt gtcagaatgg ggggcagcca ccactgctga
 180
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<211> 351

<212> PRT

<213> Homo sapiens

<400> 3950

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Glu Tyr Leu Gln Lys Glu Met Gln Leu Ile Ile Glu Asn Pro Pro Ile
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Val Val Gln Leu Ser Asp Ala Cys Asp Met Leu Gly Asp His Ile Val
290              295              300
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Gly Ile His Pro Arg Thr Ala Asp Pro Ala Ile Leu Pro Asn Ile Leu
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<211> 1012

<212> DNA

<213> Homo sapiens

<400> 3951

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<211> 188

<212> PRT

<213> Homo sapiens

<400> 3952

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 Arg Glu Asn Phe Leu Ser Lys Leu Asn Arg Glu Leu Ile Glu Thr Ile
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<211> 2900

<212> DNA

<213> Homo sapiens

<400> 3953

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<211> 627

<212> PRT

<213> Homo sapiens

<400> 3954

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Leu	His	Pro	Ser

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Val	Ser	Glu	Ala	Val	Pro	Leu	Gly	Ala	Ala	Ala	Leu	Val	Pro	Ala	Phe				
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Leu	Tyr	Pro	Phe	Phe	Gly	Val	Leu	Arg	Ser	Asn	Glu	Val	Ala	Ala	Glu				
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Tyr	Phe	Lys	Asn	Thr	Thr	Leu	Leu	Leu	Val	Gly	Val	Ile	Cys	Val	Ala				
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Cys	Cys	Thr	Thr	Leu	Leu	Ser	Met	Trp	Leu	Ser	Asn	Thr	Ser	Thr	Thr				
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 Val Ser Ile Val Thr Glu Phe Val Ser Asn Pro Ala Thr Ile Thr Ile
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 545 550 555
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 580 585 590
 Gly Leu Val Ile Val Met Val Ala Ile Asn Thr Trp Gly Val Ser Leu
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<211> 522

<212> DNA

<213> Homo sapiens

<400> 3955

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<213> Homo sapiens

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 35           40           45
Lys Glu Val Ser Ser Ser Glu Asn Pro Ser Ser His Ser Lys Val Arg
 50           55           60
Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
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Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
 85           90           95
Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
 100          105          110
Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile
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Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
 130          135          140
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<212> DNA

<213> Homo sapiens

<400> 3957

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3891

<210> 3958

<211> 440
 <212> PRT
 <213> Homo sapiens

<400> 3958

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      20              25              30
Thr Glu Pro Ala Gln Ala Gln Lys Cys Tyr Arg Asp Leu Ala Leu Val
 35              40              45
Ser Arg Asp Gly Met Asn Ile Val Leu Asn Lys Ile Asn Gln Ile Leu
 50              55              60
Met Glu Lys Tyr Leu Lys Leu Gln Asp Thr Cys Arg Thr Gln Leu Val
 65              70              75              80
Trp Leu Val Arg Glu Leu Val Lys Ser Gly Val Leu Gly Ala Asp Gly
      85              90              95
Val Cys Met Thr Phe Met Lys Gln Ile Ala Gly Gly Asp Val Thr Ala
 100              105              110
Lys Asn Ile Trp Leu Ala Glu Ser Val Leu Asp Ile Leu Thr Glu Gln
 115              120              125
Arg Glu Trp Val Leu Lys Ser Ser Ile Leu Ile Ala Met Ala Val Tyr
 130              135              140
Thr Tyr Leu Arg Leu Ile Val Asp His His Gly Thr Ala Gln Leu Gln
 145              150              155              160
Ala Leu Arg Gln Lys Glu Val Asp Phe Cys Ile Ser Leu Leu Arg Glu
 165              170              175
Arg Phe Met Glu Cys Leu Met Ile Gly Arg Asp Leu Val Arg Leu Leu
 180              185              190
Gln Asn Val Ala Arg Ile Pro Glu Phe Glu Leu Leu Trp Lys Asp Ile
 195              200              205
Ile His Asn Pro Gln Ala Leu Ser Pro Gln Phe Thr Gly Ile Leu Gln
 210              215              220
Leu Leu Gln Ser Arg Thr Ser Arg Lys Phe Leu Ala Cys Arg Leu Thr
 225              230              235              240
Pro Asp Met Glu Thr Lys Leu Leu Phe Met Thr Ser Arg Val Arg Phe
 245              250              255
Gly Gln Gln Lys Arg Tyr Gln Asp Trp Phe Gln Arg Gln Tyr Leu Ser
 260              265              270
Thr Pro Asp Ser Gln Ser Leu Arg Cys Asp Leu Ile Arg Tyr Ile Cys
 275              280              285
Gly Val Val His Pro Ser Asn Glu Val Leu Ser Ser Asp Ile Leu Pro
 290              295              300
Arg Trp Ala Ile Ile Gly Trp Leu Leu Thr Thr Cys Thr Ser Asn Val
 305              310              315              320
Ala Ala Ser Asn Ala Lys Leu Ala Leu Phe Tyr Asp Trp Leu Phe Phe
 325              330              335
Ser Pro Asp Lys Asp Ser Ile Met Asn Ile Glu Pro Ala Ile Leu Val
 340              345              350
Met His His Ser Met Lys Pro His Pro Ala Ile Thr Ala Thr Leu Leu
 355              360              365
Asp Phe Met Cys Arg Ile Ile Pro Asn Phe Tyr Pro Pro Leu Glu Gly
 370              375              380
His Val Arg Gln Gly Val Phe Ser Ser Leu Asn His Ile Val Glu Lys

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385              390              395              400
Arg Val Leu Ala Cys Lys Lys Tyr Trp Leu Tyr Leu Arg Leu Leu Gly
              405              410              415
Ile Cys Leu Leu Xaa Leu Leu Glu Glu Phe Leu Ser Cys His Arg Ile
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Thr Lys Thr Pro Ser Ser Pro Val
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<210> 3959

<211> 752

<212> DNA

<213> Homo sapiens

<400> 3959

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600
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660
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<210> 3960

<211> 94

<212> PRT

<213> Homo sapiens

<400> 3960

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Pro Leu Gly Arg Pro Gly Ala His Arg Ala Phe Ile Trp Leu Tyr Lys
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Gly Pro Asn Ser Pro Leu Asp Phe Leu Phe Ser Phe Gln Asn Ala Val
              20              25              30
Ser Lys Tyr Gly Ser Gln Phe Gln Gly Asn Ser Gln His Asp Ala Leu
              35              40              45
Glu Phe Leu Leu Trp Leu Leu Asp Arg Val His Glu Asp Leu Glu Gly

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50	55	60
Ser Ser Arg Trp Ala Arg Cys Arg Arg Ser Phe Arg Leu Lys Pro Leu		
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Lys Pro Leu Arg Thr Ala Cys His His Gln Leu Ser Phe Leu		80
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<210> 3961
 <211> 2505
 <212> DNA
 <213> Homo sapiens

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 120
 tcctggggca gaggaggttg tggcggtggc tggagaaagc ggcggcgagg gatggaggaa
 180
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 cgagtcaact ggcccgccac cgagttctct ctgcccacaa ctggagtttt atataaagaa
 360
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 780
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 1080
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 1200
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<210> 3962

<211> 306

<212> PRT

<213> Homo sapiens

<400> 3962

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 20 25 30
 Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu Ser

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      35              40              45
Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr Pro
  50              55              60
Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val Asn
  65              70              75
Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu Thr
      85              90              95
Leu Arg Gln Leu Glu Gln Gln Glu Ile Leu Arg Val Pro Phe Arg
      100              105              110
Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe Pro
      115              120              125
Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr Val
      130              135              140
Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys Glu
      145              150              155
Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp Lys
      165              170              175
Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp Lys
      180              185              190
Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu Glu
      195              200              205
His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu Gln
      210              215              220
Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly Asn
      225              230              235
Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val Lys
      245              250              255
Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr Met
      260              265              270
Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro Val
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Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser Leu
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Pro Asn
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<210> 3963

<211> 1513

<212> DNA

<213> Homo sapiens

<400> 3963

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  360

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<210> 3964

<211> 436

<212> PRT

<213> Homo sapiens

<400> 3964

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 35 40 45
 Gln Ser Asn Lys Met Asp Leu Ser Gly Gly Met Leu Gln Asp Lys Arg

50		55		60	
Met Glu Ile Asp Lys His	Ser Leu Asn Ile Gly Asp Tyr Asn Arg Thr				
65	70	75	80		
Val Gly Lys Gly Pro Gly Ser Arg Pro Gln Ile Ser Lys Glu Ser Ser					
	85	90	95		
Met Glu Arg Asn Pro Tyr Phe Asp Lys Asn Gly Asn Pro Ser Met Phe					
	100	105	110		
Gly Val Gly Asn Thr Ala Ala Gln Pro Arg Gly Met Gln Gln Pro Pro					
	115	120	125		
Ala Gln Pro Leu Ser Ser Ser Gln Pro Asn Leu Arg Ala Gln Val Pro					
	130	135	140		
Pro Pro Leu Leu Ser Pro Gln Val Pro Val Ser Leu Leu Lys Tyr Ala					
	145	150	155	160	
Pro Asn Asn Gly Gly Leu Asn Pro Leu Phe Gly Pro Gln Gln Val Ala					
	165	170	175		
Met Leu Asn Gln Leu Ser Gln Leu Asn Gln Leu Ser Gln Ile Ser Gln					
	180	185	190		
Leu Gln Arg Leu Leu Ala Gln Gln Gln Arg Ala Gln Ser Gln Arg Ser					
	195	200	205		
Val Pro Ser Gly Asn Arg Pro Gln Gln Asp Gln Gln Gly Arg Pro Leu					
	210	215	220		
Ser Val Gln Gln Gln Met Met Gln Gln Ser Arg Gln Leu Asp Pro Asn					
	225	230	235	240	
Leu Leu Val Lys Gln Gln Thr Pro Pro Ser Gln Gln Gln Pro Leu His					
	245	250	255		
Gln Pro Ala Met Lys Ser Phe Leu Asp Asn Val Met Pro His Thr Thr					
	260	265	270		
Pro Glu Leu Gln Lys Gly Pro Ser Pro Ile Asn Ala Phe Ser Asn Phe					
	275	280	285		
Pro Ile Gly Leu Asn Ser Asn Leu Asn Val Asn Met Asp Met Asn Ser					
	290	295	300		
Ile Lys Glu Pro Gln Ser Arg Leu Arg Lys Trp Thr Thr Val Asp Ser					
	305	310	315	320	
Ile Ser Val Asn Thr Ser Leu Asp Gln Asn Ser Ser Lys His Gly Ala					
	325	330	335		
Ile Ser Ser Gly Phe Arg Leu Glu Glu Ser Pro Phe Val Pro Tyr Asp					
	340	345	350		
Phe Met Asn Ser Ser Thr Ser Pro Ala Ser Pro Pro Gly Ser Ile Gly					
	355	360	365		
Asp Gly Trp Pro Arg Ala Lys Ser Pro Asn Gly Ser Ser Ser Val Asn					
	370	375	380		
Trp Pro Pro Glu Phe Arg Pro Gly Glu Pro Trp Lys Gly Tyr Pro Asn					
	385	390	395	400	
Ile Asp Pro Glu Thr Asp Pro Tyr Val Thr Pro Gly Ser Val Ile Asn					
	405	410	415		
Asn Leu Pro Ile Asn Thr Val Arg Glu Val Asp His Leu Arg Asp Arg					
	420	425	430		
Asn Ser Gly Thr					
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<210> 3965

<211> 2850

<212> DNA

<213> Homo sapiens

<400> 3965
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 1920
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 1980
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 2040
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 2100
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 2160
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 2280
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 2340
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 2400
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 2460
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 2700
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 2850

<210> 3966

<211> 782

<212> PRT

<213> Homo sapiens

<400> 3966

Met Gly Pro Pro Leu Ala Pro Arg Pro Ala His Val Pro Gly Glu Ala
 1 5 10 15
 Gly Pro Arg Arg Thr Arg Glu Ser Arg Pro Gly Ala Val Ser Phe Ala

```

      20      25      30
Asp Val Ala Val Tyr Phe Ser Pro Glu Glu Trp Glu Cys Leu Arg Pro
      35      40      45
Ala Gln Arg Ala Leu Tyr Arg Asp Val Met Arg Glu Thr Phe Gly His
      50      55      60
Leu Gly Ala Leu Gly Glu Ala Gly Pro Ser Gly Arg Asp Pro Gln Ser
      65      70      75      80
Val Gly Phe Ser Val Pro Lys Pro Ala Phe Ile Ser Trp Val Glu Gly
      85      90      95
Glu Val Glu Ala Trp Ser Pro Glu Ala Gln Asp Pro Asp Gly Glu Ser
      100      105      110
Ser Ala Ala Phe Ser Arg Gly Gln Gly Gln Glu Ala Gly Ser Arg Asp
      115      120      125
Gly Asn Glu Glu Lys Glu Arg Leu Lys Lys Cys Pro Lys Gln Lys Glu
      130      135      140
Val Ala His Glu Val Ala Val Lys Glu Trp Trp Pro Ser Val Ala Cys
      145      150      155      160
Pro Glu Phe Cys Asn Pro Arg Gln Ser Pro Met Asn Pro Trp Leu Lys
      165      170      175
Asp Thr Leu Thr Arg Arg Leu Pro His Ser Cys Pro Asp Cys Gly Arg
      180      185      190
Asn Phe Ser Tyr Pro Ser Leu Leu Ala Ser His Gln Arg Val His Ser
      195      200      205
Gly Glu Arg Pro Phe Ser Cys Gly Gln Cys Gln Ala Arg Phe Ser Gln
      210      215      220
Arg Arg Tyr Leu Leu Gln His Gln Phe Ile His Thr Gly Glu Lys Pro
      225      230      235      240
Tyr Pro Cys Pro Asp Cys Gly Arg Arg Phe Arg Gln Arg Gly Ser Leu
      245      250      255
Ala Ile His Arg Arg Ala His Thr Gly Glu Lys Pro Tyr Ala Cys Ser
      260      265      270
Asp Cys Lys Ser Arg Phe Thr Tyr Pro Tyr Leu Leu Ala Ile His Gln
      275      280      285
Arg Lys His Thr Gly Glu Lys Pro Tyr Ser Cys Pro Asp Cys Ser Leu
      290      295      300
Arg Phe Ala Tyr Thr Ser Leu Leu Ala Ile His Arg Arg Ile His Thr
      305      310      315      320
Gly Glu Lys Pro Tyr Pro Cys Pro Asp Cys Gly Arg Arg Phe Thr Tyr
      325      330      335
Ser Ser Leu Leu Ser His Arg Arg Ile His Ser Asp Ser Arg Pro
      340      345      350
Phe Pro Cys Val Glu Cys Gly Lys Gly Phe Lys Arg Lys Thr Ala Leu
      355      360      365
Glu Ala His Arg Trp Ile His Arg Ser Cys Ser Glu Arg Arg Ala Trp
      370      375      380
Gln Gln Ala Val Val Gly Arg Ser Glu Pro Ile Pro Val Leu Gly Gly
      385      390      395      400
Lys Asp Pro Pro Val His Phe Arg His Phe Pro Asp Ile Phe Gln Glu
      405      410      415
Phe Cys Gln Gln Arg Leu Gln Asp Arg Gly Val Pro Ser Asn Ala Pro
      420      425      430
Pro Val Pro Gly Gln Ser Pro Arg Ser Phe Phe Arg Asp Arg Gln
      435      440      445
Ser Ser Ala Val Ala Tyr Cys Gly His Arg Gly Val Ser Glu Ala Ser

```



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      450              455              460
Gly Pro Tyr Ile Phe Leu Glu Gly Lys Lys Pro Leu Leu Tyr Phe Pro
465              470              475              480
Asp Thr Pro Pro Pro Leu Glu Lys Ala Ala Glu Ala Ala Leu Phe
      485              490              495
Lys Gly Lys Trp Asp Asp Glu Ala Arg Glu Met Ala Pro Pro Ala
      500              505              510
Pro Leu Leu Ala Pro Arg Pro Gly Glu Thr Arg Pro Gly Cys Arg Lys
      515              520              525
Pro Gly Thr Val Ser Phe Ala Asp Val Ala Val Tyr Phe Ser Pro Glu
      530              535              540
Glu Trp Gly Cys Leu Arg Pro Ala Gln Arg Ala Leu Tyr Arg Asp Val
      545              550              555              560
Met Gln Glu Thr Tyr Gly His Leu Gly Ala Leu Gly Phe Pro Gly Pro
      565              570              575
Lys Pro Ala Leu Ile Ser Trp Met Glu Gln Glu Ser Glu Ala Trp Ser
      580              585              590
Pro Ala Ala Gln Asp Pro Glu Lys Gly Glu Arg Leu Gly Gly Ala Arg
      595              600              605
Arg Gly Asp Val Pro Asn Arg Lys Glu Glu Glu Pro Glu Glu Val Pro
      610              615              620
Arg Ala Lys Gly Pro Arg Lys Ala Pro Val Lys Glu Ser Pro Glu Val
      625              630              635              640
Leu Val Glu Arg Asn Pro Asp Pro Ala Ile Ser Val Ala Pro Ala Arg
      645              650              655
Ala Gln Pro Pro Lys Asn Ala Ala Trp Asp Pro Thr Thr Gly Ala Gln
      660              665              670
Pro Pro Ala Pro Ile Pro Ser Met Asp Ala Gln Ala Gly Gln Arg Arg
      675              680              685
His Val Cys Thr Asp Cys Gly Arg Arg Phe Thr Tyr Pro Ser Leu Leu
      690              695              700
Val Ser His Arg Arg Met His Ser Gly Glu Arg Pro Phe Pro Cys Pro
      705              710              715              720
Glu Cys Gly Met Arg Phe Lys Arg Lys Phe Ala Val Glu Ala His Gln
      725              730              735
Trp Ile His Arg Ser Cys Ser Gly Gly Arg Arg Gly Arg Arg Pro Gly
      740              745              750
Ile Arg Ala Val Pro Arg Ala Pro Val Arg Gly Asp Arg Asp Pro Pro
      755              760              765
Val Leu Phe Arg His Tyr Pro Asp Ile Phe Glu Glu Cys Gly
      770              775              780

```

<210> 3967

<211> 892

<212> DNA

<213> Homo sapiens

<400> 3967

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atcctgcccc gtggccgccc ccgtctcgta ggggacaccc tgggtgtttaa ggaatggccag
120
tactggatcc gagccggac ctcaaggac atcatcaaga ctggaggcta caaggtcagc
180

```

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gccctggagg tggagtggca cctgctggcc caccacagca tcacagatgt ggctgtgatt
240
ggagttccgg atatgacatg gggccagcgg gtcactgctg tggtagacct ccgagaagga
300
cactcactgt cccacaggga gctcaaagag tgggccagaa atgtcctggc ccgctacggg
360
gtgacctcgg agctggtgct ggtggaggag atcccgcgga accagatggg caagattgac
420
aagaaggcgc tcacaggga cttccacccc tcatgacccg gcagactggg actgcgggtc
480
tgggtggggag cagcagacgt ccccttcaca ccgagaacca cgggggcccg tccaagacct
540
ggcctccctt aaacctgaac ccccaaatc aggtcacgta gaatacaaaa ctgtttggga
600
tgaaatcacc atgtggggtc cccagcctcg ggccagttgt tgcagctcaa ggagaccgtc
660
cctggtgtca cctctgcctg gtcaccgccc acctcatctg tgcagcgcgg tgcaccgagc
720
ccctggcccc acgtgctgag gcacctccc cccacacagt ccctgcagtt gccaggctct
780
ccaggggcagg tccagagggt ttcccacaaa aaacaaataa agactccact ggaggaaaaa
840
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892

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<210> 3968

<211> 151

<212> PRT

<213> Homo sapiens

<400> 3968

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Val Ala Arg Gln Ile Leu Pro Arg Gly Arg Gly Arg Leu Val Gly Asp
20 25 30
Thr Val Val Phe Lys Asp Gly Gln Tyr Trp Ile Arg Gly Arg Thr Ser
35 40 45
Val Asp Ile Ile Lys Thr Gly Gly Tyr Lys Val Ser Ala Leu Glu Val
50 55 60
Glu Trp His Leu Leu Ala His Pro Ser Ile Thr Asp Val Ala Val Ile
65 70 75 80
Gly Val Pro Asp Met Thr Trp Gly Gln Arg Val Thr Ala Val Val Thr
85 90 95
Leu Arg Glu Gly His Ser Leu Ser His Arg Glu Leu Lys Glu Trp Ala
100 105 110
Arg Asn Val Leu Ala Pro Tyr Ala Val Pro Ser Glu Leu Val Leu Val
115 120 125
Glu Glu Ile Pro Arg Asn Gln Met Gly Lys Ile Asp Lys Lys Ala Leu
130 135 140
Ile Arg His Phe His Pro Ser
145 150

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<210> 3969

<211> 915

<212> DNA

<213> Homo sapiens

<400> 3969

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120
ggattgcaac tcggggaggg atggagcacg cgtcgtcgcc tgggaaacgg gtgcagccgc
180
ggaaggcgag cgggtgggac ttccggagca gttaatggtg gggaaacttt ctagtggatg
240
tgggaggagg cgggacttcc tgcagcaaat tggggctgtg cgcgctcaa gcccgtttac
300
ctgctcccca ggcgggcacc caggatgggc gaggtggagg ccccgggcgc ctgtgtggctc
360
gagagcccc ctgggggagc gccccccatc ttcctgccct cgagcgggca agccctggtc
420
ctgggcaggg gaccctgac ccagggttac gaccggaagt gctccagaac tcaagtggag
480
ctgtctcgag atcctgagac ccggacagtg gcagtgaac aggtatcagt gcctctgcaa
540
gggcccagca ggcctgggga tgggatttgg ggaggaattg caagccgtca gtgaaggggt
600
acattaggaa aatctgattg gggccgggcg tgggtggctc agcctgtaat cccagcactt
660
tgggaggccg aggcgggagg atcgcttgaa cccaggagtt cgagaccagc ctgagcgaca
720
tggtgaaacc tgtctctcta aaaaattagc ggggaatggt gcgcgtcctt gtagttccta
780
atcggggagg tgaagcggga ggatcccttg agcccagtag gtcaagggtg tagtgagcag
840
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900
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915

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<210> 3970

<211> 89

<212> PRT

<213> Homo sapiens

<400> 3970

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Met Gly Glu Val Glu Ala Pro Gly Arg Leu Trp Leu Glu Ser Pro Pro
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Gly Gly Ala Pro Pro Ile Phe Leu Pro Ser Asp Gly Gln Ala Leu Val
20      25      30
Leu Gly Arg Gly Pro Leu Thr Gln Val Thr Asp Arg Lys Cys Ser Arg
35      40      45
Thr Gln Val Glu Leu Val Ala Asp Pro Glu Thr Arg Thr Val Ala Val
50      55      60
Lys Gln Val Ser Val Pro Leu Gln Gly Pro Ala Arg Pro Gly Asp Gly
65      70      75      80
Ile Trp Gly Gly Ile Ala Ser Arg Gln

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85

<210> 3971
 <211> 433
 <212> DNA
 <213> Homo sapiens

<400> 3971
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 120
 ctggggaacg ggtaatcaga gaaacctca ctcatagggt ggtgcccttt atgcagagac
 180
 ttaaaggaag gagggagggt ccctgacaga gagaatggta agtgcaaagg tcctgggtgg
 240
 gcttggtgtg aggaagagca aggccagtgt ggctggaaca gaggtagtga aggggagaga
 300
 gttgtaagca atgagcttag acaggaaatg gggctctggt cacatgggaa atggtaggac
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 420
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 433

<210> 3972
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 3972
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 Ser Leu Leu Thr Thr Leu Ser Pro Ser Leu Thr Leu Phe Gln Pro His
 20 25 30
 Trp Pro Cys Ser Ser Ser Thr Gln Ala His Pro Gly Pro Leu His Leu
 35 40 45
 Pro Phe Ser Leu Ser Gly Asp Leu Pro Pro Ser Phe Lys Ser Leu His
 50 55 60
 Lys Gly His His Pro Met Ser Glu Gly Phe Ser Asp Tyr Pro Phe Pro
 65 70 75 80
 Ser Arg Ala Leu Pro Ser Met Leu His Phe Phe Pro Arg Ala Leu Asn
 85 90 95
 Thr Thr Tyr Leu Ser Phe Ile Phe Ser Leu Ser Phe Phe Cys Leu Leu
 100 105 110
 Pro Leu Glu His His Gln Ser Arg
 115 120

<210> 3973
 <211> 984
 <212> DNA
 <213> Homo sapiens

<400> 3973

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 120
 tgctccacct acttgacgtc gagatattac agggccccgt agatcatcct tgggtttacca
 180
 ttttgtgagg caattgacat gtgggtccctg ggctgtgtta ttgcagaatt gttcctgggt
 240
 tggccggttat atccaggagc ttcgaggtat gatcagattc ggtatatattc acaaacacag
 300
 gggtttgcctg ctgaatattt attaagcgcc gggacaaaga caactaggtt tttcaaccgt
 360
 gacacgggact caccatatcc tttgtggaga ctgaagacac cagatgacca tgaagcagag
 420
 acagggatta agtcaaaaga agcaagaaag tacattttca actgtttaga tgatatggcc
 480
 caggtgaaca tgacgacaga ttggaaggg agcgacatgt tggtagaaaa gggtgacggg
 540
 cgggagttca ttgacctgtt gaagaagatg ctgaccattg atgctgacaa gagaatcact
 600
 ccaatcgaaa ccctgaacca tccctttgtc accatgacac acttactcga ttttccccac
 660
 agcacacacg tcaaatcatg tttccagaac atggagatct gcaagcgctg ggtgaatatg
 720
 tatgacacgg tgaaccagag caaaaccctt ttcacacgc acgtggcccc cagcacgtcc
 780
 accaacctga ccatgacctt taacaaccag ctgaccactg tccacaacca gccctcagcg
 840
 gcatccatgg ctgcagcggc ccagcggagc atgccccctg agacaggaac agcccagatt
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 960
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 984

<210> 3974

<211> 328

<212> PRT

<213> Homo sapiens

<400> 3974

Leu Gly Leu Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu Val
 1 5 10 15
 Asp Pro Ser Arg Gln Pro Tyr Arg Val Lys Val Ile Asp Phe Gly Ser
 20 25 30
 Ala Ser His Val Ser Lys Ala Val Cys Ser Thr Tyr Leu Gln Ser Arg
 35 40 45
 Tyr Tyr Arg Ala Pro Glu Ile Ile Leu Gly Leu Pro Phe Cys Glu Ala
 50 55 60
 Ile Asp Met Trp Ser Leu Gly Cys Val Ile Ala Glu Leu Phe Leu Gly
 65 70 75 80
 Trp Pro Leu Tyr Pro Gly Ala Ser Glu Tyr Asp Gln Ile Arg Tyr Ile
 85 90 95
 Ser Gln Thr Gln Gly Leu Pro Ala Glu Tyr Leu Leu Ser Ala Gly Thr

```

100      105      110
Lys Thr Thr Arg Phe Phe Asn Arg Asp Thr Asp Ser Pro Tyr Pro Leu
115      120      125
Trp Arg Leu Lys Thr Pro Asp Asp His Glu Ala Glu Thr Gly Ile Lys
130      135      140
Ser Lys Glu Ala Arg Lys Tyr Ile Phe Asn Cys Leu Asp Asp Met Ala
145      150      155      160
Gln Val Asn Met Thr Thr Asp Leu Glu Gly Ser Asp Met Leu Val Glu
165      170      175
Lys Ala Asp Arg Arg Glu Phe Ile Asp Leu Leu Lys Lys Met Leu Thr
180      185      190
Ile Asp Ala Asp Lys Arg Ile Thr Pro Ile Glu Thr Leu Asn His Pro
195      200      205
Phe Val Thr Met Thr His Leu Leu Asp Phe Pro His Ser Thr His Val
210      215      220
Lys Ser Cys Phe Gln Asn Met Glu Ile Cys Lys Arg Arg Val Asn Met
225      230      235      240
Tyr Asp Thr Val Asn Gln Ser Lys Thr Pro Phe Ile Thr His Val Ala
245      250      255
Pro Ser Thr Ser Thr Asn Leu Thr Met Thr Phe Asn Asn Gln Leu Thr
260      265      270
Thr Val His Asn Gln Pro Ser Ala Ala Ser Met Ala Ala Ala Gln
275      280      285
Arg Ser Met Pro Leu Gln Thr Gly Thr Ala Gln Ile Cys Ala Arg Pro
290      295      300
Asp Pro Phe Gln Gln Ala Leu Ile Val Cys Pro Pro Gly Leu Gln Ala
305      310      315      320
Leu Gln Ala Ser Pro Phe Thr Arg
325

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<210> 3975

<211> 593

<212> DNA

<213> Homo sapiens

<400> 3975

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120
gctcttggggg gctcaaggga gcttgggcct ctgccagcct gcaagctgcc tccaactctc
180
agtcaggatt tggatgcccc cagtgcagtc ctgaggccgc cgcctcccat cctactatcc
240
tgcttctgag gcgtctcgga atcataggcc tcccgtggaa ggggagcagc aggcgaggtc
300
tgcgtagacc ccacagatgc ccgctcgct gccagactta aaagtctgtg cccctccccc
360
accaccaggg taccagatc ccaggcggct cagccaggcc cagagcccca agagctggggc
420
tggtctctcc aactgggata tggggtaggg gctgctcccc caagtccttg ggggactgtc
480
tgggacatcc aggcctgtc ttctgtctt aacctcac aacagagaac acgatgttct
540

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gtccacgaaa gaaggcccca cactctctccc atccggcctc cactgaaacg cgt
593

<210> 3976

<211> 101

<212> PRT

<213> Homo sapiens

<400> 3976

Met	Gly	Phe	Ser	Leu	Leu	Glu	Gly	Pro	Ala	Ser	Leu	Gln	Pro	Pro	His
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Arg	Glu	Ser	Leu	Pro	Leu	His	Ser	Leu	Pro	Arg	Asp	Gly	Ser	Trp	Gly
			20					25					30		
Leu	Lys	Gly	Ala	Trp	Ala	Ser	Ala	Ser	Leu	Gln	Ala	Ala	Ser	Asn	Ser
			35				40					45			
Gln	Ser	Gly	Phe	Gly	Cys	Pro	Gln	Cys	Ser	Pro	Glu	Ala	Ala	Ala	Pro
			50			55				60					
His	Pro	Thr	Ile	Leu	Leu	Leu	Arg	Arg	Leu	Gly	Ile	Ile	Gly	Leu	Pro
65				70						75				80	
Trp	Lys	Gly	Ser	Ser	Arg	Arg	Gly	Leu	Arg	Glu	Pro	His	Arg	Cys	Pro
				85					90					95	
Leu	Ala	Cys	Gln	Thr											
				100											

<210> 3977

<211> 2668

<212> DNA

<213> Homo sapiens

<400> 3977

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120
ttgtctcggg ggggttgattc ggcacaaacc gcccgaccca ggggcgggtg cgcgtgtgga
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240
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300
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360
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420
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480
ccatctcaac agggccaagg tgggtttacat ggaatctacc tgcgggcctt ctgcacaggg
540
ctggattctg ttttgagcc ttatcgccaa gcactgcttg atttgaaca agagttcctg
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ggtgatcccc atctctccat atcacatgac aactacttcc tagaccagtt ccagcttctt
660
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720

atcctggaaa cagtcacaa acacagctgt ggggggttgc ctctgttcg aagtgcactg
 780
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 840
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 900
 aatgtcagtg ccagccaga agaggacgag gaggatctgg gcattggggg actgacagga
 960
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 1020
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 1080
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 1200
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 1980
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 2340

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 2580
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<211> 667

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<213> Homo sapiens

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<211> 2746

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<210> 3981

<211> 4447

<212> DNA

<213> Homo sapiens

<400> 3981

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<212> PRT

<213> Homo sapiens

<400> 3982

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<212> DNA

<213> Homo sapiens

<400> 3983

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<212> PRT

<213> Homo sapiens

<400> 3984

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[illegible]

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<212> DNA
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<212> PRT

<213> Homo sapiens

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 Ser Arg Phe Pro Gln His Tyr Lys Ser Leu Tyr Arg Leu Ala Phe Leu
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 1940 1945 1950
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 1955 1960 1965
 Ala Leu Ala Ala Ala Thr Thr Ile Ile Thr Cys Pro Pro Ser Ala Ser
 1970 1975 1980
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 2005 2010 2015
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 2020 2025 2030
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 2035 2040 2045
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 2065 2070 2075 2080
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 2100 2105 2110
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 2115 2120 2125
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 2130 2135 2140
 Pro Pro Glu Ile Thr Val Thr Pro Pro Thr Pro Thr Leu Leu Ser Pro

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		2180		2185		2190
Pro Ala Leu Glu Val Leu Glu Thr Ser Ser Gln Glu Ser Ser Leu Glu						
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<210> 3999

<211> 2546

<212> DNA

<213> Homo sapiens

<400> 3999

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<210> 4000

<211> 606

<212> PRT

<213> Homo sapiens

<400> 4000

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35      40      45
Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile Cys Glu Asn Ala Thr
50      55      60
Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro Val Ala Leu Val Val
65      70      75      80
His Met Ala Pro Ala Ser Val Leu Val Asp Ser Arg Tyr Gln Gln Trp
85      90      95
Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu Val Leu Asn Glu Asn
100     105     110
Cys Ala Ser Val His Asn Leu Arg Ser His Lys Ile Gln Thr Gln Leu
115     120     125
Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu Thr Ser Phe Arg Cys
130     135     140
Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met Val Gln Gly Glu Cys
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Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu Trp Gln Arg Asp Ala
165     170     175
Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val Glu Ala Leu Gln Leu
180     185     190
Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg Arg Ser Ala Gln Asp
195     200     205
Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr Pro Glu Ile Ile Phe
210     215     220
Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile Arg Asn Val Ser Ala
225     230     235     240
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245     250     255
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260     265     270
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275     280     285
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305     310     315     320
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325     330     335
Val Leu His His Ile Ser Met Ile Pro Ala Lys Cys Leu Gln Glu Gly
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Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu Ile Ser Ser Leu Leu
355     360     365
Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys Leu Val Arg His Cys
370     375     380
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 Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser Pro Asn Phe Ser Glu
 465 470 475 480
 Lys Val Gly Val Ala Phe Asp His Met Lys Val Cys Phe Gly Asp Phe
 485 490 495
 Pro Thr Met Pro Lys Leu Ile Pro Pro Thr Glu Ser Pro Val Cys Trp
 500 505 510
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 515 520 525
 Gly Ala Gly Gly Pro Pro Val Gln Gly Ala Gly Arg Arg Pro Gly Gly
 530 535 540
 Trp Gly Ala Ser Ala Glu Ala Gly Pro His Arg Gly Ala Thr Gly Gln
 545 550 555 560
 Glu Gly Gln Ser Pro Val Lys Ile Trp Glu Thr Leu Asn Ser Glu Gly
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<210> 4001

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 4001

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<211> 417

<212> PRT

<213> Homo sapiens

<400> 4002

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Leu	Ser	Asp	Ser	Leu	Gly	Val	Ser	Val	Met	Ala	Thr	Asp	Gln	Asp	Ser
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Tyr	Ser	Thr	Ser	Ser	Thr	Glu	Glu	Glu	Leu	Glu	Gln	Phe	Ser	Ser	Pro
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Ser	Val	Lys	Lys	Lys	Pro	Ser	Met	Ile	Leu	Gly	Lys	Ala	Arg	His	Arg
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Leu	Ser	Phe	Ala	Ser	Phe	Ser	Ser	Met	Phe	His	Ala	Phe	Leu	Ser	Asn
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Asn	Arg	Lys	Leu	Tyr	Lys	Lys	Val	Val	Glu	Leu	Ala	Gln	Asp	Lys	Gly
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Ser	Tyr	Phe	Gly	Ser	Leu	Val	Gln	Asp	Tyr	Lys	Val	Tyr	Ser	Leu	Glu
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Thr	Met	Met	Thr	Gln	Leu	Lys	Ser	Tyr	Leu	Leu	Gln	Ser	Thr	Glu	Leu
145					150					155					160
Lys	Ala	Leu	Val	Asp	Pro	Ala	Leu	His	Ser	Glu	Glu	Glu	Leu	Glu	Ala
			165						170					175	
Ile	Val	Glu	Ser	Ala	Leu	Tyr	Lys	Cys	Val	Leu	Lys	Pro	Leu	Lys	Glu
		180						185					190		
Ala	Ile	Asn	Ser	Cys	Leu	His	Gln	Ile	His	Ser	Lys	Asp	Gly	Ser	Leu
		195					200					205			
Gln	Gln	Leu	Lys	Glu	Asn	Gln	Leu	Val	Ile	Leu	Ala	Thr	Thr	Thr	Thr
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<211> 581
<212> DNA
<213> Homo sapiens
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420
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<210> 4004

<211> 160
 <212> PRT
 <213> Homo sapiens

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Leu Ala Leu Lys Phe Thr Cys Ser Arg Ala Lys Asp Val Ile Ile Pro
           35           40           45
Ala Lys Pro Pro Val Ser Phe Phe Ser Leu Arg Ser Pro Val Leu Asp
           50           55           60
Leu Phe Gln Gly Gln Leu Asp Tyr Ala Glu Tyr Val Arg Arg Asp Ser
65           70           75           80
Glu Val Val Leu Leu Phe Phe Tyr Ala Pro Trp Cys Gly Gln Ser Ile
           85           90           95
Ala Ala Arg Ala Glu Ile Glu Gln Ala Ala Ser Arg Leu Ser Asp Gln
           100          105          110
Val Leu Phe Val Ala Ile Asn Cys Trp Trp Asn Gln Gly Lys Cys Arg
           115          120          125
Lys Gln Lys His Phe Phe Tyr Phe Pro Val Ile Tyr Leu Tyr His Arg
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<210> 4005
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 <212> DNA
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<210> 4006
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<212> PRT
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35 40 45
Pro Lys Met Thr Arg Ser Lys Leu Lys Glu Val Val Glu Lys Gly Met
50 55 60
Val Ile Pro Thr Trp Asn Ile Ser Pro Ile Lys Lys Ala Asn Glu Ile
65 70 75 80
Lys Pro Pro Gln Phe Val Asp Ile His Leu Glu Glu Asp Asp Ser Ser
85 90 95
Asp Glu Glu Tyr Gln Pro Asp Asp Glu Glu Asp Glu Thr Ala Glu
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Glu Ser Leu Leu Glu Ser Asp Val Glu Ser Thr Ala Ser Ser Pro Arg
115 120 125
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130 135 140
Asp Glu Glu Ser Gly Ile Leu Ser Glu Ala Glu Lys Val Thr Thr Pro
145 150 155 160
Ala Ile Arg His Ile Ser Ala Glu Val Val Pro Met Gly Pro Pro Pro
165 170 175
Pro Pro Lys Pro Lys Gln Thr Arg Asp Ser Thr Phe Met Glu Lys Leu
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Phe Gln Pro Met Asp Asp Ser Leu Ile Ala Phe Arg Thr Arg
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<210> 4007
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<212> DNA
<213> Homo sapiens

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1920

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 2040
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 2100
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 2160
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<210> 4008

<211> 290

<212> PRT

<213> Homo sapiens

<400> 4008

Gly	Lys	Arg	Lys	Arg	Ser	Ser	Ser	Glu	Asp	Ala	Glu	Ser	Leu	Ala	Pro
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Arg	Ser	Lys	Val	Lys	Lys	Ile	Ile	Gln	Lys	Asp	Ile	Ile	Lys	Glu	Ala
			20					25					30		
Ser	Glu	Ala	Ser	Lys	Glu	Asn	Arg	Asp	Ile	Glu	Ile	Ser	Thr	Glu	Glu
		35				40						45			
Glu	Lys	Asp	Thr	Gly	Asp	Leu	Lys	Asp	Ser	Ser	Leu	Leu	Lys	Thr	Lys
		50			55						60				
Arg	Lys	His	Lys	Lys	Lys	His	Lys	Glu	Arg	His	Lys	Met	Gly	Glu	Glu
65				70					75					80	
Val	Ile	Pro	Leu	Arg	Val	Leu	Ser	Lys	Ser	Glu	Trp	Met	Asp	Leu	Lys
			85						90					95	
Lys	Glu	Tyr	Leu	Ala	Leu	Gln	Lys	Ala	Ser	Met	Ala	Ser	Leu	Lys	Lys
			100					105					110		
Thr	Ile	Ser	Gln	Ile	Lys	Ser	Glu	Ser	Glu	Met	Glu	Thr	Asp	Ser	Gly
			115				120					125			
Val	Pro	Gln	Asn	Thr	Gly	Met	Lys	Asn	Glu	Lys	Thr	Ala	Asn	Arg	Glu
			130			135					140				
Glu	Cys	Arg	Thr	Gln	Glu	Lys	Val	Asn	Ala	Thr	Gly	Pro	Gln	Phe	Val
145				150					155						160
Ser	Gly	Val	Ile	Val	Lys	Ile	Ile	Ser	Thr	Glu	Pro	Leu	Pro	Gly	Arg
			165					170						175	
Lys	Gln	Val	Arg	Asp	Thr	Leu	Ala	Ala	Ile	Ser	Glu	Val	Leu	Tyr	Val
			180				185					190			
Asp	Leu	Leu	Glu	Gly	Asp	Thr	Glu	Cys	His	Ala	Arg	Phe	Lys	Thr	Pro
		195				200					205				
Glu	Asp	Ala	Gln	Ala	Val	Ile	Asn	Ala	Tyr	Thr	Glu	Ile	Asn	Lys	Lys
					210		215				220				
His	Cys	Trp	Lys	Leu	Glu	Ile	Leu	Ser	Gly	Asp	His	Glu	Gln	Arg	Tyr
225				230						235					240
Trp	Gln	Lys	Ile	Leu	Val	Asp	Arg	Gln	Ala	Lys	Leu	Asn	Gln	Pro	Arg
			245						250					255	
Glu	Lys	Lys	Arg	Gly	Thr	Glu	Lys	Leu	Ile	Thr	Lys	Ala	Glu	Lys	Ile

	260		265		270
Arg	Leu	Ala	Lys	Thr	Gln
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Tyr	Asp				
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<210> 4009
 <211> 675
 <212> DNA
 <213> Homo sapiens

<400> 4009
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 120
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 180
 aatgaaaaaa ccataggcag tctctctaata gagttttact gttctgaaaa cacttctgtc
 240
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 420
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 480
 tatcatgtga gaaggaataa tttagacaat gtatcatgc cactgggttt ggaggtgcca
 540
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 675

<210> 4010
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 4010
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 Ser Val Gln Asp Pro Ala Ser Ser Pro Ser Ile Gln Asp Gly Gly Leu
 20 25 30
 Met Gln Ala Ser Val Pro Gly Pro Ser Glu Glu Pro Val Val Tyr Asn
 35 40 45
 Pro Thr Thr Ala Ala Phe Ile Cys Asp Ser Leu Val Asn Glu Lys Thr
 50 55 60
 Ile Gly Ser Pro Pro Asn Glu Phe Tyr Cys Ser Glu Asn Thr Ser Val
 65 70 75 80
 Pro Asn Glu Ser Asn Lys Ile Leu Val Asn Lys Asp Val Pro Gln Lys

85 90 95
 Pro Gly Gly Glu Thr Thr Pro Ser Val Thr Asp Leu Leu Asn Tyr Phe
 100 105 110
 Leu Ala Pro Glu Ile Leu Thr Gly Asp Asn Gln Tyr Tyr Cys Glu Asn
 115 120 125
 Cys Ala Ser Leu Gln Asn Ala Glu Lys Thr Met Gln Ile Thr Glu Glu
 130 135 140
 Pro Glu Tyr Leu Ile Leu Thr Leu Leu Arg Phe Ser Tyr Asp Gln Lys
 145 150 155 160
 Tyr His Val Arg Arg Lys Ile Leu Asp Asn Val Ser Leu Pro Leu Val
 165 170 175
 Leu Glu Leu Pro Val Lys Arg Ile Thr Ser Phe Ser Ser Leu Ser Glu
 180 185 190
 Ser Trp Ser Val Asp Val Asp Phe Thr Asp Leu Ser Glu Asn Leu Ala
 195 200 205
 Lys Lys Leu Lys Pro Ser Gly Thr Asp Glu Ala Ser Cys Thr Lys Leu
 210 215 220
 Val
 225

 <210> 4011
 <211> 1371
 <212> DNA
 <213> Homo sapiens

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 180
 gccaccatga agggcatcac gaccgaacag ctggacgctc tgggttgccg catctgcctg
 240
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 300
 ctccacggct tcatgaattg gcttcataat ctgctaacgc tttgcggtgg ggtttccctt
 360
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 480
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 540
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 660
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 720
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 780
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 840

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<210> 4012

<211> 419

<212> PRT

<213> Homo sapiens

<400> 4012

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			20					25					30		
Ser	Arg	Ser	Arg	Ala	Arg	Ala	Gly	Glu	Leu	Trp	Leu	Pro	His	Gly	Thr
			35				40					45			
Val	Ala	Thr	Pro	Val	Phe	Met	Pro	Val	Gly	Thr	Gln	Ala	Thr	Met	Lys
			50			55					60				
Gly	Ile	Thr	Thr	Glu	Gln	Leu	Asp	Ala	Leu	Gly	Cys	Arg	Ile	Cys	Leu
65				70					75					80	
Gly	Asn	Thr	Tyr	His	Leu	Gly	Leu	Arg	Pro	Gly	Pro	Glu	Leu	Ile	Gln
				85					90					95	
Lys	Ala	Asn	Gly	Leu	His	Gly	Phe	Met	Asn	Trp	Pro	His	Asn	Leu	Leu
			100					105					110		
Thr	Leu	Cys	Gly	Gly	Val	Ser	Leu	Asp	Ser	Gly	Gly	Phe	Gln	Met	Val
			115				120					125			
Ser	Leu	Val	Ser	Leu	Ser	Glu	Val	Thr	Glu	Glu	Gly	Val	Arg	Phe	Arg
			130				135				140				
Ser	Pro	Tyr	Asp	Gly	Asn	Glu	Thr	Leu	Leu	Ser	Pro	Glu	Lys	Ser	Val
145				150					155					160	
Gln	Ile	Gln	Asn	Ala	Leu	Gly	Ser	Asp	Ile	Ile	Met	Gln	Leu	Asp	Asp
			165						170					175	
Val	Val	Ser	Ser	Thr	Val	Thr	Gly	Pro	Arg	Val	Glu	Glu	Ala	Met	Tyr
			180				185						190		
Arg	Ser	Ile	Arg	Trp	Leu	Asp	Arg	Cys	Ile	Ala	Ala	His	Gln	Arg	Pro
			195				200					205			
Asp	Lys	Gln	Asn	Leu	Phe	Ala	Ile	Ile	Gln	Gly	Gly	Leu	Asp	Ala	Asp
			210				215					220			
Leu	Arg	Ala	Thr	Cys	Leu	Glu	Glu	Met	Thr	Lys	Arg	Asp	Val	Pro	Gly

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225                230                235                240
Phe Ala Ile Gly Gly Leu Ser Gly Gly Glu Ser Lys Ser Gln Phe Trp
                245                250                255
Arg Met Val Ala Leu Ser Thr Ser Arg Leu Pro Lys Asp Lys Pro Arg
                260                265                270
Tyr Leu Met Gly Val Gly Tyr Ala Thr Asp Leu Val Val Cys Val Ala
                275                280                285
Leu Gly Cys Asp Met Phe Asp Cys Val Phe Pro Thr Arg Thr Ala Arg
                290                295                300
Phe Gly Ser Ala Leu Val Pro Thr Gly Asn Leu Gln Leu Arg Lys Lys
305                310                315
Val Phe Glu Lys Asp Phe Gly Pro Ile Asp Pro Glu Cys Thr Cys Pro
                325                330                335
Thr Cys Gln Lys His Ser Arg Ala Phe Leu His Ala Leu Leu His Ser
                340                345                350
Asp Asn Thr Ala Ala Leu His His Leu Thr Val His Asn Ile Ala Tyr
                355                360                365
Gln Leu Gln Leu Met Ser Ala Val Arg Thr Ser Ile Val Glu Lys Arg
                370                375                380
Phe Pro Asp Phe Val Arg Asp Phe Met Gly Ala Met Tyr Gly Asp Pro
385                390                395                400
Thr Leu Cys Pro Thr Trp Ala Thr Asp Ala Leu Ala Ser Val Gly Ile
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Thr Leu Gly

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<210> 4013

<211> 1419

<212> DNA

<213> Homo sapiens

<400> 4013

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120
agagcttccc ccatcccccg cagccccgac cggtctgcgt gccaacagct gctccagcag
180
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240
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360
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420
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480
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540
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600
gacaagcact ttgggtctgg cgacctgatg gaccccgaa tactggggct gacctacatc
660

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aaaggggct ccaccgacag tggcatcgac acggccccct gcattgctgc caccatcctc
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780
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900
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<210> 4014

<211> 473

<212> PRT

<213> Homo sapiens

<400> 4014

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20           25           30
Thr Pro Ala Leu Gln Pro Leu Ser Arg Ala Ser Pro Ile Pro Gly Thr
35           40           45
Pro Asp Arg Leu Pro Cys Gln Gln Leu Leu Gln Gln Ala Gln Ala Ala
50           55           60
Ile Pro Arg Ser Thr Ser Phe Asp Arg Lys Leu Pro Asp Gly Thr Arg
65           70           75           80
Ser Ser Pro Ser Asn Gln Ser Ser Ser Ser Asp Pro Gly Pro Gly Gly
85           90           95
Ser Gly Pro Trp Arg Pro Gln Val Gly Tyr Asp Gly Cys Gln Ser Pro
100          105          110
Leu Leu Leu Glu His Gln Gly Ser Gly Pro Leu Glu Cys Asp Gly Ala
115          120          125
Arg Glu Arg Glu Asp Thr Met Glu Ala Ser Arg His Pro Glu Thr Lys
130          135          140
Trp His Gly Pro Pro Ser Lys Val Leu Gly Ser Tyr Lys Glu Arg Ala
145          150          155          160
Leu Gln Lys Asp Gly Ser Cys Lys Asp Ser Pro Asn Lys Leu Ser His

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165      170      175
Ile Gly Asp Lys Ser Cys Ser Ser His Ser Ser Ser Asn Thr Leu Ser
180      185      190
Ser Asn Thr Ser Ser Asn Ser Asp Asp Lys His Phe Gly Ser Gly Asp
195      200      205
Leu Met Asp Pro Glu Leu Leu Gly Leu Thr Tyr Ile Lys Gly Ala Ser
210      215      220
Thr Asp Ser Gly Ile Asp Thr Ala Pro Cys Met Pro Ala Thr Ile Leu
225      230      235
Gly Pro Val His Leu Ala Gly Ser Arg Ser Leu Ile His Ser Arg Ala
245      250      255
Glu Gln Trp Ala Asp Ala Ala Asp Val Ser Gly Pro Asp Asp Glu Pro
260      265      270
Ala Lys Leu Tyr Ser Val His Gly Tyr Ala Ser Thr Ile Ser Ala Gly
275      280      285
Ser Ala Ala Glu Gly Ser Met Gly Asp Leu Ser Glu Ile Ser Ser His
290      295      300
Ser Ser Gly Ser His His Ser Gly Ser Pro Ser Ala His Cys Ser Lys
305      310      315
Ser Ser Gly Ser Leu Asp Ser Ser Lys Val Tyr Ile Val Ser His Ser
325      330      335
Ser Gly Gln Gln Val Pro Gly Ser Met Ser Lys Pro Tyr His Arg Gln
340      345      350
Gly Ala Val Asn Lys Tyr Val Ile Gly Trp Lys Lys Ser Glu Gly Ser
355      360      365
Pro Pro Pro Glu Glu Pro Glu Val Thr Glu Cys Pro Gly Met Tyr Ser
370      375      380
Glu Leu Asp Val Met Ser Thr Ala Thr Gln His Gln Thr Val Val Gly
385      390      395
Asp Ala Val Ala Glu Thr Gln His Val Leu Ser Lys Glu Asp Phe Leu
405      410      415
Lys Leu Met Leu Pro Asp Ser Pro Leu Val Glu Glu Gly Arg Arg Lys
420      425      430
Phe Ser Phe Tyr Gly Asn Leu Ser Pro Arg Arg Ser Leu Tyr Arg Thr
435      440      445
Leu Ser Asp Glu Ser Ile Cys Ser Asn Arg Arg Gly Ser Ser Phe Gly
450      455      460
Ser Ser Arg Ser Ser Val Leu Asp Gln
465      470

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<210> 4015

<211> 823

<212> DNA

<213> Homo sapiens

<400> 4015

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120
atagtgctgc agggcggcgg cctggagtct cccaccaagc ccaaggggag gcccaagaag
180
aactcaattc caacgagcga gcagcttact gagcaggagc gcgccaagga tgcagagaaa
240

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ccccgcggagg tgcggggcga gccacgcgac aggagccgcg aggactgagg gcggtatacg
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420
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600
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720
ccgtcggcat gcctggaggc cgggtccccg atgtcgtcgg ggcacctacc cctcgtgcg
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<210> 4016

<211> 95

<212> PRT

<213> Homo sapiens

<400> 4016

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Asn Arg Arg Met Lys Trp Lys Lys Ile Val Leu Gln Gly Gly Gly Leu
35 40 45
Glu Ser Pro Thr Lys Pro Lys Gly Arg Pro Lys Lys Asn Ser Ile Pro
50 55 60
Thr Ser Glu Gln Leu Thr Glu Gln Glu Arg Ala Lys Asp Ala Glu Lys
65 70 75 80
Pro Ala Glu Val Pro Gly Glu Pro Ser Asp Arg Ser Arg Glu Asp
85 90 95

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<210> 4017

<211> 1521

<212> DNA

<213> Homo sapiens

<400> 4017

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120
agcaccgtcc tacagggcct gccctttggg gccgtcccca ccgtgctggc cttggacttc
180
acgtgcttcc tcgccctgct gttcttattc tccatcctcc ggaaggtggc ctgggactat
240

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gggcggctgg ccttggtgac agatgcagac aggccttcggc ggcaggagag ggaccgagtg
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360
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780
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1521

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<210> 4018

<211> 480

<212> PRT

<213> Homo sapiens

<400> 4018

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[illegible]

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1320

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<212> PRT

<213> Homo sapiens

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      115          120          125
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Ser Pro Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp
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<210> 4021

<211> 4209

<212> DNA

<213> Homo sapiens

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<211> 885

<212> PRT

<213> Homo sapiens

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Pro Tyr Gly Asp Val Ile Gly Leu Gln Val Asp Tyr Trp Leu Gly His
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His Met Leu Gln	Thr Phe Asp Tyr Ser Arg Asp	Pro Gln Glu Arg Glu	
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Phe Thr Thr Ala	Val Ser Ser Pro Gly Gly Gln	Ser Val Val Leu Gly	
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Ser Tyr Asp Arg	Leu Arg Val Phe Asn Trp Ile	Pro Arg Arg Ser Ile	
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Phe Met Asn Pro	His Leu Ile Ser Val Arg Ile	Asn Glu Arg Cys Gln	
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Arg Gly Thr Glu	Asp Asn Lys Lys Leu Ala Tyr	Leu Ile Asp Ile Lys	
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300
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360
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420
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480
gtcttgggtg gtaatcagtt ggtgatcatt gtgggaattg tctgtgccac aatcctgctg
540
ctccctgttc tgatattgat cgtgaagaag acctgtggaa ataagagttc agtgaattct
600
acagtcttgg tgaagaacac gaagaagact aatccagaga tgaagaaaaa accctgccat
660

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tttgaagat gtgaagggga ggtgaacaca cgcttcagcc taaaacacta agtagatgca
720
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780
caggccagt cttggcacag agcagggact caggaagcct ttgtcactaa agtaagagcc
840
tctgcggagt acagtgcagt gggctcgctg ggacaccccc aggcagcaga tctctggatt
900
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941

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<210> 4028

<211> 236

<212> PRT

<213> Homo sapiens

<400> 4028

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20 25 30
Lys Glu Leu Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val
35 40 45
Phe Gln Ser Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe
50 55 60
Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe Arg Tyr Tyr His Lys
65 70 75 80
Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp Gly His Phe Gln Asn
85 90 95
Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn Asp Gly Ser Ile Met
100 105 110
Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn Tyr Thr Cys Ser Ile
115 120 125
His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile Val Leu His Val Ser
130 135 140
Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala Ala Leu Arg Pro Leu
145 150 155 160
Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val Gly Ile Val Cys Ala
165 170 175
Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile Val Lys Lys Thr Cys
180 185 190
Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu Val Lys Asn Thr Lys
195 200 205
Lys Thr Asn Pro Glu Met Lys Glu Lys Pro Cys His Phe Glu Arg Cys
210 215 220
Glu Gly Glu Val Asn Thr Arg Phe Ser Leu Lys His
225 230 235

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<210> 4029

<211> 909

<212> DNA

<213> Homo sapiens

<400> 4029

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 120
 ctacatgctg ctgctgggtg tgccgtgctg ggcgctcagc gaggtcagca tgcaggcgca
 180
 gcacatagcg ccgcagaaga tgatgctgta cccggtgctc agtctcgcca ccgtcaatgt
 240
 ggtggggcgt gctggcgcgc gccgccaaca tggcgctgtt ccgggacagc cgtgtctcgg
 300
 ccattcttctg ccgcaaaaac gtgggtggcg tcgccaccaa ggctgcacc tnttctgga
 360
 gtaccgcccg cagggtgcgc acttcccnnng ccgcctgcgc tatcactgga gctgcagccg
 420
 ccacccccgc agcgcaactc ggtgcccgcg ccgcgcgcgc cgctgcacgg ccgcctggg
 480
 ncgccccac atgtctctgc ccacgcgtga cccctggac acgtgacagg gcccgcgccg
 540
 ccccgacac gccctgggg cgagagaca ccgggttggc ttggggcgcg cggtttgcac
 600
 gggatggggt gggggcgggc tcccctaggg acagggtcct cgagtgcgcg tcctgggggt
 660
 ccgcggcgcg cttcttctc tcaggaatct ctcggaccgc ggatcctcag ccccgctcc
 720
 accagccccg ccagcgcggt ggtctctgtt gggaggcctg gccggagca gagcagagg
 780
 gatccggccc ctgcctgctg ggcggcccg gttggaagg agggcagtg gggcgagagat
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 aaagactcg
 909

<210> 4030

<211> 169

<212> PRT

<213> Homo sapiens

<400> 4030

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Ala	Gly	Gln	Pro	Val	Gly	Ala	Ala	Leu	Arg	Ala	Ala	Ala	Val	Gly	
		20					25					30			
Arg	Gly	Pro	His	Leu	Leu	Leu	Leu	His	Ala	Ala	Ala	Gly	Ala	Ala	
		35				40					45				
Val	Arg	Gly	Ala	Gln	Arg	Gly	Gln	His	Ala	Gly	Arg	Ala	His	Ser	Ala
		50				55					60				
Ala	Glu	Asp	Asp	Ala	Val	Pro	Gly	Ala	Gln	Ser	Arg	His	Arg	Gln	Cys
		65			70					75				80	
Gly	Gly	Pro	Cys	Trp	Arg	Ala	Pro	Pro	Thr	Trp	Arg	Cys	Ser	Gly	Thr
			85					90					95		
Ala	Val	Ser	Arg	Pro	Ser	Ser	Ser	Ala	Lys	Thr	Trp	Trp	Arg	Ser	Pro
			100					105					110		
Pro	Arg	Pro	Ala	Pro	Xaa	Pro	Gly	Val	Pro	Pro	Pro	Gly	Ala	Arg	Leu

ggtcggataa gagttaagga caaggagggt aatgtgctaa tggacacgga gctgtgacga
 1260
 tcctcatgtg atcatgaagt aacagtaact gactttttat gttaaaaaat gtacatttac
 1320
 tgtggattct gtttaattta ttgtgtatgt gtggggaaaa gattggattc taaaataaaa
 1380
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 1406

<210> 4032

<211> 418

<212> PRT

<213> Homo sapiens

<400> 4032

Xaa	Ala	Glu	Asn	Ala	Ser	Leu	Ala	Lys	Leu	Arg	Ile	Glu	Arg	Glu	Ser
1			5					10						15	
Ala	Leu	Glu	Lys	Leu	Arg	Lys	Glu	Ile	Ala	Gly	Phe	Glu	Gln	Gln	Lys
		20					25						30		
Ala	Lys	Glu	Leu	Ala	Arg	Ile	Glu	Glu	Phe	Lys	Lys	Glu	Glu	Met	Arg
		35					40					45			
Lys	Leu	Gln	Lys	Glu	Arg	Lys	Val	Phe	Glu	Lys	Tyr	Thr	Thr	Ala	Ala
	50				55						60				
Arg	Thr	Phe	Pro	Asp	Lys	Lys	Glu	Arg	Glu	Glu	Ile	Gln	Thr	Leu	Lys
65				70					75					80	
Gln	Gln	Ile	Ala	Asp	Leu	Arg	Glu	Asp	Leu	Lys	Arg	Lys	Glu	Thr	Lys
			85					90						95	
Trp	Ser	Ser	Thr	His	Ser	Arg	Leu	Arg	Ser	Gln	Ile	Gln	Met	Leu	Val
			100					105					110		
Arg	Glu	Asn	Thr	Asp	Leu	Arg	Glu	Glu	Ile	Lys	Val	Met	Glu	Arg	Phe
		115					120					125			
Arg	Leu	Asp	Ala	Trp	Lys	Arg	Ala	Glu	Ala	Ile	Glu	Ser	Ser	Leu	Glu
		130				135					140				
Val	Glu	Lys	Lys	Asp	Lys	Leu	Ala	Asn	Thr	Ser	Val	Arg	Phe	Gln	Asn
145				150					155					160	
Ser	Gln	Ile	Ser	Ser	Gly	Thr	Gln	Val	Glu	Lys	Tyr	Lys	Lys	Asn	Tyr
			165					170						175	
Leu	Pro	Met	Gln	Gly	Asn	Pro	Pro	Arg	Arg	Ser	Lys	Ser	Ala	Pro	Pro
		180					185						190		
Arg	Asp	Leu	Gly	Asn	Leu	Asp	Lys	Gly	Gln	Ala	Ala	Ser	Pro	Arg	Glu
		195					200					205			
Pro	Leu	Glu	Pro	Leu	Asn	Phe	Pro	Asp	Pro	Glu	Tyr	Lys	Glu	Glu	Glu
		210				215					220				
Glu	Asp	Gln	Asp	Ile	Gln	Gly	Glu	Ile	Ser	His	Pro	Asp	Gly	Lys	Val
225				230					235					240	
Glu	Lys	Val	Tyr	Lys	Asn	Gly	Cys	Arg	Val	Ile	Leu	Phe	Pro	Asn	Gly
			245					250						255	
Thr	Arg	Lys	Glu	Val	Ser	Ala	Asp	Gly	Lys	Thr	Ile	Thr	Val	Thr	Phe
			260				265						270		
Phe	Asn	Gly	Asp	Val	Lys	Gln	Val	Met	Pro	Asp	Gln	Arg	Val	Ile	Tyr
		275					280					285			
Tyr	Tyr	Ala	Ala	Ala	Gln	Thr	Thr	His	Thr	Thr	Tyr	Pro	Glu	Gly	Leu
	290				295						300				
Glu	Val	Leu	His	Phe	Ser	Ser	Gly	Gln	Ile	Glu	Lys	His	Tyr	Pro	Asp


```

305          310          315          320
Gly Arg Lys Glu Ile Thr Phe Pro Asp Gln Thr Val Lys Asn Leu Phe
          325          330          335
Pro Asp Gly Gln Glu Glu Ser Ile Phe Pro Asp Gly Thr Ile Val Arg
          340          345          350
Val Gln Arg Asp Gly Asn Lys Leu Ile Glu Phe Asn Asn Gly Gln Arg
          355          360          365
Glu Leu His Thr Ala Gln Phe Lys Arg Arg Glu Tyr Pro Asp Gly Thr
          370          375          380
Val Lys Thr Val Tyr Ala Asn Gly His Gln Glu Thr Lys Tyr Arg Ser
385          390          395          400
Gly Arg Ile Arg Val Lys Asp Lys Glu Gly Asn Val Leu Met Asp Thr
          405          410          415
Glu Leu

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<210> 4033

<211> 487

<212> DNA

<213> Homo sapiens

<400> 4033

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120
tcaagaagag cctcctagt ttggctcta actggctgtg cgacccaggg caggtcactt
180
gtcctctctg ggaagcagct gaataatgaa cactgggatt tccccaggct ggcttctcac
240
tgcagagcag aggaagaaagca ttctgggggc ctgctatgga gggtcattta tccagtttac
300
aacttccacg gccggccctc aatggcttcc ttctctccc acaagagcgc tgggccaagc
360
cagctctgca ccagttggac gccttccaag aaaaactcag gctccggggg ctgcttgta
420
ggaccagacg ggaggcctgg cgccccgcc cgccatgtgt ggggagcggg cctctccaag
480
ccagtcc
487

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<210> 4034

<211> 94

<212> PRT

<213> Homo sapiens

<400> 4034

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Met Asn Thr Gly Ile Phe Pro Gly Trp Leu Leu Thr Ala Glu Gln Arg
1          5          10          15
Lys Ser Ile Leu Gly Ala Cys Tyr Gly Gly Ser Phe Ile Gln Phe Thr
          20          25          30
Thr Ser Thr Ala Gly Pro Gln Trp Leu Pro Phe Ser Pro Thr Arg Ala
          35          40          45
Leu Gly Gln Ala Ser Ser Ala Pro Val Gly Arg Leu Pro Arg Lys Thr

```

50					55					60					
Gln	Ala	Pro	Gly	Ala	Ala	Cys	Gln	Asp	Gln	Thr	Gly	Gly	Leu	Ala	Pro
65					70					75					80
Pro	Pro	Ala	Met	Cys	Gly	Glu	Arg	Ala	Ser	Pro	Ser	Gln	Ser		
				85					90						

<210> 4035

<211> 343

<212> DNA

<213> Homo sapiens

<400> 4035

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nnncttaata gcagtgttat ggaattccat gtgaggcaca aacattcaga caatcctagc
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aatgttcttg aatcctatgt gagggacaaa cattcagacc ccagcagcaa tgttctggaa
120
tcctatggga gggacaaact ctcagaaaaa agcaagagta ttttggaaat ctatctgagg
180
tataaacact cagaacctca tagcagtgtt caggaatcct atgtgagggg caaacattca
240
gaccacagca ggagcattct agaatcctat ttgaggaaca aacattcaga caatcgtagc
300
agtgttcttg aatccttttt ttttttgaag ctttcaatct ctt
343

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<210> 4036

<211> 114

<212> PRT

<213> Homo sapiens

<400> 4036

Xaa	Leu	Asn	Ser	Ser	Val	Met	Glu	Phe	His	Val	Arg	His	Lys	His	Ser
1				5						10				15	
Asp	Asn	Pro	Ser	Asn	Val	Leu	Glu	Ser	Tyr	Val	Arg	Asp	Lys	His	Ser
			20					25					30		
Asp	Pro	Ser	Ser	Asn	Val	Leu	Glu	Ser	Tyr	Gly	Arg	Asp	Lys	Leu	Ser
			35				40					45			
Glu	Asn	Ser	Lys	Ser	Ile	Leu	Glu	Ser	Tyr	Leu	Arg	Tyr	Lys	His	Ser
	50					55				60					
Glu	Pro	His	Ser	Ser	Val	Gln	Glu	Ser	Tyr	Val	Arg	Asp	Lys	His	Ser
65					70					75					80
Asp	His	Ser	Arg	Ser	Ile	Leu	Glu	Ser	Tyr	Leu	Arg	Asn	Lys	His	Ser
				85					90				95		
Asp	Asn	Arg	Ser	Ser	Val	Leu	Glu	Ser	Phe	Phe	Leu	Lys	Leu	Ser	
			100					105					110		
Ile	Ser														

<210> 4037

<211> 741

<212> DNA

<213> Homo sapiens

<400> 4037

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tttttttttt ttttttttgg aaagagaaaa tatatttact attcattaag tggatgcggg
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tcatacataaa ggtcttcatt ctcatcctct tcacgttgag taggctgagg aggaggaaga
120
ggaggagaag gggttggtct tgctgtctca gggcggcaga ggcagaagag aatctgagca
180
tacgtggacc tgtagccagg tgggcataga taaaaggaaa tattgtttgc cagtcctctgc
240
tggaatgatg cctttacaca tctgtctgat ctgattgctc cactgttttc tgacttctct
300
tccctttcca gggttctagc ctgttcatct agcccccata tggctgttga catcgagtac
360
agatacaact gcatggctcc ttccttgcgc caagagaggt ttgcctttaa gatctcacca
420
aagcccagca aaccactgag gccttgtatt cagctgagca gcaagaatga agccagtgga
480
atgggtggccc cggtgtcca ggagaagaag gtgaaaaagc ggggtgtcctt cgagacaaac
540
caggggctgg ccctgacaat ggtcaaagtg ttctcggaat tctgatgacc gctagatatg
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ccattcaaca tcaccagact cctagacaac attgtgagct tgacgacagc agagagcggag
660
agctttgttc tggatttttc ccagccctct gcagattact tagactttag aaatcgactt
720
caggccgacc acgtctgcct t
741

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<210> 4038

<211> 134

<212> PRT

<213> Homo sapiens

<400> 4038

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Met Ala Val Asp Ile Glu Tyr Arg Tyr Asn Cys Met Ala Pro Ser Leu
  1             5             10            15
Arg Gln Glu Arg Phe Ala Phe Lys Ile Ser Pro Lys Pro Ser Lys Pro
  20            25            30
Leu Arg Pro Cys Ile Gln Leu Ser Ser Lys Asn Glu Ala Ser Gly Met
  35            40            45
Val Ala Pro Ala Val Gln Glu Lys Lys Val Lys Lys Arg Val Ser Phe
  50            55            60
Ala Asp Asn Gln Gly Leu Ala Leu Thr Met Val Lys Val Phe Ser Glu
  65            70            75            80
Phe Asp Asp Pro Leu Asp Met Pro Phe Asn Ile Thr Glu Leu Leu Asp
  85            90            95
Asn Ile Val Ser Leu Thr Thr Ala Glu Ser Glu Ser Phe Val Leu Asp
 100           105           110
Phe Ser Gln Pro Ser Ala Asp Tyr Leu Asp Phe Arg Asn Arg Leu Gln
 115           120           125
Ala Asp His Val Cys Leu
 130

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<210> 4039

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 4039

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gctgcgcgcg tcggagagggc tcttggggaa actcccacgg ccaggggact ttgaaagca
120
gagcggagag ccttcgcacg cgctagtctg cgaagtgcgcg ctacagcccg cacctgttcc
180
tccagcgcgcg ccgccttccc acccctcgga ccgcgcgcgc tcggggcgcc cgccgttcc
240
tgctatgaat ccggccctag gcaaccagac ggacgtggcg ggccttctcg gccaacagca
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gcgaggcgct ggagcgagcc gtgcgctgct gcaccagggc gtccgtggcg accgacgacg
360
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420
cgggtcatgtg cgtgctctca ctacacgtgg tcttcggcat cttcttcctc ggctgcaatc
480
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600
ccacgcctg cccactttgc tagcccggtc gtgcccctca ctatcagaga ctggggcgaag
660
caaacctgtc ggagtcaatt atttctctcg acttcggcct ttcggaaaga agcgaccggt
720
ttctccctcg cctctgaaa gtctcatgc ctggcagtcg gaggagagcg ccagactct
780
gaaactcagca gaaagtggca agaagagggc gattagggcg cagaactttg gaagctgcta
840
cttacttgga atgcggggag accgacggcg cgaaggccct tctccaccgc caggtgggccc
900
aagctctggg ggcaggtgga gagggcgggc aggggagaga ccagcgcca ctgacgcct
960
tgtgaccgga agagtgcact gttaaaagcc acgcagcaga ctcatggggg ctacacaaatc
1020
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1080
gataaatacc tttgattgta acgtgccgtt ttaagaggtt ttgtgtttgt ttgcttgaat
1140
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1200
agttttgtca ttgtggaaga aggggtgggg ggagggggag cctgcgaatt tgaacggggg
1260
gagttgtttc ttttagtgca ttcccaactg ggtcttttgg gaggcgtcta cggttcctgc
1320
tggccctggg acaaagaccg agaatagaac tcgtagctcg tgactgcacg gtttacgcca
1380
caaaagtgtc cttgacatcc gtgacaccgt ttgacttttt tgttttttct ttaatttaaca
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1500

aaa
1503

<210> 4040
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4040
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Thr Ala Gln Gly Leu Ser Lys Ala Glu Arg Gly Ala Leu Ala Arg Ala
20 25 30
Ser Leu Arg Val Ser Ala Gln Pro Gly Thr Cys Ser Ser Ser Ala Ala
35 40 45
Ala Phe Pro Pro Leu Gly Pro Ala Pro Leu Ala Ala Pro Ala Arg Ser
50 55 60
Cys Asp Glu Ser Gly Pro Arg Gln Pro Asp Gly Arg Gly Gly Pro Ser
65 70 75 80
Trp Pro Thr Ala Ala Arg Arg Trp Ser Glu Pro Cys Ala Ala Pro
85 90 95
Arg Arg Pro Trp
100

<210> 4041
<211> 573
<212> DNA
<213> Homo sapiens

<400> 4041
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ggtagagattc cagctgaatt aaggggcggcg gccactgacc accggcagga gctaattgaa
120
tgtgttgcca attcagatga acagcttggt gagatgttct tggaaagaaa aatccccctcg
180
atttctgatt taaagctagc aattcgaaga gctactctga aaagatcatt tactcctgta
240
tttttgggaa gcgccttgaa gaacaaagga gttcagcctc ttttagatgc tgttttagaa
300
tacctcccaa atccatctga agtccagaac tatgctatct tcaataaaga ggatgactca
360
aaagagaaaa ccaaaatcct aatgaactcc agtagagaca attccccccc attttaggag
420
ctggctttta aactggaggt aggtcgattt ggacaattaa cttatgttgc cagttatcag
480
ggagagctaa agaagggtga caccatctat aacacaagga caagaaagaa agtacggttg
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caacggctgg ctgcgatgca tgccgacatg atg
573

<210> 4042
<211> 191
<212> PRT

<213> Homo sapiens

<400> 4042

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Asp Leu Ile Glu Glu Arg Ala Ile Tyr Phe Asp Gly Asp Phe Gly Gln
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Ile Val Arg Tyr Gly Glu Ile Pro Ala Glu Leu Arg Ala Ala Ala Thr
          20           25           30
Asp His Arg Gln Glu Leu Ile Glu Cys Val Ala Asn Ser Asp Glu Gln
          35           40           45
Leu Gly Glu Met Phe Leu Glu Glu Lys Ile Pro Ser Ile Ser Asp Leu
          50           55           60
Lys Leu Ala Ile Arg Arg Ala Thr Leu Lys Arg Ser Phe Thr Pro Val
65           70           75           80
Phe Leu Gly Ser Ala Leu Lys Asn Lys Gly Val Gln Pro Leu Leu Asp
          85           90           95
Ala Val Leu Glu Tyr Leu Pro Asn Pro Ser Glu Val Gln Asn Tyr Ala
          100          105          110
Ile Leu Asn Lys Glu Asp Asp Ser Lys Glu Lys Thr Lys Ile Leu Met
          115          120          125
Asn Ser Ser Arg Asp Asn Ser His Pro Phe Val Gly Leu Ala Phe Lys
          130          135          140
Leu Glu Val Gly Arg Phe Gly Gln Leu Thr Tyr Val Arg Ser Tyr Gln
145          150          155          160
Gly Glu Leu Lys Lys Gly Asp Thr Ile Tyr Asn Thr Arg Thr Arg Lys
          165          170          175
Lys Val Arg Leu Gln Arg Leu Ala Arg Met His Ala Asp Met Met
          180          185          190

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<210> 4043

<211> 744

<212> DNA

<213> Homo sapiens

<400> 4043

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120
ctcccaaaaa aagacccaaa agttaaaggt gtccaatcag cagctgtaca agcttttctt
180
aaaaggaaag aagaggagct gagacgaaaa gccttagagg agaaaaggag aaaagaggaa
240
ctagtgaaaa agcgaattga gctcaaacat gacaagaaa caagagctat ggccaagagg
300
acaaaggata atttccatgg ttacaatggg attcctattg aggaaaaagtc aaagaagagg
360
caggcaacag aaagccatac cagccaagga accgaccgag agtatgaaat ggaagaagag
420
aatgaattcc tcgagtacaa tcacgcagag tcagagcagg agtatgagga agagcaagaa
480
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540
ttcactgatt tactcaggct ggctgagaaa aagcagtttg aaccagtgga aatcaaggta
600

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gtgaagaaat cagaagagcg acctatgacc gcagaagaac ttaggggagcg agaattcctt
 660
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 720
 aaaaaggcac ctctcggacg gaag
 744

<210> 4044
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 4044
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 20 25 30
 Arg Lys Glu Glu Leu Arg Arg Lys Ala Leu Glu Glu Lys Arg Arg
 35 40 45
 Lys Glu Glu Leu Val Lys Lys Arg Ile Glu Leu Lys His Asp Lys Lys
 50 55 60
 Ala Arg Ala Met Ala Lys Arg Thr Lys Asp Asn Phe His Gly Tyr Asn
 65 70 75
 Gly Ile Pro Ile Glu Glu Lys Ser Lys Lys Arg Gln Ala Thr Glu Ser
 85 90 95
 His Thr Ser Gln Gly Thr Asp Arg Glu Tyr Glu Met Glu Glu Glu Asn
 100 105 110
 Glu Phe Leu Glu Tyr Asn His Ala Glu Ser Glu Gln Glu Tyr Glu Glu
 115 120 125
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<211> 437

<212> PRT

<213> Homo sapiens

<400> 4046

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Thr	Val	Val	Thr	Ala	Ile	Phe	Gly	Gly	Ile	Leu	Gln	Asn	Glu	Val	Asn
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      290                295                300
Cys Lys Xaa Lys Gln Lys Ser Thr Lys Lys Phe Trp Ile Gln Lys Leu
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Pro Lys Val Leu Cys Leu His Leu Lys Arg Phe His Trp Thr Ala Tyr
      325                330                335
Leu Arg Asn Lys Val Asp Thr Tyr Val Glu Phe Pro Leu Arg Gly Leu
      340                345                350
Asp Met Lys Cys Tyr Leu Leu Asp Pro Glu Asn Ser Gly Pro Glu Ser
      355                360                365
Cys Leu Tyr Asp Leu Ala Ala Val Val Val His His Gly Ser Gly Val
      370                375                380
Gly Ser Gly His Tyr Thr Ala Tyr Ala Thr His Glu Gly Arg Trp Phe
      385                390                395                400
His Phe Asn Asp Ser Thr Val Thr Leu Thr Asp Glu Glu Thr Val Val
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<211> 809

<212> DNA

<213> Homo sapiens

<400> 4047

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720

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<210> 4048

<211> 118

<212> PRT

<213> Homo sapiens

<400> 4048

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Val	Ala	Ile	Gly	Phe	Thr	Gly	Gly	Leu	Val	Phe	Met	Tyr	Val	Gln	Cys
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Lys	Val	Tyr	Val	Gln	Leu	Trp	Arg	Arg	Leu	Lys	Ala	Tyr	Asn	Arg	Val
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Ile	Phe	Val	Gln	Asn	Cys	Pro	Asp	Thr	Ala	Lys	Lys	Leu	Glu	Lys	Asn
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Phe	Ser	Cys	Asn	Val	Asn	Thr	Asp	Ile	Lys	Asp	Ala	Val	Val	Val	Pro
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<211> 1211

<212> DNA

<213> Homo sapiens

<400> 4049

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<211> 403

<212> PRT

<213> Homo sapiens

<400> 4050

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 35 40 45
 Ile Val Ser Arg Asp Arg Lys Val Ser Pro Lys Ser Glu Phe Thr Ser
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 Arg Asp Ser Gln Ser Ser Asp Lys Gln Ile Leu Asn Ile Tyr Asp Leu
 65 70 75 80
 Cys Asn Lys Phe Ile Ala Tyr Ser Thr Val Phe Glu Asp Val Val Asp
 85 90 95
 Val Leu Ala Glu Trp Gly Ser Leu Tyr Val Leu Thr Arg Asp Gly Arg
 100 105 110
 Val His Ala Leu Gln Glu Lys Asp Thr Gln Thr Lys Leu Glu Met Leu
 115 120 125
 Phe Lys Lys Asn Leu Phe Glu Met Ala Ile Asn Leu Ala Lys Ser Gln
 130 135 140
 His Leu Asp Ser Asp Gly Leu Ala Gln Ile Phe Met Gln Tyr Gly Asp
 145 150 155 160
 His Leu Tyr Ser Lys Gly Asn His Asp Gly Ala Val Gln Gln Tyr Ile
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 Arg Thr Ile Gly Lys Leu Glu Pro Ser Tyr Val Ile Arg Lys Phe Leu
 180 185 190
 Asp Ala Gln Arg Ile His Asn Leu Thr Ala Tyr Leu Gln Thr Leu His

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Lys	Ser	Glu	Ser	Glu	Val	His	Phe	Asp	Val	Glu	Thr	Ala	Ile	Lys	Val														
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<210> 4051

<211> 1645

<212> DNA

<213> Homo sapiens

<400> 4051

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<211> 93

<212> PRT

<213> Homo sapiens

<400> 4052

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<211> 461

<212> DNA

<213> Homo sapiens

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<211> 96

<212> PRT

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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Ser Cys Arg Ala Ser Thr Leu Leu Ala Glu Leu Asp Asp Asp Glu Asp		1480
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<400> 4057

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<211> 714

<212> PRT

<213> Homo sapiens

<400> 4060

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 Gln Ala Gln Glu Trp Asp Met Asp Ala Arg Arg Pro Met Pro Phe Gln
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 Tyr Lys Thr Leu Met Ser Leu Asp Ala Glu Gly Ser Val Pro Lys Pro
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 Gln Arg His Pro Glu Glu Arg Glu Ile Pro Met Asp Pro Glu Ala Gly
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 Ala Glu Pro Leu Val Pro Ala Gln Asp Ala Ser Ser Gln Val Lys Arg
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 Ile Pro Thr Glu Ser Ile Thr Val Asp Ser Pro Ile Ser Ala Gln Asp
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Glu	Cys	Glu	Lys	Ser	Phe	Asn	Cys	His	Ser	Gly	Leu	Ile	Arg	His	Gln	Glu	Cys	Glu	Lys	Ser	Phe	Asn	Cys	His	Ser	Gly	Leu	Ile	Arg	His	Gln	Glu	Cys	Glu	Lys	Ser	Phe	Asn	Cys	His	Ser	Gly	Leu	Ile	Arg	His	Gln
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625										630										635																											
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675										680										685																											
Lys	Asp	His	Leu	Arg	Val	His	Ser	Gly	Gly	Pro	Gly	Pro	Gly	Ala	Pro	Lys	Asp	His	Leu	Arg	Val	His	Ser	Gly	Gly	Pro	Gly	Pro	Gly	Ala	Pro	Lys	Asp	His	Leu	Arg	Val	His	Ser	Gly	Gly	Pro	Gly	Pro	Gly	Ala	Pro
690										695										700																											
Arg	Gln	Leu	Pro	Pro	Pro	Pro	Glu	Arg	Asp							Arg	Gln	Leu	Pro	Pro	Pro	Pro	Glu	Arg	Asp							Arg	Gln	Leu	Pro	Pro	Pro	Pro	Glu	Arg	Asp						
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<210> 4061

<211> 519

<212> DNA

<213> Homo sapiens

<400> 4061

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<210> 4062

<211> 165

<212> PRT

<213> Homo sapiens

<400> 4062

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Glu	Leu	Ala	Ala	Ile	Ile	Pro	Leu	Val	Val	Lys	Ser	Val	Lys	Cys	Ala

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<210> 4064

<211> 818

<212> PRT

<213> Homo sapiens

<400> 4064

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Met Cys Cys Pro Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His
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Asn His Asn Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp
          50          55          60
Gln Ala Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr
65          70          75          80
Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
          85          90          95
Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys Asn
          100          105          110
Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys Glu Lys
          115          120          125
His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu Ile Thr Asn
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Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met Tyr Pro His Arg
          145          150          155          160
Pro Val Leu Met Val Ile Ser His Ala Ala Pro His Gly Pro Glu Asp
          165          170          175
Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro Asn Ala Ser Gln His Ile
          180          185          190
Thr Pro Ser Tyr Asn Tyr Ala Pro Asp Pro Asp Lys His Trp Ile Met
          195          200          205
Arg Tyr Thr Gly Pro Met Lys Pro Ile His Met Glu Phe Thr Asn Met
          210          215          220
Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser Met
          225          230          235          240
Glu Thr Ile Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Asp Asn Thr
          245          250          255
Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly
          260          265          270
Leu Val Lys Gly Lys Ser Met Pro Tyr Glu Phe Asp Ile Arg Val Pro
          275          280          285
Phe Tyr Val Arg Gly Pro Asn Val Glu Ala Gly Cys Leu Asn Pro His
          290          295          300
Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly
          305          310          315          320
Leu Asp Ile Pro Ala Asp Met Asp Gly Lys Ser Ile Leu Lys Leu Leu
          325          330          335
Asp Thr Glu Arg Pro Val Asn Arg Phe His Leu Lys Lys Lys Met Arg
          340          345          350
Val Trp Arg Asp Ser Phe Leu Val Glu Arg Gly Lys Leu Leu His Lys
          355          360          365
Arg Asp Asn Asp Lys Val Asp Ala Gln Glu Glu Asn Phe Leu Pro Lys

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370	375	380
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385	390	395
Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys Val Glu Asp Ala Thr Gly		400
	405	415
Lys Leu Lys Leu His Lys Cys Lys Gly Pro Met Arg Leu Gly Gly Ser		
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Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr Tyr Gly Gln Gly Ser Glu		
	435	445
Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys Leu Ser Leu Ala Gly Arg		
	450	460
Arg Lys Lys Xaa Leu Gln Glu Glu Xaa Tyr Lys Ala Ser Tyr Val Arg		
	465	475
Asn Arg Ser Ile Arg Ser Val Ala Ile Glu Val Asp Gly Arg Val Tyr		
	485	495
His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg Asn Leu Thr Lys Arg		
	500	510
His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp		
	515	525
Xaa Ser Val Ala Leu Glu Ala Phe Pro Thr Thr Gln Pro Pro Thr Xaa		
	530	540
Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln		
	545	555
Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys Asp His Lys		
	565	575
Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys Ile Lys Asn		
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Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro Glu Glu Cys		
	595	605
Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly Arg Leu Lys		
	610	620
His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu Gln Glu Lys		
	625	635
Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys Lys Leu Arg		
	645	655
Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys Ser Met Pro Gly		
	660	670
Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln Thr Ala Pro Phe		
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Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala Asn Asn Asn Thr		
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Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn Phe Leu Phe Cys		
	705	715
Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu Asn Thr Asp Pro		
	725	735
Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg Asp Val Leu Asn		
	740	750
Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Gly Tyr Lys		
	755	765
Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly Leu Lys Asp Gly		
	770	780
Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Lys Trp Pro Glu		
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810

815

Glu Gly

<210> 4065
<211> 696
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Phe Pro Leu Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile
35 40 45
Pro Phe Ser Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr
50 55 60
Ile Asn Val Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys
65 70 75 80
Ala Ile Val Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn
85 90 95
Glu Ile Asp Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr

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<211> 521

<212> PRT

<213> Homo sapiens

<400> 4068

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 Gln Ala Phe Leu Glu Met Ala Ser Glu Glu Ala Val Thr Met Val
 65 70 75 80
 Asn Tyr Tyr Thr Pro Ile Thr Pro His Leu Arg Ser Gln Pro Val Tyr
 85 90 95
 Ile Gln Tyr Ser Asn His Arg Glu Leu Lys Thr Asp Asn Leu Pro Asn
 100 105 110
 Gln Ala Arg Ala Gln Ala Ala Leu Gln Ala Val Ser Ala Val Gln Ser
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 Gly Ser Leu Ala Leu Ser Gly Gly Pro Ser Asn Glu Gly Thr Val Leu
 130 135 140
 Pro Gly Gln Ser Pro Val Leu Arg Ile Ile Ile Glu Asn Leu Phe Tyr


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145          150          155          160
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Val Leu Lys Ile Ile Thr Phe Thr Lys Asn Asn Gln Phe Gln Ala Leu
180          185          190
Leu Gln Tyr Ala Asp Pro Val Asn Ala His Tyr Ala Lys Met Ala Leu
195          200          205
Asp Gly Gln Asn Ile Tyr Asn Ala Cys Cys Thr Leu Arg Ile Asp Phe
210          215          220
Ser Lys Leu Thr Ser Leu Asn Val Lys Tyr Asn Asn Asp Lys Ser Arg
225          230          235
Asp Phe Thr Arg Leu Asp Leu Pro Thr Gly Asp Gly Gln Pro Ser Leu
245          250          255
Glu Pro Pro Met Ala Ala Ala Phe Gly Ala Pro Gly Ile Ile Ser Ser
260          265          270
Pro Tyr Ala Gly Ala Ala Gly Phe Ala Pro Ala Ile Gly Phe Pro Gln
275          280          285
Ala Thr Gly Leu Ser Val Pro Ala Val Pro Gly Ala Leu Gly Pro Leu
290          295          300
Thr Ile Thr Ser Ser Ala Val Thr Gly Arg Met Ala Ile Pro Gly Ala
305          310          315
Ser Gly Ile Pro Gly Asn Ser Val Leu Leu Val Thr Asn Leu Asn Pro
325          330          335
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370          375          380
Ser Gly Gln Arg Leu Tyr Gly Lys Val Leu Arg Ala Thr Leu Ser Lys
385          390          395
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405          410          415
Thr Lys Asp Phe Ser Asn Ser Pro Leu His Arg Phe Lys Lys Pro Gly
420          425          430
Ser Lys Asn Phe Gln Asn Ile Phe Pro Pro Ser Ala Thr Leu His Leu
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450          455          460
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465          470          475
Arg Lys Met Ala Leu Ile Gln Leu Gly Ser Val Glu Glu Ala Ile Gln
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<210> 4069

<211> 714

<212> DNA

<213> Homo sapiens

<400> 4069

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<210> 4070
<211> 113
<212> PRT
<213> Homo sapiens

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Gln Thr Ser Thr Met Thr Phe Ala Pro Phe Glu Asp Thr Leu Ser Trp
50 55 60
Met Leu Phe Gly Trp Gln Gln Pro Phe Ser Ser Cys Glu Lys Lys Ser
65 70 75 80
Glu Ala Lys Ser Pro Ser Asn Gly Val Gly Ser Leu Ala Ser Lys Pro
85 90 95
Val Asp Val Ala Ser Asp Asn Val Lys Lys His Thr Lys Lys Asn
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Glu

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<210> 4071
<211> 601
<212> DNA
<213> Homo sapiens

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<400> 4071

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 480
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<210> 4072

<211> 175

<212> PRT

<213> Homo sapiens

<400> 4072

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Cys	Ala	Leu	Val	Pro	Arg	Leu	Val	Arg	Met	Lys	Val	Phe	His	Leu	Ser
		20					25					30			
Leu	Ser	Gln	Ser	Val	Val	Leu	Arg	His	His	Trp	Ile	Leu	Pro	Phe	Val
		35				40					45				
Gln	Ala	Leu	Lys	Ala	Arg	Met	Thr	Ser	Phe	His	Arg	Phe	Phe	Phe	Thr
		50				55					60				
Ala	Asn	Gln	Val	Lys	Ile	Tyr	Thr	Asn	Gln	Glu	Lys	Thr	Arg	Thr	Phe
65					70					75				80	
Ile	Gly	Leu	Glu	Val	Thr	Ser	Gly	His	Ala	Gln	Phe	Leu	Asp	Leu	Val
			85						90				95		
Ser	Glu	Val	Asp	Arg	Val	Met	Glu	Glu	Phe	Asn	Leu	Thr	Thr	Phe	Tyr
			100					105					110		
Gln	Asp	Pro	Ser	Phe	His	Leu	Ser	Leu	Ala	Trp	Cys	Val	Gly	Asp	Ala
		115					120					125			
Arg	Leu	Gln	Leu	Glu	Gly	Gln	Cys	Leu	Gln	Glu	Leu	Gln	Ala	Ile	Val
		130				135					140				
Asp	Gly	Phe	Glu	Asp	Ala	Glu	Val	Leu	Leu	Arg	Val	His	Thr	Glu	Gln
145					150					155					160
Val	Arg	Cys	Lys	Ser	Gly	Asn	Lys	Phe	Phe	Ser	Met	Pro	Leu	Lys	
			165						170					175	

<210> 4073

<211> 1864

<212> DNA

<213> Homo sapiens

<400> 4073

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180
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360
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420
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480
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540
aaagaccaga gtaatgcgga gaagcacgca gatggaatga taagtactat taatcccgta
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gatgcaatat atcaacctag tcctttggaa cctgtgatca gcacaatgcc ttccagact
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720
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780
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1440
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1500

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 1560
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 1620
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 1680
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 1740
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 attg
 1864

<210> 4074

<211> 456

<212> PRT

<213> Homo sapiens

<400> 4074

Met	Val	Glu	Ser	Ile	Lys	His	Cys	Ile	Val	Leu	Leu	Gln	Ile	Ala	Lys
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Asp	Gln	Ser	Asn	Ala	Glu	Lys	His	Ala	Asp	Gly	Met	Ile	Ser	Thr	Ile
			20					25				30			
Asn	Pro	Val	Asp	Ala	Ile	Tyr	Gln	Pro	Ser	Pro	Leu	Glu	Pro	Val	Ile
		35					40					45			
Ser	Thr	Met	Pro	Ser	Gln	Thr	Val	Leu	Pro	Pro	Glu	Pro	Val	Gln	Leu
		50				55					60				
Cys	Lys	Ser	Glu	Gln	Arg	Pro	Ser	Ser	Leu	Pro	Val	Gly	Pro	Val	Leu
65					70					75				80	
Ala	Thr	Leu	Gly	His	His	Gln	Thr	Pro	Thr	Pro	Asn	Ser	Thr	Gly	Ser
				85					90				95		
Gly	His	Ser	Pro	Pro	Ser	Ser	Ser	Leu	Thr	Ser	Pro	Ser	His	Val	Asn
			100					105					110		
Leu	Ser	Pro	Asn	Thr	Val	Pro	Glu	Phe	Ser	Tyr	Ser	Ser	Ser	Glu	Asp
			115				120						125		
Glu	Phe	Tyr	Asp	Ala	Asp	Glu	Phe	His	Gln	Ser	Gly	Ser	Ser	Pro	Lys
		130				135					140				
Arg	Leu	Ile	Asp	Ser	Ser	Gly	Ser	Ala	Ser	Val	Leu	Thr	His	Ser	Ser
145					150					155					160
Ser	Gly	Asn	Ser	Leu	Lys	Arg	Pro	Asp	Thr	Thr	Glu	Ser	Leu	Asn	Ser
				165					170					175	
Ser	Leu	Ser	Asn	Gly	Thr	Ser	Asp	Ala	Asp	Leu	Phe	Asp	Ser	His	Asp
			180				185						190		
Asp	Arg	Asp	Asp	Asp	Ala	Glu	Ala	Gly	Ser	Val	Glu	Glu	His	Lys	Ser
		195					200								
Val	Ile	Met	His	Leu	Leu	Ser	Gln	Val	Arg	Leu	Gly	Met	Asp	Leu	Thr
		210				215					220				
Lys	Val	Val	Leu	Pro	Thr	Phe	Ile	Leu	Glu	Arg	Arg	Ser	Leu	Leu	Glu
225					230					235					240
Met	Tyr	Ala	Asp	Phe	Phe	Ala	His	Pro	Asp	Leu	Phe	Val	Ser	Ile	Ser
				245					250					255	
Asp	Gln	Lys	Asp	Pro	Lys	Asp	Arg	Met	Val	Gln	Val	Val	Lys	Trp	Tyr

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                260                265                270
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   275                280                285
Tyr Asn Pro Ile Leu Gly Glu Ile Phe Gln Cys His Trp Thr Leu Pro
   290                295                300
Asn Asp Thr Glu Glu Asn Thr Glu Leu Val Ser Glu Gly Pro Val Pro
   305                310                315
Trp Val Ser Lys Asn Ser Val Thr Phe Val Ala Glu Gln Val Ser His
   320                325                330                335
His Pro Pro Ile Ser Ala Phe Tyr Ala Glu Cys Phe Asn Lys Lys Ile
   340                345                350
Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser
   355                360                365
Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr
   370                375                380
Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile
   385                390                395                400
Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys
   405                410                415
Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe
   420                425                430
Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn
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Asp Lys Lys Ser Phe Cys Ser Ile
   450                455

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<210> 4075

<211> 2492

<212> DNA

<213> Homo sapiens

<400> 4075

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120
gtgcacatat ccagggtaaa gtcagttaac ctcgaccagt ggactcaaga acagattcag
180
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240
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300
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360
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420
aaggtgaaaa tgccacagaa aaaagaagac ccacagctac ctcggaaaaa cttccccgaa
480
tccacagcgc ctgtcatgga ttgttgggc cttgatgctc ctgtggcctg ctccattgca
540
aatagtaaga ccagcaatac cctagagaag gatttagatc tgttggcctc tgttccatcc
600
ccttctctct cgggttccag aaaggttgta ggttccatgc caactgcagg gagtgccggc
660

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780
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840
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 2492

<210> 4076

<211> 410

<212> PRT

<213> Homo sapiens

<400> 4076

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			20					25					30		
Ala	Gly	Ile	His	Arg	Asn	Leu	Gly	Val	His	Ile	Ser	Arg	Val	Lys	Ser
		35					40					45			
Val	Asn	Leu	Asp	Gln	Trp	Thr	Gln	Glu	Gln	Ile	Gln	Cys	Met	Gln	Glu
	50					55					60				
Met	Gly	Asn	Gly	Lys	Ala	Asn	Arg	Leu	Tyr	Glu	Ala	Tyr	Leu	Pro	Glu
	65				70				75					80	
Thr	Phe	Arg	Arg	Pro	Gln	Ile	Asp	Pro	Ala	Val	Glu	Gly	Phe	Ile	Arg
			85						90					95	
Asp	Lys	Tyr	Glu	Lys	Lys	Lys	Tyr	Met	Asp	Arg	Ser	Leu	Asp	Ile	Asn
			100					105					110		
Ala	Phe	Arg	Lys	Glu	Lys	Asp	Asp	Lys	Trp	Lys	Arg	Gly	Ser	Glu	Pro
		115					120					125			
Val	Pro	Glu	Lys	Lys	Leu	Glu	Pro	Val	Val	Phe	Glu	Lys	Val	Lys	Met
					135						140				
Pro	Gln	Lys	Lys	Glu	Asp	Pro	Gln	Leu	Pro	Arg	Lys	Ser	Ser	Pro	Lys
	145				150					155				160	
Ser	Thr	Ala	Pro	Val	Met	Asp	Leu	Leu	Gly	Leu	Asp	Ala	Pro	Val	Ala
			165					170						175	
Cys	Ser	Ile	Ala	Asn	Ser	Lys	Thr	Ser	Asn	Thr	Leu	Glu	Lys	Asp	Leu
		180						185					190		
Asp	Leu	Leu	Ala	Ser	Val	Pro	Ser	Pro	Ser	Ser	Ser	Gly	Ser	Arg	Lys
		195				200						205			
Val	Val	Gly	Ser	Met	Pro	Thr	Ala	Gly	Ser	Ala	Gly	Ser	Val	Pro	Glu
		210				215					220				
Asn	Leu	Asn	Leu	Phe	Pro	Glu	Pro	Gly	Ser	Lys	Ser	Glu	Glu	Ile	Gly
				230					235					240	
Lys	Lys	Gln	Leu	Ser	Lys	Asp	Ser	Ile	Leu	Ser	Leu	Tyr	Gly	Ser	Gln
			245						250					255	
Thr	Pro	Gln	Met	Pro	Thr	Gln	Ala	Met	Phe	Met	Ala	Pro	Ala	Gln	Met
			260					265						270	
Ala	Tyr	Pro	Thr	Ala	Tyr	Pro	Ser	Phe	Pro	Gly	Val	Thr	Pro	Pro	Asn
		275					280					285			
Ser	Ile	Met	Gly	Ser	Met	Met	Pro	Pro	Pro	Val	Gly	Met	Val	Ala	Gln
	290					295					300				
Pro	Gly	Ala	Ser	Gly	Met	Val	Ala	Pro	Met	Ala	Met	Pro	Ala	Gly	Tyr


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305          310          315          320
Met Gly Gly Met Gln Ala Ser Met Met Gly Val Pro Asn Gly Met Met
          325          330          335
Thr Thr Gln Gln Ala Gly Tyr Met Ala Gly Met Ala Ala Met Pro Gln
          340          345          350
Thr Val Tyr Gly Val Gln Pro Ala Gln Gln Leu Gln Trp Asn Leu Thr
          355          360          365
Gln Met Thr Gln Gln Met Ala Gly Met Asn Phe Tyr Gly Ala Asn Gly
          370          375          380
Met Met Asn Tyr Gly Gln Ser Met Ser Gly Gly Asn Gly Gln Ala Ala
385          390          395          400
Asn Gln Thr Leu Ser Pro Gln Met Trp Lys
          405          410

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<210> 4077

<211> 684

<212> DNA

<213> Homo sapiens

<400> 4077

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<210> 4078

<211> 194

<212> PRT

<213> Homo sapiens

<400> 4078

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Arg Val Val His Asn Trp Asp Phe Glu Pro Arg Lys Val Ser Arg Cys
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Ser Met Arg Tyr Leu Ala Leu Met Val Ser Arg Pro Val Leu Arg Leu

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                20                25                30
Arg Glu Ile Asn Pro Leu Leu Phe Ser Tyr Val Glu Glu Leu Val Glu
   35                40                45
Ile Arg Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile
   50                55                60
Thr Cys Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Leu Gln Asp
   65                70                75                80
Arg Gln His Phe Val Glu Asn Asp Glu Met Tyr Ser Val Gln Asp Leu
                85                90                95
Leu Asp Val His Ala Gly Arg Leu Gly Cys Ser Leu Thr Glu Ile His
                100                105                110
Thr Leu Phe Ala Lys His Ile Lys Leu Asp Cys Glu Arg Cys Gln Ala
                115                120                125
Lys Gly Phe Val Cys Glu Leu Cys Arg Glu Gly Asp Val Leu Phe Pro
                130                135                140
Phe Asp Ser His Thr Ser Val Cys Ala Asp Cys Ser Ala Val Phe His
   145                150                155                160
Arg Asp Cys Tyr Tyr Asp Asn Ser Thr Thr Cys Pro Lys Cys Ala Arg
                165                170                175
Leu Ser Leu Arg Lys Gln Ser Leu Phe Gln Glu Pro Gly Pro Asp Val
                180                185                190
Glu Ala

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<210> 4079

<211> 783

<212> DNA

<213> Homo sapiens

<400> 4079

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120
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240
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300
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360
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420
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540
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660
ctgttatgac ctcatctctc ccatgaggaa gccagggttc agagaagttg aaggcatgag
720

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 780
 nta
 783

<210> 4080
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 4080
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 35 40 45
 Glu Ala Leu His Ala Gln Pro Gly Glu Gln Gly Trp Met Gly Leu Lys
 50 55 60
 Arg Ala Gln Pro Ser Pro Glu Arg Thr Leu His Ser Asn Leu Pro Gln
 65 70 75 80
 Ser Trp Gly Lys His Glu Gly Cys Pro Ser Thr Glu Val Asn Pro Gly
 85 90 95
 His Ala Arg Thr Lys
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<210> 4081
 <211> 645
 <212> DNA
 <213> Homo sapiens

<400> 4081
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 120
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<211> 362

<212> PRT

<213> Homo sapiens

<400> 4084

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<212> DNA

<213> Homo sapiens

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<211> 789

<212> PRT

<213> Homo sapiens

<400> 4086

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Lys Gly Pro Pro Phe Met Glu Ser Leu Pro Glu Asn Lys Pro Leu Val
705          710          715          720
Trp Ser Leu Ala Val Ser Leu Leu Ala Ile Ile Gly Leu Leu Gly
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<211> 959

<212> DNA

<213> Homo sapiens

<400> 4087

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 ctcaccatga gggccaatga cttggttgga accagtatga ctgtcctaca ggagcagcag
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<210> 4088

<211> 319

<212> PRT

<213> Homo sapiens

<400> 4088

Arg	Gly	Ser	Leu	Glu	Lys	Ala	Leu	Phe	Gln	Leu	Leu	Lys	Val	Trp	Gly
1				5					10					15	
Gln	Trp	Ala	Glu	Gln	Thr	Arg	Arg	Leu	Gln	Arg	Leu	Asp	Val	Ser	Leu
		20						25					30		
Ala	Val	Ala	Arg	Val	Arg	Ser	Ala	Gly	Pro	Ser	Cys	Gln	Asn	Lys	Gly
		35					40					45			
Asp	Leu	Val	Met	Glu	Ala	Leu	Leu	Glu	Gly	Ile	Gln	Asn	Arg	Gly	His
	50					55					60				
Gly	Gly	Gly	Phe	Leu	Thr	Ser	Cys	Glu	Ala	Glu	Leu	Gln	Glu	Leu	Met
65					70					75					80
Lys	Gln	Ile	Asp	Ile	Met	Val	Ala	His	Lys	Lys	Ser	Glu	Trp	Glu	Gly
			85						90					95	
Arg	Thr	His	Ala	Leu	Glu	Thr	Cys	Leu	Lys	Ile	Arg	Glu	Gln	Glu	Leu
			100					105					110		
Lys	Ser	Leu	Arg	Ser	Gln	Leu	Asp	Val	Thr	His	Lys	Glu	Val	Gly	Met
		115				120						125			
Leu	His	Gln	Gln	Val	Glu	Glu	His	Glu	Lys	Ile	Lys	Gln	Glu	Met	Thr
	130					135					140				
Met	Glu	Tyr	Lys	Gln	Glu	Leu	Lys	Lys	Leu	His	Glu	Glu	Leu	Cys	Ile
			145			150				155				160	
Leu	Lys	Arg	Ser	Tyr	Glu	Lys	Leu	Gln	Lys	Lys	Gln	Met	Arg	Glu	Phe
			165					170					175		
Arg	Gly	Asn	Thr	Lys	Asn	His	Arg	Glu	Asp	Arg	Ser	Glu	Ile	Glu	Arg
		180					185						190		
Leu	Thr	Ala	Lys	Ile	Glu	Glu	Phe	Arg	Gln	Lys	Ser	Leu	Asp	Trp	Glu
		195					200					205			
Lys	Gln	Arg	Leu	Ile	Tyr	Gln	Gln	Gln	Val	Ser	Ser	Leu	Glu	Ala	Gln
		210				215					220				
Arg	Lys	Ala	Leu	Ala	Glu	Gln	Ser	Glu	Ile	Ile	Gln	Ala	Gln	Leu	Val
					230					235				240	
Asn	Arg	Lys	Gln	Lys	Leu	Glu	Ser	Val	Glu	Leu	Ser	Ser	Gln	Ser	Glu
			245						250					255	
Ile	Gln	His	Leu	Ser	Ser	Lys	Leu	Glu	Arg	Ala	Asn	Asp	Thr	Ile	Cys
			260				265					270			
Ala	Asn	Glu	Leu	Glu	Ile	Glu	Arg	Leu	Thr	Met	Arg	Val	Asn	Asp	Leu
		275					280					285			
Val	Gly	Thr	Ser	Met	Thr	Val	Leu	Gln	Glu	Gln	Gln	Gln	Lys	Glu	Glu
		290				295					300				
Lys	Leu	Arg	Glu	Ser	Glu	Lys	Leu	Leu	Glu	Ala	Leu	Gln	Glu	Lys	
305					310					315					

<210> 4089

<211> 511

<212> DNA

<213> Homo sapiens

<400> 4089

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 120
 aaccctgtgg ggctggcccc tacacagttt ttaaggggta caggggaaggg aagaacagg
 180
 caccatgtgg ggcagggggt ctgcttctat catatttcca tttgtgtgtt ttaggagatc
 240
 cttccaactc tcaactaacat tattttccag agaacaaaag aaaaactatg ctctccaaga
 300
 acatgtttcc tttgtaattt ttctgtcttc aaactttttc tggagagatg agtcatttga
 360
 cctgacattg agaataggct tgaagccctt tgagaggaca aaggagatag agtcagcatt
 420
 cctatctcca tgctctgaag atccaagtca cttggttact gctccctggg ctgtctattt
 480
 tcaactgttta tggaagatag agtacacctg t
 511

<210> 4090

<211> 109

<212> PRT

<213> Homo sapiens

<400> 4090

Met	Trp	Gly	Arg	Gly	Ser	Ala	Ser	Ile	Ile	Phe	Pro	Phe	Cys	Cys	Phe
1				5					10				15		
Arg	Arg	Ser	Phe	Gln	Leu	Ser	Leu	Thr	Leu	Phe	Ser	Arg	Glu	Gln	Lys
			20					25					30		
Lys	Asn	Tyr	Ala	Leu	Gln	Glu	His	Val	Ser	Phe	Val	Ile	Phe	Leu	Ser
	35						40				45				
Ser	Asn	Phe	Phe	Trp	Arg	Asp	Glu	Ser	Phe	Asp	Leu	Thr	Leu	Arg	Ile
	50				55						60				
Gly	Leu	Lys	Pro	Phe	Glu	Arg	Thr	Lys	Glu	Ile	Glu	Ser	Ala	Phe	Leu
	65				70				75				80		
Ser	Pro	Cys	Ser	Glu	Asp	Pro	Ser	His	Leu	Val	Thr	Ala	Pro	Trp	Ala
			85					90					95		
Val	Tyr	Phe	His	Cys	Leu	Trp	Lys	Ile	Glu	Tyr	Thr	Cys			
			100					105							

<210> 4091

<211> 1526

<212> DNA

<213> Homo sapiens

<400> 4091

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 60

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120
caaggaaggg cccccgggag ctctatatgg aggaaggagc ccagaatggg gtgcaccagg
180
aagacaaaaa ctttgggtgc cacttgctg atcctgagcg gcatgactaa catcatctgc
240
ctgctctacg tgggctgggt caccaactac atcgccagcg tgtatgtgcy ggggcaggag
300
ccggcgcccg acaagaagct ggaggaagac aaaggggaca ctctgaagat tattgagcgg
360
ctggaccacc tggagaatgt catcaagcag cacattcaag gctataggag aaatttctcc
420
cttctgaatg tgtccaacta actctgttca cctgagaaat catattcccc agctctgggt
480
atccctgaat aaccacagga gaacagttcc aggccctgat aagtcagcta ttgcaagggg
540
gacctggctg gaagatatga aggaaaaata tcattcttga actaataagt tgagagatca
600
cagccttcag gggaccagaa ggggaaggctg aacagagaag ggcaatttca cgttcgccat
660
gtccatattt ctatcgctcat gagccatctc accttacagg cagggaagtt ttgagcttag
720
agaatgggat gcgtcaagaa aaccgtggct ccccgagctc tgttcttgga ttcatgtcct
780
gttgtttcat cctgtgtaga ctggagtcag ggtctacaca gttggaattc tatggaacca
840
agatgctgtg tggcagatgg atgtggactc caactgtgac aatccagaag gccttgggga
900
cttgtttcat gaacagctcc ctgtaggatc tctgttgggg tgggggattc taggggcatc
960
tcgcagttt tcttctgaaa acaaaacgaa tacaagttgg gcagggtcaa caactgtgca
1020
tgcagtcccc tcccagggtt ggctagcagt attgttgggt accgtaagca cttagcattg
1080
ttaagtgcgc ataagtaaca agatgcaaca gcctctggcc aagttttgaa gattttgtt
1140
taaatgtatg ttttagatgt tgacattcat gattattaaa aggaacaaaa ctcaatttgg
1200
ggtctcaaga gccacaattc tagacttcta ggatgtcagg agccatgctc ttaagcttct
1260
cacccctgctg ttttaatgag attaatgatt attttccact gaggacctac ctgtgatgtt
1320
cataaaaaag tgaaataaat gactcacatg gagatttga aggatattcac tgtggaaggt
1380
agatgttaac agcctctaga aatatgataa ttatcagcta ttgagatgc agtcactgta
1440
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1500
gttataagaa aaaaaaaaaa aaaaaa
1526

<210> 4092

<211> 146

<212> PRT

<213> Homo sapiens

<400> 4092

His Gly Gly Tyr Thr Gly Ser Gly Pro Gly Phe Gly Glu Pro Arg Asp
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 Ser Gly Ala Glu Val Pro Ser Gly Ser Gly Arg Ala Thr Gly Cys Glu
 20 25 30
 Arg Gly Gly Val Arg Gly Ala Arg Gln Gly Arg Ala Pro Gly Ser Ser
 35 40 45
 Ile Trp Arg Lys Glu Pro Arg Met Val Cys Thr Arg Lys Thr Lys Thr
 50 55 60
 Leu Val Ser Thr Cys Val Ile Leu Ser Gly Met Thr Asn Ile Ile Cys
 65 70 75 80
 Leu Leu Tyr Val Gly Trp Val Thr Asn Tyr Ile Ala Ser Val Tyr Val
 85 90 95
 Arg Gly Gln Glu Pro Ala Pro Asp Lys Lys Leu Glu Glu Asp Lys Gly
 100 105 110
 Asp Thr Leu Lys Ile Ile Glu Arg Leu Asp His Leu Glu Asn Val Ile
 115 120 125
 Lys Gln His Ile Gln Gly Tyr Arg Arg Asn Phe Ser Leu Leu Asn Val
 130 135 140
 Ser Asn
 145

<210> 4093

<211> 1519

<212> DNA

<213> Homo sapiens

<400> 4093

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 120
 gaggaaaaga ggcgggggcg cgctgggggg tgagagcatg agggaggccg gggggggctg
 180
 cttggagcgc tgctagggag cggtgccgcc gcacacccgc ctggggcgcg cggaggggcg
 240
 ggagcgggca ggtcgcgcct cgccgcagcg accgcgggga gctgttctga ttccgcagcg
 300
 gcacctaggg gcccgagca ccccccgcgc cgccgcgcgc cgcacatggg caacgcaggg
 360
 agcatggatt cgcagcagac cgatttcagg gcgcacaacg tgcctttgaa gctgccgatg
 420
 ccagagccag gtgaactgga ggagcgattt gccatcgctg tgaacgctat gaacctaccc
 480
 cctgacaaa ccaggttact cgggcagtat gataatgaga aaaaatggga actgatttgt
 540
 gatcaggaac gattccaggt gaagaatcct ccccatatat acattcaaaa gctcaaaagg
 600
 tatctggatc cagctgtaac caggaagaaa ttcagacggc gtgttcaaga atctacacaa
 660
 gtgctaagag aactggaaat ttctttaaga actaaccaca ttggatgggt cagagaattt
 720

ctgaatgaag aaaacaaagg tcttgatggt ctatgggaat atctctcatt tgcacagtac
 780
 gcggtaactt ttgactttga aagtggtggag agtactgtgg agagctcggt ggacaaatca
 840
 aagccctgga gttaggtccat cgaggacctg cacagagggga gcaacctgcc ctcacctgtg
 900
 ggcaacagtgt tctcccgctc tggaagacat tctgcactgc gatataatac attgccaagc
 960
 agaagaactc tgaaaaattc aagattagtg agtaagaaag atgatgtgca tgtctgtatc
 1020
 atgtgtttac gtgccatcat gaattatcag tatggtttca acatgggtcat gtctcatcca
 1080
 cagcgtgtca atgagattgc actaagcctg aacaacaaga atcccagaac aaaagccctt
 1140
 gtcttagaac tgttggcagc cgtttgtctt gtcagaggcg ggcatgaaat cattttatca
 1200
 gcatttgata actttaaaga ggtttggga gaaaaacagc gctttgagaa gttgatggaa
 1260
 catttcagga atgaagacaa taacatagat tttatgggtg cttctatgca gtttattaat
 1320
 attgtagtcc attcagtaga agatatgaat ttcagagttc acctgcagta tgaatttacc
 1380
 aaattaggcc tggacgaata cttggacaag ctgaaacaca ctgagagtga caagcttcaa
 1440
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<210> 4094

<211> 391

<212> PRT

<213> Homo sapiens

<400> 4094

Met	Gly	Asn	Ala	Gly	Ser	Met	Asp	Ser	Gln	Gln	Thr	Asp	Phe	Arg	Ala
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His	Asn	Val	Pro	Leu	Lys	Leu	Pro	Met	Pro	Glu	Pro	Gly	Glu	Leu	Glu
			20					25					30		
Glu	Arg	Phe	Ala	Ile	Val	Leu	Asn	Ala	Met	Asn	Leu	Pro	Pro	Asp	Lys
		35					40					45			
Ala	Arg	Leu	Leu	Arg	Gln	Tyr	Asp	Asn	Glu	Lys	Lys	Trp	Glu	Leu	Ile
	50				55					60					
Cys	Asp	Gln	Glu	Arg	Phe	Gln	Val	Lys	Asn	Pro	Pro	His	Thr	Tyr	Ile
	65				70				75					80	
Gln	Lys	Leu	Lys	Gly	Tyr	Leu	Asp	Pro	Ala	Val	Thr	Arg	Lys	Lys	Phe
			85					90					95		
Arg	Arg	Arg	Val	Gln	Glu	Ser	Thr	Gln	Val	Leu	Arg	Glu	Leu	Glu	Ile
			100					105					110		
Ser	Leu	Arg	Thr	Asn	His	Ile	Gly	Trp	Val	Arg	Glu	Phe	Leu	Asn	Glu
		115					120					125			
Glu	Asn	Lys	Gly	Leu	Asp	Val	Leu	Val	Glu	Tyr	Leu	Ser	Phe	Ala	Gln
		130				135					140				
Tyr	Ala	Val	Thr	Phe	Asp	Phe	Glu	Ser	Val	Glu	Ser	Thr	Val	Glu	Ser


```

145          150          155          160
Ser Val Asp Lys Ser Lys Pro Trp Ser Arg Ser Ile Glu Asp Leu His
          165          170          175
Arg Gly Ser Asn Leu Pro Ser Pro Val Gly Asn Ser Val Ser Arg Ser
          180          185          190
Gly Arg His Ser Ala Leu Arg Tyr Asn Thr Leu Pro Ser Arg Arg Thr
          195          200          205
Leu Lys Asn Ser Arg Leu Val Ser Lys Lys Asp Asp Val His Val Cys
          210          215          220
Ile Met Cys Leu Arg Ala Ile Met Asn Tyr Gln Tyr Gly Phe Asn Met
225          230          235          240
Val Met Ser His Pro His Ala Val Asn Glu Ile Ala Leu Ser Leu Asn
          245          250          255
Asn Lys Asn Pro Arg Thr Lys Ala Leu Val Leu Glu Leu Ala Ala
          260          265          270
Val Cys Leu Val Arg Gly Gly His Glu Ile Ile Leu Ser Ala Phe Asp
          275          280          285
Asn Phe Lys Glu Val Cys Gly Glu Lys Gln Arg Phe Glu Lys Leu Met
          290          295          300
Glu His Phe Arg Asn Glu Asp Asn Asn Ile Asp Phe Met Val Ala Ser
305          310          315          320
Met Gln Phe Ile Asn Ile Val Val His Ser Val Glu Asp Met Asn Phe
          325          330          335
Arg Val His Leu Gln Tyr Glu Phe Thr Lys Leu Gly Leu Asp Glu Tyr
          340          345          350
Leu Asp Lys Leu Lys His Thr Glu Ser Asp Lys Leu Gln Val Gln Ile
          355          360          365
Gln Ala Tyr Leu Asp Asn Val Phe Asp Val Gly Ala Leu Leu Glu Asp
          370          375          380
Ala Glu Thr Lys Asn Ala Ala
385          390

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<210> 4095

<211> 253

<212> DNA

<213> Homo sapiens

<400> 4095

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120
agagagatca agtagcatcc ccagcgaaat ctgaggcctc tggagggcc tgtgcacgtg
180
tgtctggaag tgtgtgtcca gccagcatat ctgcatgtgt gtgcctgtcc agacagcata
240
tctgtgcacg cgt
253

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<210> 4096

<211> 83

<212> PRT

<213> Homo sapiens

<400> 4096

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Met Gly Gly Gly Glu Gln Ala Ser Ala Gly Arg Val Pro Lys Arg Gln
 1           5           10           15
Pro Arg Glu Gln Gly Gln Ile Val Gly Gly Gly Phe Ser Ser Thr Val
      20           25           30
Gln Val Arg Lys Leu Arg Leu Lys Arg Asp Gln Val Ala Ser Pro Ala
      35           40           45
Lys Ser Glu Ala Ser Gly Gly Ala Cys Ala Arg Val Ser Gly Ser Val
      50           55           60
Cys Pro Gly Ser Ile Ser Ala Cys Val Cys Leu Ser Arg Gln His Ile
      65           70           75           80
Cys Ala Arg

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<210> 4097

<211> 1385

<212> DNA

<213> Homo sapiens

<400> 4097

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ctgggacgcg tgccgcgcac tggcacgcga gggcgcgcag ccaggctgca cgattcactg
120
cgtgctgttc tcacttggtc tacaatgagt gccaaatctg ctatcagcaa ggaaattttt
180
gcacctcttg atgaaaggat gctgggagct gtccaagtca agaggaggac aaagaaaaag
240
attcctttct tggcaactgg aggtcaaggc gaatatattaa cttatatctg cctgtcagtg
300
acaaacaaga aaccacaca ggcgtccatc acaaaggcca aacagtttga aggctccaca
360
tcatttggtc ggagatcaca gtggatgctc gagcagcttc gccaggttaa tggtatcgat
420
cctaattggg attcggcaga gtttgatttg ttgtttgaat atgcttttga ccagtgggta
480
gccagcacag cgtcagaaaa atgcaccttc ttccagatcc tccaccatac ctgccagagg
540
tacctcacgc acaggaagcc agagtattat aactgccaat ccaaaattat gggaggaaac
600
agcatcctcc attcagctgc tgacagcgtg accagcgcag tgcagaaggc aagccaggcc
660
ttgaatgagc gtggagagcg attaggccga gcagaggaga agacagaaga cctgaagaac
720
agcgcgccagc agtttgaga aactgcgcac aagcttgcca tgaagcacia atgttgagaa
780
actgcctatc ctggtgactc ttcttaagag aaactgaaga gtttggttcag cagtttttcc
840
aagaattcgg gacctccgct tgctttcttt tttccaatat ttggacactt agagtgggtt
900
ttgttttttc ttttcagatg ttaatgtgaa agaaaggggtg ttgcattttt acatttccct
960
aatgatcttg ctaataaatg ctacaatagc atcagcttca ttttgggttt ttgcctcctc
1020

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ccactgtgtg tatgtgtgta tatgtatgtt ttgaatatgt tttctttatt aaaaaatatt
 1080
 ttttgtagtt tgaatatgaa atttggaacca aatgataaac tgcgctgagt ctaaactggc
 1140
 aacatgtatt tttttctctg atattaagca ggaaggcatt ttaatgtggg gacatcagat
 1200
 gttatttttc ctagatgaaa ataaaagtca agcagtgatt agtttccactc actgtcctag
 1260
 ctacacttaa tttgaagatt aaaattctac attgtggaaa acaattgaat tttattgggaa
 1320
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 1380
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 1385

<210> 4098

<211> 258

<212> PRT

<213> Homo sapiens

<400> 4098

Ser Gly Ala Arg Ser Pro Glu Pro Arg Ala Gly Gln Pro Pro Gly Glu
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 20 25 30
 Arg Ala Arg Leu His Asp Ser Leu Arg Ala Val Leu Thr Cys Ser Thr
 35 40 45
 Met Ser Ala Lys Ser Ala Ile Ser Lys Glu Ile Phe Ala Pro Leu Asp
 50 55 60
 Glu Arg Met Leu Gly Ala Val Gln Val Lys Arg Thr Lys Lys Lys
 65 70 75 80
 Ile Pro Phe Leu Ala Thr Gly Gly Gln Gly Glu Tyr Leu Thr Tyr Ile
 85 90 95
 Cys Leu Ser Val Thr Asn Lys Lys Pro Thr Gln Ala Ser Ile Thr Lys
 100 105 110
 Val Lys Gln Phe Glu Gly Ser Thr Ser Phe Val Arg Arg Ser Gln Trp
 115 120 125
 Met Leu Glu Gln Leu Arg Gln Val Asn Gly Ile Asp Pro Asn Gly Asp
 130 135 140
 Ser Ala Glu Phe Asp Leu Leu Phe Glu Asn Ala Phe Asp Gln Trp Val
 145 150 155 160
 Ala Ser Thr Ala Ser Glu Lys Cys Thr Phe Phe Gln Ile Leu His His
 165 170 175
 Thr Cys Gln Arg Tyr Leu Thr Asp Arg Lys Pro Glu Phe Ile Asn Cys
 180 185 190
 Gln Ser Lys Ile Met Gly Gly Asn Ser Ile Leu His Ser Ala Ala Asp
 195 200 205
 Ser Val Thr Ser Ala Val Gln Lys Ala Ser Gln Ala Leu Asn Glu Arg
 210 215 220
 Gly Glu Arg Leu Gly Arg Ala Glu Glu Lys Thr Glu Asp Leu Lys Asn
 225 230 235 240
 Ser Ala Gln Gln Phe Ala Glu Thr Ala His Lys Leu Ala Met Lys His
 245 250 255
 Lys Cys

<210> 4099
 <211> 511
 <212> DNA
 <213> Homo sapiens

<400> 4099
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 attagggaaa ggttttctgt gaaattacct tctgattgta gccacatgaa acacatcaac
 120
 ttaacaata aaaaattgta taatggaatt ggatcagggg gttcccaaaa ccccttcac
 180
 tgaggtttgg caattcactg agaaggactc acaggactca gcagatagtc atactggggg
 240
 ctttgattta ttacatttaa tacagcaaaa agacacaaag caacatttga gaaaggaaaa
 300
 ggtgcatgtg tcaagtctg gaggaagcca ggcacaagct acaggagtca tctcctgtgt
 360
 agctagcagg atatgcttaa ttccccagc ctcaaatttt gacgacacat gtgcaatgtt
 420
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 480
 acataggcaa cctctctctt cctcacgcy t
 511

<210> 4100
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 4100
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 1 5 10 15
 Gln Phe Thr Glu Lys Asp Ser Gln Asp Ser Ala Asp Ser His Thr Trp
 20 25 30
 Gly Phe Asp Leu Leu His Leu Ile Gln Lys Asp Thr Lys Gln His
 35 40 45
 Leu Arg Lys Glu Lys Val His Val Ser Lys Ser Gly Gly Ser Gln Ala
 50 55 60
 Gln Ala Thr Gly Val Ile Ser Cys Val Ala Ser Arg Ile Cys Leu Ile
 65 70 75 80
 Pro Pro Ala Ser Asn Phe Asp Asp Thr Cys Ala Met Leu Ser Thr Leu
 85 90 95
 Pro Glu Phe His
 100

<210> 4101
 <211> 536
 <212> DNA
 <213> Homo sapiens

<400> 4101

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tttttttttt tttttttttt tttttttttt tttttgagga accccagaaa tgtgtttatt
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aagttggact cgtattgctg tgtgggggtcc cagtgcacgc gtgtgcaccc gctacaagat
120
ccaggaaaga tggcacacgg cagacgacga caggaaggac acctgtctccc cacccttccc
180
gggacccccg catgtgcaaa attcagctg gggctctgcag ctgcttgagg agaccaggg
240
cctcttgctc cacagcctgc aaggtctgag caggcaacgg ccttggggcg gtgaggcccc
300
cgcttggtca ctccccgcgc ccccatgca ggcagtggag gggaggacac gcaggaggac
360
cagacgctaa aggtgtaaac gggcagccgt ggcactcctc acctctcaat aaataagata
420
ataactaaa taaataaaca actaataaaa gacatgaagg aatggatgca gagcgtgaa
480
cggatggcgc aggacgtccc tgggtggggc cacggtcccc ttaaggcatg tgggag
536

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<210> 4102
 <211> 106
 <212> PRT
 <213> Homo sapiens

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<400> 4102
Met Cys Leu Leu Ser Trp Thr Arg Ile Ala Val Trp Gly Pro Ser Ala
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Arg Val Cys Thr Arg Tyr Lys Ile Gln Glu Arg Trp His Thr Ala Asp
20          25          30
Asp Asp Arg Lys Asp Thr Cys Ser Pro Pro Phe Pro Gly Pro Arg His
35          40          45
Val Gln Asn Ser Ser Trp Gly Leu Gln Leu Leu Gly Thr Gln Gly
50          55          60
Leu Leu Leu His Ser Leu Gln Gly Leu Ser Arg Gln Arg Pro Trp Gly
65          70          75          80
Gly Glu Ala Pro Ala Trp Ser Leu Pro Ala Pro Pro Met Gln Ala Val
85          90          95
Glu Gly Arg Thr Arg Arg Arg Thr Arg Arg
100          105

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<210> 4103
 <211> 3040
 <212> DNA
 <213> Homo sapiens

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<400> 4103
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120
gaggaggaag gcggtgacga gtctgacctg agttcggaat ccagcattaa gaagaaatct
180
caagaggaaa ggaagaccg acagtccttg gataagccag ccaggaaaag gaggcggaga
240

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agtagaaaaga agcccagcgg tgccctcggg tctgagtcgt ataagtcac tgacggaagc
 300
 gctgagcaga cggcaccagg agacagcaca gggtagatgg aagtttctct ggactccctg
 360
 gatctccgag tcaaaggaat tctgtcttca caagcagaag ggttgcccaa cggccagat
 420
 gtgtcggaga cagacggcct ccaggaaagt cctctctgca gctgccggat ggaacacccg
 480
 aagagtcgag agatcaccac actggccaac aacagtgca tggctacaga gagcgtggac
 540
 catgaattgg gccggtgcac aaacagcgtg gtcaagtatg agctgatgag cccctccaac
 600
 aaggccccgc tctcgtgct gtgtgaagac caccggggcc gcatgggtgaa gcaccagtg
 660
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 720
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 780
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 840
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 1020
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 1080
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 1140
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 1680
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 1860
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 1980
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 2160
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 2220
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 2280
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 2340
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 2580
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 2640
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 2700
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 2760
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 2880
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 2940
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<210> 4104

<211> 978

<212> PRT

<213> Homo sapiens

<400> 4104

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Ser	Glu	Ala	Asp	Arg	Ala	Gln	Lys	Met	Asp	Gly	Glu	Ser	Glu	Glu	Glu
			20					25					30		
Gln	Glu	Ser	Val	Asp	Thr	Gly	Glu	Glu	Glu	Gly	Gly	Asp	Glu	Ser	
			35				40				45				
Asp	Leu	Ser	Ser	Glu	Ser	Ser	Ile	Lys	Lys	Lys	Ser	Gln	Glu	Glu	Arg
	50					55				60					
Lys	Asp	Arg	Gln	Ser	Leu	Asp	Lys	Pro	Ala	Arg	Lys	Arg	Arg	Arg	Arg

```

65          70          75          80
Ser Arg Lys Lys Pro Ser Gly Ala Leu Gly Ser Glu Ser Tyr Lys Ser
      85          90          95
Ser Ala Gly Ser Ala Glu Gln Thr Ala Pro Gly Asp Ser Thr Gly Tyr
      100          105          110
Met Glu Val Ser Leu Asp Ser Leu Asp Leu Arg Val Lys Gly Ile Leu
      115          120          125
Ser Ser Gln Ala Glu Gly Leu Ala Asn Gly Pro Asp Val Leu Glu Thr
      130          135          140
Asp Gly Leu Gln Glu Val Pro Leu Cys Ser Cys Arg Met Glu Thr Pro
      145          150          155          160
Lys Ser Arg Glu Ile Thr Thr Leu Ala Asn Asn Gln Cys Met Ala Thr
      165          170          175
Glu Ser Val Asp His Glu Leu Gly Arg Cys Thr Asn Ser Val Val Lys
      180          185          190
Tyr Glu Leu Met Arg Pro Ser Asn Lys Ala Pro Leu Leu Val Leu Cys
      195          200          205
Glu Asp His Arg Gly Arg Met Val Lys His Gln Cys Cys Pro Gly Cys
      210          215          220
Gly Tyr Phe Cys Thr Ala Gly Asn Phe Met Glu Cys Gln Pro Glu Ser
      225          230          235          240
Ser Ile Ser His Arg Phe His Lys Asp Cys Ala Ser Arg Val Asn Asn
      245          250          255
Ala Ser Tyr Cys Pro His Cys Gly Glu Glu Ser Ser Lys Ala Lys Glu
      260          265          270
Val Thr Ile Ala Lys Ala Asp Thr Thr Ser Thr Val Thr Pro Val Pro
      275          280          285
Gly Gln Glu Lys Gly Ser Ala Xaa Gly Gly Arg Ala Asp Thr Thr Thr
      290          295          300
Gly Ser Ala Xaa Pro Gly His His Ser Arg Arg Thr Thr Ser Cys Arg
      305          310          315          320
Val Gln Pro Pro Thr Xaa Pro Glu Gly Phe Asp Pro Thr Gly Pro Ala
      325          330          335
Gly Leu Gly Arg Pro Thr Pro Gly Leu Ser Gln Gly Pro Gly Lys Glu
      340          345          350
Thr Leu Glu Ser Ala Leu Ile Ala Leu Asp Ser Glu Lys Pro Lys Lys
      355          360          365          370
Leu Arg Phe His Pro Lys Gln Leu Tyr Phe Ser Ala Arg Gln Gly Glu
      375          380          385
Leu Gln Lys Val Leu Leu Met Leu Val Asp Gly Ile Asp Pro Asn Phe
      390          395          400
Lys Met Glu His Gln Asn Lys Arg Ser Pro Leu His Ala Ala Ala Glu
      405          410          415
Ala Gly His Val Asp Ile Cys His Met Leu Val Gln Ala Gly Ala Asn
      420          425          430
Ile Asp Thr Cys Ser Glu Asp Gln Arg Thr Pro Leu Met Glu Ala Ala
      435          440          445
Glu Asn Asn His Leu Glu Ala Val Lys Tyr Leu Ile Lys Ala Gly Ala
      450          455          460
Leu Val Asp Pro Lys Asp Ala Glu Gly Ser Thr Cys Leu His Leu Ala
      465          470          475          480
Ala Lys Lys Gly His Tyr Glu Val Val Gln Tyr Leu Leu Ser Asn Gly
      485          490          495
Arg Met Asp Val Asn Cys Gln Asp Asp Gly Gly Trp Thr Pro Met Ile

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500										505					510				
Trp	Ala	Thr	Glu	Tyr	Lys	His	Val	Asp	Leu	Val	Lys	Leu	Leu	Leu	Ser				
515										520					525				
Lys	Gly	Ser	Asp	Ile	Asn	Ile	Arg	Asp	Asn	Glu	Glu	Asn	Ile	Cys	Leu				
530										535					540				
His	Trp	Ala	Ala	Phe	Ser	Gly	Cys	Val	Asp	Ile	Ala	Glu	Ile	Leu	Leu				
545										555					560				
Ala	Ala	Lys	Cys	Asp	Leu	His	Ala	Val	Asn	Ile	His	Gly	Asp	Ser	Pro				
565										570					575				
Leu	His	Ile	Ala	Ala	Arg	Glu	Asn	Arg	Tyr	Asp	Cys	Val	Val	Leu	Ph				
580										585					590				
Leu	Ser	Arg	Asp	Ser	Asp	Val	Thr	Leu	Lys	Asn	Lys	Glu	Gly	Glu	Thr				
595										600					605				
Pro	Leu	Gln	Cys	Ala	Ser	Leu	Asn	Ser	Gln	Val	Trp	Ser	Ala	Leu	Gln				
610										615					620				
Met	Ser	Lys	Ala	Leu	Gln	Asp	Ser	Ala	Pro	Asp	Arg	Pro	Ser	Pro	Val				
625										630					635				
Glu	Arg	Ile	Val	Ser	Arg	Asp	Ile	Ala	Arg	Gly	Tyr	Glu	Arg	Ile	Pro				
645										650					655				
Ile	Pro	Cys	Val	Asn	Ala	Val	Asp	Ser	Glu	Pro	Cys	Pro	Ser	Asn	Tyr				
660										665					670				
Lys	Tyr	Val	Ser	Gln	Asn	Cys	Val	Thr	Ser	Pro	Met	Asn	Ile	Asp	Arg				
675										680					685				
Asn	Ile	Thr	His	Leu	Gln	Tyr	Cys	Val	Cys	Ile	Asp	Asp	Cys	Ser	Ser				
690										695					700				
Ser	Asn	Cys	Met	Cys	Gly	Gln	Leu	Ser	Met	Arg	Cys	Trp	Tyr	Asp	Lys	</			

[illegible]

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<210> 4105
<211> 775
<212> DNA
<213> Homo sapiens
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120
ctgatcgacg gcggggagca ttactgggag gtgcgctacg agccggacag caagcgcttc
180
gcgctggggc tggcctaccg cagcctgggc cgcttcgagc aactgggcaa gacggccgccc
240
tcctggtgccc tgcaactaac aattggctgc aggtcagctt cacggaagca cgccaacaag
300
gtcaagggtgc tggacgcccc cgtgcccagc tgccctgggtg tgcactgtga cttccaccaa
360
ggcctcctgt ccttctacaa tgccccgacc aaacaagtgc tgcacacttt caagaccagg
420
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480
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540
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660
gccttaactc cagatggggg gggtcaccaag agggagtggtg caccctggcg ggccctctcc
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775

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<210> 4106
<211> 186
<212> PRT
<213> Homo sapiens
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>400> 4106
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Lys Arg Met Pro Ser Gly Arg Gly Gly Arg Asp Arg Phe Thr Ala Glu
20 25 30
Ser Tyr Thr Val Leu Gly Asp Thr Leu Ile Asp Gly Gly Glu His Tyr
35 40 45
Trp Glu Val Arg Tyr Glu Pro Asp Ser Lys Ala Phe Gly Val Gly Val

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50	55	60
Ala Tyr Arg Ser Leu Gly	Arg Phe Glu Gln Leu Gly	Lys Thr Ala Ala
65	70	75
Ser Trp Cys Leu His Ser	Thr Ile Gly Cys Arg	Ser Ala Ser Arg Lys
85	90	95
His Ala Asn Lys Val Lys	Val Leu Asp Ala Pro	Val Pro Asp Cys Leu
100	105	110
Gly Val His Cys Asp Phe	His Gln Gly Leu Leu	Ser Phe Tyr Asn Ala
115	120	125
Arg Thr Lys Gln Val Leu	His Thr Phe Lys Thr	Arg Phe Thr Gln Pro
130	135	140
Leu Leu Pro Ala Phe Thr	Val Trp Cys Gly Ser	Phe Gln Val Thr Thr
145	150	155
Gly Leu Gln Val Pro Ser	Ala Val Arg Cys Leu	Gln Lys Arg Gly Ser
165	170	175
Ala Thr Ser Ser Ser Asn	Thr Ser Leu Thr	
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<210> 4107

<211> 1442

<212> DNA

<213> Homo sapiens

<400> 4107

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 120
 cgcgtcactg tcgggtcggc gagccacggg ggcgcgcga gcacatggc gaccaccgtc
 180
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 240
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 360
 aattacggca tgaccgcgat ggaccctac tgccgactgc gcctgggcta cgcggtgtac
 420
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 480
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 720
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<210> 4108

<211> 273

<212> PRT

<213> Homo sapiens

<400> 4108

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Leu	Pro	Gln	Asp	Phe	Leu	Arg	Ile	Thr	Pro	Thr	Gln	Gln	Gln	Arg	Gln
			20					25					30		
Val	Gln	Leu	Asp	Ala	Gln	Ala	Pro	Ser	Ser	Cys	Ser	Thr	Glu	Ala	Gln
			35				40					45			
Gly	Thr	Val	Gly	Arg	Leu	Asn	Ile	Thr	Val	Val	Gln	Ala	Lys	Leu	Ala
			50			55					60				
Lys	Asn	Tyr	Gly	Met	Thr	Arg	Met	Asp	Pro	Tyr	Cys	Arg	Leu	Arg	Leu
65					70					75				80	
Gly	Tyr	Ala	Val	Tyr	Glu	Thr	Pro	Thr	Ala	His	Asn	Gly	Ala	Lys	Asn
			85						90					95	
Pro	Arg	Trp	Asn	Lys	Val	Ile	His	Cys	Thr	Val	Pro	Pro	Gly	Val	Asp
			100					105					110		
Ser	Phe	Tyr	Leu	Glu	Ile	Phe	Asp	Glu	Arg	Ala	Phe	Ser	Met	Asp	Asp
			115				120						125		
Arg	Ile	Ala	Trp	Thr	His	Ile	Thr	Ile	Pro	Glu	Ser	Leu	Arg	Gln	Gly
			130			135				140					
Lys	Val	Glu	Asp	Lys	Trp	Tyr	Ser	Leu	Ser	Gly	Arg	Gln	Gly	Asp	Asp
145					150					155				160	
Lys	Glu	Gly	Met	Ile	Asn	Leu	Val	Met	Ser	Tyr	Ala	Leu	Leu	Pro	Ala
				165						170				175	
Ala	Met	Val	Met	Pro	Pro	Gln	Pro	Val	Val	Leu	Met	Pro	Thr	Val	Tyr
			180					185					190		
Gln	Gln	Gly	Val	Gly	Tyr	Val	Pro	Ile	Thr	Gly	Met	Pro	Ala	Val	Cys
			195				200					205			
Ser	Pro	Gly	Met	Val	Pro	Val	Ala	Leu	Pro	Pro	Ala	Ala	Val	Asn	Ala

210		215		220
Gln Pro Arg Cys Ser Glu Glu Asp Leu Lys Ala Ile Gln Asp Met Phe				
225		230		235
Pro Asn Met Asp Gln Glu Val Ile Arg Ser Val Leu Glu Ala Gln Arg				
	245		250	255
Gly Asn Lys Asp Ala Ala Ile Asn Ser Leu Leu Gln Met Gly Glu Glu				
	260	265		270
Pro				

<210> 4109

<211> 1637

<212> DNA

<213> Homo sapiens

<400> 4109

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 180
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 240
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 300
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 360
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 480
 gagctccacg ggaacatgta cattgaagtc tgtacctcct gcgttcccaa cagggagtac
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 720
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 1020
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 1080
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tgaagaacag ttggcacttt gcagatggcc agtgtcacgg tgaaggctgg gttgccccca
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 1620
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 1637

<210> 4110

<211> 375

<212> PRT

<213> Homo sapiens

<400> 4110

Ala	Ala	Leu	Lys	Leu	His	Gly	Lys	Cys	Asp	Asp	Val	Met	Arg	Leu	Leu
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Met	Ala	Glu	Leu	Gly	Leu	Glu	Ile	Pro	Ala	Tyr	Ser	Arg	Trp	Gln	Asp
		20						25					30		
Pro	Ile	Phe	Ser	Leu	Ala	Thr	Pro	Leu	Arg	Ala	Gly	Glu	Glu	Gly	Ser
		35					40						45		
His	Ser	Arg	Lys	Ser	Leu	Cys	Arg	Ser	Arg	Glu	Glu	Leu	Arg	Gly	Lys
	50					55				60					
Val	Arg	Glu	Leu	Ala	Ser	Ala	Val	Arg	Asn	Ala	Lys	Tyr	Leu	Val	Val
	65				70				75					80	
Tyr	Thr	Gly	Ala	Gly	Ile	Ser	Thr	Ala	Ala	Ser	Ile	Pro	Asp	Tyr	Arg
			85						90					95	
Gly	Pro	Asn	Gly	Val	Trp	Thr	Leu	Leu	Gln	Lys	Gly	Arg	Ser	Val	Ser
			100						105					110	
Ala	Ala	Asp	Leu	Ser	Glu	Ala	Glu	Pro	Thr	Leu	Thr	His	Met	Ser	Ile
		115					120						125		
Thr	Arg	Leu	His	Glu	Gln	Lys	Leu	Val	Gln	His	Val	Val	Ser	Gln	Asn
		130				135					140				
Cys	Asp	Gly	Leu	His	Leu	Arg	Ser	Gly	Leu	Pro	Arg	Thr	Ala	Ile	Ser
	145				150				155					160	
Glu	Leu	His	Gly	Asn	Met	Tyr	Ile	Glu	Val	Cys	Thr	Ser	Cys	Val	Pro
			165						170					175	
Asn	Arg	Glu	Tyr	Val	Arg	Val	Phe	Asp	Val	Thr	Glu	Arg	Thr	Ala	Leu
		180					185						190		
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Arg	Asp	Thr	Ile	Val	His	Phe	Gly	Glu	Arg	Gly	Thr	Leu	Gly	Gln	Pro
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Trp	Cys	Met	Thr	Lys	Pro	Pro
		260		265		270
Leu	Gln	Trp	Thr	Pro	Lys	Asp
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Lys	Cys	Asp	Asp	Val	Met	Arg
		290		295		300
Ile	Pro	Ala	Tyr	Ser	Arg	Trp
		305		310		315
Pro	Leu	Arg	Ala	Gly	Glu	Gly
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<210> 4111

<211> 2599

<212> DNA

<213> Homo sapiens

<400> 4111

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asp Lys Ala Thr Gly Ile Leu Leu Tyr Gly Leu Ala Ser Arg Leu Arg
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 Asp Thr Arg Arg Leu Ser Phe Leu Val Ser Tyr Ile Ala Ser Lys Lys
 65 70 75 80
 Ile His Thr Glu Pro Gln Leu Ser Ala Ala Leu Glu Tyr Val Arg Ser
 85 90 95
 His Pro Leu Asp Pro Ile Asp Thr Val Asp Phe Glu Arg Glu Cys Gly
 100 105 110
 Val Gly Val Ile Val Thr Pro Glu Gln Ile Glu Glu Ala Val Glu Ala
 115 120 125
 Ala Ile Asn Arg His Arg Pro Gln Leu Leu Val Glu Arg Tyr His Phe
 130 135 140
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 145 150 155 160
 Asp Gly Lys Met Ile Lys Asn Glu Val Asp Met Gln Val Leu His Leu
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 180 185 190
 Lys Ala Arg Leu Glu Glu Thr Asp Arg Arg Thr Ala Lys Asp Val Val
 195 200 205
 Glu Asn Gly Glu Thr Ala Asp Gln Thr Leu Ser Leu Met Glu Gln Leu
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 Arg Gly Glu Ala Leu Lys Phe His Lys Pro Gly Glu Asn Tyr Lys Thr
 225 230 235 240
 Pro Gly Tyr Val Val Thr Pro His Thr Met Asn Leu Leu Lys Gln His
 245 250 255
 Leu Glu Ile Thr Gly Gly Gln Val Arg Thr Arg Phe Pro Pro Glu Pro
 260 265 270
 Asn Gly Ile Leu His Ile Gly His Ala Lys Ala Ile Asn Phe Asn Phe
 275 280 285
 Gly Tyr Ala Lys Ala Asn Asn Gly Ile Cys Phe Leu Arg Phe Asp Asp
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 Thr Asn Pro Glu Lys Glu Glu Ala Lys Phe Phe Thr Ala Ile Cys Asp
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<210> 4113
<211> 1894
<212> DNA
<213> Homo sapiens

<400> 4113
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1320

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<210> 4114

<211> 389

<212> PRT

<213> Homo sapiens

<400> 4114

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			20					25					30		
Lys	Ala	Leu	Cys	Thr	Ala	His	Glu	Lys	Phe	Cys	Phe	Trp	Pro	Asp	Ser
	35						40					45			
Pro	Ser	Pro	Asp	Arg	Phe	Gly	Met	Leu	Pro	Leu	Asp	Glu	Pro	Ala	Ile
	50					55				60					
Leu	Val	Ser	Glu	Phe	Leu	Asp	Arg	Phe	Gln	Ser	Leu	Cys	His	Leu	Asp
65					70				75					80	
Leu	Gln	Leu	Pro	Ser	Leu	Arg	Pro	Glu	Asp	Leu	Lys	Thr	Met	Cys	Leu
			85					90					95		
Thr	Glu	Asp	Lys	Ile	Ser	Leu	Leu	His	Leu	Leu	Glu	Asp	Glu	Leu	
			100					105				110			
Asp	His	Arg	Thr	Asp	Glu	Arg	Lys	Thr	Thr	Ile	Lys	Leu	Gly	Ser	Asp
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	130					135					140				
Cys	Ser	Ser	Ser	Leu	Glu	Ser	Met	Gln	Leu	Ser	Leu	Ile	Ala	Cys	Ser
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Gln	Cys	Met	Arg	Lys	Val	Gly	Leu	Trp	Gly	Phe	Gln	Gln	Ile	Glu	Ser
			165					170					175		
Ser	Met	Thr	Asp	Leu	Asp	Ala	Ser	Phe	Gly	Leu	Thr	Ser	Ser	Pro	Ile
	180					185						190			
Pro	Gly	Leu	Glu	Gly	Arg	Pro	Glu	Arg	Leu	Pro	Leu	Val	Pro	Glu	Ser
	195					200					205				
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      245              250              255
Ser Pro Thr Thr Arg Thr Arg Pro Val Thr Arg Ser Met Gly Thr Gly
      260              265              270
Asp Thr Pro Gly Leu Glu Val Pro Ser Ser Xaa Ser Ala Glu Ser Gln
      275              280              285
Ala Ser Ser Leu Cys Ser Ser Ser Ser Asp Thr Ser Ser Arg Ser
      290              295              300
Phe Phe Asp Pro Thr Ser Gln His Arg Asp Trp Cys Pro Trp Val Asn
305              310              315              320
Ile Thr Leu Gly Lys Glu Ser Arg Glu Asn Gly Gly Thr Glu Pro Asp
      325              330              335
Ala Ser Ala Pro Ala Glu Pro Gly Trp Lys Ala Val Leu Thr Ile Leu
      340              345              350
Leu Ala His Lys Gln Ser Ser Gln Pro Ala Glu Thr Asp Ser Met Ser
      355              360              365
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<210> 4115

<211> 1056

<212> DNA

<213> Homo sapiens

<400> 4115

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<211> 151

<212> PRT

<213> Homo sapiens

<400> 4116

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			20					25					30		
Asn	His	Ser	Asp	Ser	Leu	Ser	Arg	Ser	Asp	Arg	Ile	Asp	Ala	Val	Thr
	35						40					45			
Pro	Thr	Leu	Gly	Ser	Ser	Asn	Asn	Gln	Leu	Asn	Ser	Ser	Leu	Leu	Gln
	50					55				60					
Val	Tyr	Ile	Pro	Asp	Tyr	Ser	Val	Arg	Ala	Leu	Ser	Asp	Leu	Gln	Phe
65					70				75					80	
Val	Lys	Ile	Ser	Arg	Gln	Gln	Tyr	Gln	Asn	Ala	Leu	Met	Ala	Ser	Arg
			85					90					95		
Met	Asp	Lys	Thr	Pro	Gln	Ser	Ser	Asp	Ser	Glu	Asn	Thr	Lys	Ile	Glu
			100					105					110		
Leu	Thr	Leu	Thr	Glu	Leu	His	Asp	Gly	Leu	Pro	Asp	Glu	Thr	Ala	Asn
		115					120					125			
Leu	Leu	Asn	Glu	Gln	Asn	Cys	Val	Thr	His	Ser	Lys	Ala	Asn	His	Ser
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<210> 4117

<211> 973

<212> DNA

<213> Homo sapiens

<400> 4117

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<210> 4118
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Arg Cys Val Gly Cys Pro Arg Pro Ala Arg Pro Ala Ser Pro Ser Pro
 50 55 60
 Gly Glu Ala Thr Pro Pro Pro Ser Ser Gly Ile Ser Ala Val Lys Pro
 65 70 75 80
 Pro Leu Arg Ser Pro Arg Thr Leu Pro Leu Glu Leu Gly Thr Gly Gly
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 Cys Val Cys Ala Gly Leu Gly Pro Asn Thr Pro Gly Cys Gln Leu His
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<210> 4119
 <211> 649
 <212> DNA
 <213> Homo sapiens

<400> 4119
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<210> 4120
 <211> 100
 <212> PRT
 <213> Homo sapiens

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 Cys Ile Leu Val Ser Ile Val Thr Glu Phe Val Ser Asn Pro Ala Thr
 35 40 45
 Ile Thr Ile Phe Leu Pro Ile Leu Cys Ser Leu Val Ser Asn Ala Glu
 50 55 60
 Leu Pro Asp Ile Gln Thr Gly Cys Pro Arg Gly Leu Glu Trp Gln Ala
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<210> 4121
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 <212> DNA
 <213> Homo sapiens

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<211> 494

<212> PRT

<213> Homo sapiens

<400> 4122

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          450          455          460
Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu Glu Cys Glu Thr Leu
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<211> 1095

<212> DNA

<213> Homo sapiens

<400> 4123

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<211> 155

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<212> PRT

<213> Homo sapiens

<400> 4126

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Cys	Glu	Glu	Asp	Gly	Ser	Gln	Ser	Ser	Ser	Glu	Ser	Lys	Met	Val	Ile
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<210> 4128

<211> 445

<212> PRT

<213> Homo sapiens

<400> 4128

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 35 40 45
 Glu Asn Pro Cys Leu Thr Phe Ile Ile Ser Ser Ile Leu Glu Ser Asp

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Gly	Asn	Ala	Val	Thr	Asn	Ala	Thr	Trp	Glu	Glu	Met	Trp	Leu	Ser	Glu
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					100			105					110		
Ala	Ala	Phe	Thr	Cys	Leu	Glu	Thr	Ala	Phe	Arg	Leu	Asp	Ala	Leu	His
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Arg	Gln	Met	Lys	Leu	Leu	Gly	Glu	Asp	Ser	Pro	Val	Ser	Lys	Leu	Gln
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Val	Lys	Leu	Glu	Pro	Gly	Val	Asn	Pro	Ser	His	Leu	Met	Asn	Leu	Phe
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Thr	Tyr	Glu	Lys	Gly	Tyr	Cys	Phe	Val	Tyr	Tyr	Leu	Ser	Gln	Leu	Cys
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Gly	Asp	Pro	Gln	Arg	Phe	Asp	Asp	Phe	Leu	Arg	Ala	Tyr	Val	Glu	Lys
					180			185					190		
Tyr	Lys	Phe	Thr	Ser	Val	Val	Ala	Gln	Asp	Leu	Leu	Asp	Ser	Phe	Leu
					195			200				205			
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Pro	Asp	Leu	Ser	Gln	Gly	Ser	Ser	Leu	Thr	Arg	Pro	Val	Glu	Ala	Leu
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Leu	Asp	Arg	Leu	Leu	Asp	Gly	Ser	Pro	Leu	Pro	Gln	Glu	Val	Val	Met
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Ser	Leu	Ser	Lys	Cys	Tyr	Ser	Ser	Leu	Leu	Asp	Ser	Met	Asn	Ala	Glu
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Ile	Arg	Ile	Arg	Trp	Leu	Gln	Ile	Val	Val	Arg	Asn	Asp	Tyr	Tyr	Pro
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Asp	Leu	His	Arg	Val	Arg	Arg	Phe	Leu	Glu	Ser	Gln	Met	Ser	Arg	Met
					340			345				350			
Tyr	Thr	Ile	Pro	Leu	Tyr	Glu	Asp	Leu	Cys	Thr	Gly	Ala	Leu	Lys	Ser
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<210> 4129

<211> 1749

<212> DNA

<213> Homo sapiens

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<211> 523

<212> PRT

<213> Homo sapiens

<400> 4130

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			20					25				30			
Val	Val	Asp	Gln	Gly	Ala	Gly	Ala	Ser	Arg	Gly	Gly	Asn	Thr	Arg	Lys
		35					40					45			
Ser	Leu	Glu	Asp	Asn	Gly	Ser	Thr	Arg	Val	Thr	Pro	Ser	Val	Gln	Pro
	50				55					60					
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Ser	Phe	Pro	Ser	Thr	Ala	Asn	Glu	Glu	Asn	Phe	Arg	Ser	Asn	Leu	Arg
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Glu	Val	Ala	Gln	Met	Leu	Lys	Ser	Lys	His	Gly	Gly	Asn	Tyr	Leu	Leu
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Phe	Asn	Leu	Ser	Glu	Arg	Arg	Pro	Asp	Ile	Thr	Lys	Leu	His	Ala	Lys
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145				150					155					160	
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			165					170						175	
His	Asn	Val	Val	Leu	His	Asn	Lys	Gly	Asn	Arg	Gly	Arg	Ile	Gly	
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225				230					235					240	
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			245					250					255		
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	260					265						270			
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	275					280					285				
Thr	Ser	Gly	Ile	Tyr	Asn	Ile	Pro	Gly	Asp	Ser	Gln	Thr	Ser	Val	Cys
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Cys Tyr His Lys Lys Phe Arg Ser Pro Ala Arg Asp Val Ile Phe Arg
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          340          345          350
Lys Glu Asp Leu Asp Asp Ala Phe Lys Asp Asp Arg Phe Pro Glu Tyr
          355          360          365
Gly Lys Val Glu Phe Val Phe Ser Tyr Gly Pro Glu Lys Ile Gln Gly
          370          375          380
Met Glu His Leu Glu Asn Gly Pro Ser Val Ser Val Asp Tyr Asn Thr
385          390          395          400
Ser Asp Pro Leu Ile Arg Trp Asp Ser Tyr Asp Asn Phe Ser Gly His
          405          410          415
Arg Asp Asp Gly Met Glu Glu Val Val Gly His Thr Gln Gly Pro Leu
          420          425          430
Asp Gly Ser Leu Tyr Ala Lys Val Lys Lys Lys Asp Ser Leu His Gly
          435          440          445
Ser Thr Gly Ala Val Asn Ala Thr Arg Pro Thr Leu Ser Ala Thr Pro
          450          455          460
Asn His Val Glu His Thr Leu Ser Val Ser Ser Asp Ser Gly Asn Ser
465          470          475          480
Thr Ala Ser Thr Lys Thr Asp Lys Thr Asp Glu Pro Val Pro Gly Ala
          485          490          495
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<211> 608
<212> DNA
<213> Homo sapiens

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240
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300
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360
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480
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cgcacagc
608

<210> 4132
<211> 194
<212> PRT
<213> Homo sapiens

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35 40 45
Glu Leu Asp Ser Asp Ser Glu Asp Leu Asp Pro Asn Pro Glu Asp Leu
50 55 60
Asp Pro Val Ser Glu Asp Pro Glu Pro Asp Pro Glu Asp Leu Asn Thr
65 70 75 80
Val Pro Glu Asp Val Asp Pro Ser Tyr Glu Asp Leu Glu Pro Val Ser
85 90 95
Glu Asp Leu Asp Pro Asp Ala Glu Ala Pro Gly Ser Glu Pro Gln Asp
100 105 110
Pro Asp Pro Met Ser Ser Ser Phe Asp Leu Asp Pro Asp Val Ile Gly
115 120 125
Pro Val Pro Leu Ile Leu Asp Pro Asn Ser Asp Thr Leu Ser Pro Gly
130 135 140
Asp Pro Lys Val Asp Pro Xaa Ser Pro Leu Ala Ser Leu Arg Ala Pro
145 150 155 160
Arg Ser Trp Pro Pro Ala Pro Arg Cys Ser Pro Pro Pro Ala Arg
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Pro Gly Pro Ser Pro Ala Arg Ile Ala Ala Lys Pro Ser Ala Ala
180 185 190
Pro Gly

<210> 4133
<211> 1646
<212> DNA
<213> Homo sapiens

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<210> 4134

<211> 329

<212> PRT

<213> Homo sapiens

<400> 4134

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<210> 4135

<211> 388

<212> DNA

<213> Homo sapiens

<400> 4135

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<210> 4136

<211> 123

<212> PRT

<213> Homo sapiens

<400> 4136

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		20					25					30			
Ser	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Leu	Thr	Thr	Gly	Arg	Ile	Ala	Glu
	35					40					45				
Leu	Leu	Ser	Pro	Asp	Tyr	Met	Asp	Leu	Glu	Asp	Pro	Arg	Pro	Ile	Phe
	50				55					60					
Asp	Trp	Met	Gln	Ile	Ile	Arg	Lys	Arg	Ala	Val	Val	Tyr	Val	Gly	Leu
65				70					75					80	
Asp	Ala	Leu	Ser	Asp	Thr	Glu	Val	Ala	Ala	Ala	Val	Gly	Asn	Ser	Met
		85						90					95		
Phe	Ser	Asp	Leu	Val	Ser	Val	Ala	Gly	His	Ile	Tyr	Lys	Phe	Gly	Ile
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<210> 4137

<211> 2255

<212> DNA

<213> Homo sapiens

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<210> 4138
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 4138

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Val	Trp	Lys	Asn	Asp	Tyr	Arg	Gln	Leu	Glu	Lys	Glu	Leu	Gln	Gly	Gln
			20					25					30		
Asn	Val	Glu	Ala	Val	Asp	Pro	Arg	Gly	Arg	Thr	Leu	Leu	His	Leu	Ala
			35				40					45			
Val	Ser	Leu	Gly	His	Leu	Glu	Ser	Ala	Arg	Val	Leu	Leu	Arg	His	Lys
	50					55				60					
Ala	Asp	Val	Thr	Lys	Glu	Asn	Arg	Gln	Gly	Trp	Thr	Val	Leu	His	Glu
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Ala	Val	Ser	Thr	Gly	Asp	Pro	Glu	Met	Val	Tyr	Thr	Val	Leu	Gln	His
				85					90					95	
Arg	Asp	Tyr	His	Asn	Thr	Ser	Met	Ala	Leu	Glu	Gly	Val	Pro	Glu	Leu
			100					105					110		
Leu	Gln	Lys	Ile	Leu	Glu	Ala	Pro	Asp	Phe	Tyr	Val	Gln	Met	Lys	Trp
		115					120					125			
Glu	Phe	Thr	Ser	Trp	Val	Pro	Leu	Val	Ser	Arg	Ile	Cys	Pro	Asn	Asp
	130					135					140				
Val	Cys	Arg	Ile	Trp	Lys	Ser	Gly	Ala	Lys	Leu	Arg	Val	Asp	Ile	Thr
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Leu	Leu	Gly	Phe	Glu	Asn	Met	Ser	Trp	Ile	Arg	Gly	Arg	Arg	Ser	Phe
			165					170						175	
Ile	Phe	Lys	Gly	Glu	Asp	Asn	Trp	Ala	Glu	Leu	Met	Glu	Val	Asn	His
			180					185					190		
Asp	Asp	Lys	Val	Val	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ser	Gln	Glu	Met
		195					200					205			
Glu	Arg	Leu	Thr	Leu	Asp	Leu	Met	Lys	Pro	Lys	Ser	Arg	Glu	Val	Glu
		210				215					220				
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225				230						235					240
Ile	Ala	Phe	Glu	Arg	Thr	Lys	Ser	Gly	Phe	Trp	Gly	Trp	Arg	Thr	Asp
			245					250					255		
Lys	Ala	Glu	Val	Val	Asn	Gly	Tyr	Glu	Ala	Lys	Val	Tyr	Thr	Val	Asn
		260						265					270		
Asn	Val	Asn	Val	Ile	Thr	Lys	Ile	Arg	Thr	Glu	His	Leu	Thr	Glu	Glu
		275					280					285			
Glu	Lys	Lys	Arg	Tyr	Lys	Ala	Asp	Arg	Asn	Pro	Leu	Glu	Ser	Leu	Leu
	290					295				300					
Gly	Thr	Val	Glu	His	Gln	Phe	Gly	Ala	Gln	Gly	Asp	Leu	Thr	Thr	Glu
305				310						315					320
Cys	Ala	Thr	Ala	Asn	Asn	Pro	Thr	Ala	Ile	Thr	Pro	Asp	Glu	Tyr	Phe
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<211> 431
<212> DNA
<213> Homo sapiens

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<210> 4140
<211> 50
<212> PRT
<213> Homo sapiens

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35 40 45
Val Pro
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<210> 4141
<211> 1182
<212> DNA
<213> Homo sapiens

<400> 4141
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120
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180

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 780
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 1080
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 1182

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<211> 311

<212> PRT

<213> Homo sapiens

<400> 4142

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		20						25				30			
Ser	Arg	Val	His	Ile	Tyr	His	His	Thr	Gly	Asn	Asn	Thr	Phe	Arg	Val
		35					40					45			
Val	Gly	Arg	Lys	Ile	Gln	Asp	His	Gln	Val	Val	Ile	Asn	Cys	Ala	Ile
		50				55					60				
Pro	Lys	Gly	Leu	Lys	Tyr	Asn	Gln	Ala	Thr	Gln	Thr	Phe	His	Gln	Trp
		65			70				75						80
Arg	Asp	Ala	Arg	Gln	Val	Tyr	Gly	Leu	Asn	Phe	Gly	Ser	Lys	Glu	Asp
			85						90				95		
Ala	Asn	Val	Phe	Ala	Ser	Ala	Met	Met	His	Ala	Leu	Glu	Val	Leu	Asn

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      115          120          125
Ala  Gln  Val  Gln  Asn  Gly  Pro  Ser  Gln  Glu  Glu  Leu  Glu  Ile  Gln  Arg
      130          135          140
Arg  Gln  Leu  Gln  Glu  Gln  Gln  Arg  Gln  Lys  Glu  Leu  Glu  Arg  Glu  Arg
145          150          155          160
Leu  Glu  Arg  Glu  Arg  Met  Glu  Arg  Glu  Arg  Leu  Glu  Arg  Glu  Arg  Leu
      165          170          175
Glu  Arg  Glu  Arg  Leu  Glu  Arg  Glu  Arg  Leu  Glu  Gln  Glu  Gln  Leu  Glu
      180          185          190
Arg  Glu  Arg  Gln  Glu  Arg  Glu  Arg  Gln  Glu  Arg  Leu  Glu  Arg  Gln  Glu
      195          200          205
Arg  Leu  Glu  Arg  Gln  Glu  Arg  Leu  Glu  Arg  Gln  Glu  Arg  Leu  Asp  Arg
      210          215          220
Glu  Arg  Glu  Arg  Gln  Glu  Arg  Glu  Arg  Leu  Glu  Arg  Leu  Glu  Arg  Glu
225          230          235          240
Arg  Gln  Glu  Arg  Glu  Arg  Gln  Glu  Gln  Leu  Glu  Arg  Glu  Gln  Leu  Glu
      245          250          255
Trp  Glu  Arg  Glu  Arg  Arg  Ile  Ser  Ser  Ala  Ala  Ala  Pro  Ala  Ser  Val
      260          265          270
Glu  Thr  Pro  Leu  Asn  Ser  Val  Leu  Gly  Asp  Ser  Ser  Ala  Ser  Glu  Pro
      275          280          285
Gly  Leu  Gln  Ala  Ala  Ser  Gln  Pro  Ala  Glu  Thr  Pro  Ser  Gln  Gln  Gly
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<210> 4143

<211> 1773

<212> DNA

<213> Homo sapiens

<400> 4143

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600

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<210> 4144

<211> 231

<212> PRT

<213> Homo sapiens

<400> 4144

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 20 25 30
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 35 40 45
 Ser Val Leu Tyr Leu His Arg Ser Leu Ala Asp Leu Gly Arg Leu Trp

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Gly Pro Leu Arg Gln Gly Leu Val Ala Ile Lys Glu Ala His Asp Ile
      85              90              95
Glu Thr Arg Leu Asn Glu Val Glu Lys Leu Leu Lys Thr Ile Ile Ser
100              105              110
Met Pro Cys Lys Tyr Ser Arg Ser Glu Val Val Leu Thr Phe Phe Glu
115              120              125
Arg Ser Pro Leu Asp Gln Val Leu Lys Asn Asp Asn Val His Lys Ile
130              135              140
Gln Pro Ser Phe Gln Ser Pro Val Lys Ile Ser Glu Ile Met Arg Ser
145              150              155              160
Asn Gly Phe Cys Leu Ala Asn Thr Glu Thr Ile Val Ile Asp His Ser
165              170              175
Ile Pro Asn Gly Arg Asp Gln Gln Leu Gly Val Asp Pro Thr Glu His
180              185              190
Leu Phe Glu Asn Gly Ser Glu Phe Pro Ser Glu Leu Glu Asp Gly Asp
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<211> 400

<212> DNA

<213> Homo sapiens

<400> 4145

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<210> 4146

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<212> PRT

<213> Homo sapiens

<400> 4146

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Leu	Asp	Leu	Arg	Leu	Ile	Arg	Thr	Lys	Gly	Gly	Val	Asp	Ala	Ala	Leu
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Glu	Tyr	Ala	Lys	Thr	Trp	Ser	Arg	Tyr	Ala	Lys	Glu	Leu	Leu	Ala	Trp
65				70				75				80			
Thr	Glu	Lys	Arg	Ala	Ser	Tyr	Glu	Leu	Glu	Phe	Ala	Lys	Ser	Thr	Met
85				90				95							
Lys	Ile	Ala	Glu	Ala	Gly	Lys	Val	Ser	Ile	Gln	Gln	Gln	Ser	His	Met
100				105				110							
Pro	Leu	Gln	Tyr	Ile	Tyr	Thr	Leu	Phe	Leu	Glu	His	Asp	Leu	Ser	Leu
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130															

<210> 4147

4892

<212> DNA

<213> Homo sapiens

<400> 4147

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3960
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4020
aagacggtac ataatcctac aggttttaaa gtacataaaa atatagtttg gaattctttg
4080
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4140
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4200

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 4320
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 4380
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 4440
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 4500
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 4560
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 4680
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 4740
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<210> 4148
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 4148
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 20 25 30
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 35 40 45
 Glu Gln His Leu Phe Asp Val Asn Asn Ser Gly Gly Gln Ser Ser Glu
 50 55 60
 Asp Ser Glu Ser Gly Thr Leu Ser Ala Ser Ser Ala Thr Ser Ala Arg
 65 70 75 80
 Gln Arg Arg Arg Gln Ser Lys Glu Gln Asp Glu Val Arg His Gly Arg
 85 90 95
 Asp Lys Gly Leu Ile Asn Lys Glu Asn Thr Pro Ser Gly Phe Asn His
 100 105 110
 Leu Asp Asp Cys Ile Leu Asn Thr Gln Glu Val Glu Lys Val His Lys
 115 120 125
 Asn Thr Phe Gly Cys Ala Gly Glu Arg Ser Lys Pro Lys Arg Gln Lys
 130 135 140
 Ser Ser Thr Lys Leu Ser Glu Leu His Asp Asn Gln Asp Gly Leu Val
 145 150 155 160
 Asn Met Glu Ser Leu Asn Ser Thr Arg Ser His Glu Arg Thr Gly Pro
 165 170 175
 Asp Asp Phe Glu Trp Met Ser Asp Glu Arg Lys Gly Asn Glu Lys Asp

180 185 190
 Gly Gly His Thr Gln His Phe Glu Ser Pro Thr Met Lys Ile Gln Glu
 195 200 205
 His Pro Ser Leu Ser Asp Thr Lys Gln Gln Arg Asn Gln Asp Ala Gly
 210 215 220
 Asp Gln Glu Glu Ser Phe Val Ser Glu Val Pro Gln Ser Asp Leu Thr
 225 230 235 240
 Ala Leu Cys Asp Glu Lys Asn Trp Glu Glu Pro Ile Pro Ala Phe Ser
 245 250 255
 Ser Trp Gln Arg Glu Asn Ser Asp Ser Asp Glu Ala His Leu Ser Pro
 260 265 270
 Gln Ala Gly Arg Leu Ile Arg Gln Leu Leu Asp Glu Asp Ser Asp Pro
 275 280 285
 Met Leu Ser Pro Arg Phe Tyr Ala Tyr Gly Gln Ser Arg Gln Tyr Leu
 290 295 300
 Asp Asp Thr Glu Val Pro Pro Ser Pro Pro Asn Ser His Ser Phe Met
 305 310 315 320
 Arg Arg Arg Ser Ser Ser Leu Gly Ser Tyr Asp Asp Glu Gln Glu Asp
 325 330 335
 Leu Thr Pro Ala Gln Leu Thr Arg Arg Ile Gln Ser Leu Lys Lys Lys
 340 345 350
 Ile Arg Lys Phe Glu Asp Arg Phe Glu Glu Glu Lys Lys Tyr Arg Pro
 355 360 365
 Ser His Ser Asp Lys Ala Ala Asn Pro Glu Val Leu Lys Trp Thr Asn
 370 375 380
 Asp Leu Ala Lys Phe Arg Arg Gln Leu Lys Glu Ser Lys Leu Lys Ile
 385 390 395 400
 Ser Glu Glu Asp Leu Thr Pro Arg Met Arg Gln Arg Ser Asn Thr Leu
 405 410 415
 Pro Lys Ser Phe Gly Ser Gln Leu Glu Lys Glu Asp Glu Lys Lys Gln
 420 425 430
 Glu Leu Val Asp Lys Ala Ile Lys Pro Ser Val Glu Ala Thr Leu Glu
 435 440 445
 Ser Ile Gln Arg Lys Leu Gln Glu Lys Arg Ala Glu Ser Ser Arg Pro
 450 455 460
 Glu Asp Ile Lys Asp Met Thr Lys Asp Gln Ile Ala Asn Glu Lys Val
 465 470 475 480
 Ala Leu Gln Lys Ala Leu Leu Tyr Tyr Glu Ser Ile His Gly Arg Pro
 485 490 495
 Val Thr Lys Asn Glu Arg Gln Val Met Lys Pro Leu Tyr Asp Arg Tyr
 500 505 510
 Arg Leu Val Lys Gln Ile Leu Ser Arg Ala Asn Thr Ile Pro Ile Ile
 515 520 525
 Gly Ser Pro Ser Ser Lys Arg Arg Ser Pro Leu Leu Gln Pro Ile Ile
 530 535 540
 Glu Gly Glu Thr Ala Ser Phe Phe Lys Glu Ile Lys Glu Glu Glu Glu
 545 550 555 560
 Gly Ser Glu Asp Asp Ser Asn Val Lys Pro Asp Phe Met Val Thr Leu
 565 570 575
 Lys Thr Asp Phe Ser Ala Arg Cys Phe Leu Asp Gln Phe Glu Asp Asp
 580 585 590
 Ala Asp Gly Phe Ile Ser Pro Met Asp Asp Lys Ile Pro Ser Lys Cys
 595 600 605
 Ser Gln Asp Thr Gly Leu Ser Asn Leu His Ala Ala Ser Ile Pro Glu

610		615		620											
Leu	Leu	Glu	His	Leu	Gln	Glu	Met	Arg	Glu	Glu	Lys	Lys	Arg	Ile	Arg
625				630						635					640
Lys	Lys	Leu	Arg	Asp	Phe	Glu	Asp	Asn	Phe	Arg	Gln	Asn	Gly	Arg	
				645						650					655
Asn	Val	Gln	Lys	Glu	Asp	Arg	Thr	Pro	Met	Ala	Glu	Glu	Tyr	Ser	Glu
				660				665							670
Tyr	Lys	His	Ile	Lys	Ala	Lys	Leu	Arg	Leu	Leu	Glu	Val	Leu	Ile	Ser
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Lys	Arg	Asp	Thr	Asp	Ser	Lys	Ser	Met							
				690				695							

<210> 4149

<211> 1396

<212> DNA

<213> Homo sapiens

<400> 4149

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 120
 gataccggagg ccaggagctc aaccaccctt ctccggaaca gggccggcct gctgctgtgc
 180
 cctcgagcgt cgggtgctgt atctactccg gggcctaggt cggctccggg ggcggcttag
 240
 gagaaggccg ccggcgagat gttcaaaaac acgttcacga gcggtcttct ctccatcttc
 300
 tacagcatcg gcagcaagcc tctgcaaata tgggacaaaa aggtacggaa tggccacatc
 360
 aaaagaatca ctgataatga catccagtcc ctgggtgctag agattgaagg gacaaatgta
 420
 agcaccacat atatcacatg ccctgcagac cccaagaaga cgctgggaat taaacttctt
 480
 ttccttgta tgattatcaa aaacctgaag aagtatttta ccttcgaagt gcaggacta
 540
 gatgacaaga atgtgcgctg togttttcgg gcaagtaact accagagcac caccggggtc
 600
 aaacccttca tctgcacat gcccatgcgg ctggatgacg gctggaacca gattcagttc
 660
 aacttgctag acttcacacg gcgagcatac ggcaccaatt acatcgagac cctcagagtg
 720
 cagatccatg caaattgtcg catccgacgg gtttacttct cagacagact ctactcagaa
 780
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 840
 ctggaattgt gactcgaggg atagaccctt ggtatgtgact cttcttttta aaaggaaact
 900
 atgtggagga cgaatgcaaaa acatatttat cttagtttgc tctgctgtag ttctgtatt
 960
 tatacttggt gttgcttgc atggacacgg gtgaacatcg cgtaactctg tgactgcatt
 1020
 gtaagtgcag tgggggtaag cagtcctgtg agtggcgcat gaacgctgga gcttattccg
 1080


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cgcctgcc cagtgtggg ggagatacct ttaccatgaa cttacagaat taaagatggc
1140
ccataaggaa ttccagacca atatttcttc ctgcggttta ttctatgttt tatatatatt
1200
ctaaatatat gtatatgctg tgtcatactc ataactctgga aatgaataaa gtgatataatt
1260
cctggtttgt aaaaaaaaaa aaaaaatttg ctataaaatg agaagctctc ctgatagagg
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1380
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1396

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<210> 4150
<211> 193
<212> PRT
<213> Homo sapiens
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#400> 4150															
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1				5				10					15		
Ile	Gly	Ser	Lys	Pro	Leu	Gln	Ile	Trp	Asp	Lys	Lys	Val	Arg	Asn	Gly
			20					25					30		
His	Ile	Lys	Arg	Ile	Thr	Asp	Asn	Asp	Ile	Gln	Ser	Leu	Val	Leu	Glu
		35					40					45			
Ile	Glu	Gly	Thr	Asn	Val	Ser	Thr	Thr	Tyr	Ile	Thr	Cys	Pro	Ala	Asp
	50					55					60				
Pro	Lys	Lys	Thr	Leu	Gly	Ile	Lys	Leu	Pro	Phe	Leu	Val	Met	Ile	Ile
65				70						75				80	
Lys	Asn	Leu	Lys	Lys	Tyr	Phe	Thr	Phe	Glu	Val	Gln	Val	Leu	Asp	Asp
			85					90					95		
Lys	Asn	Val	Arg	Arg	Arg	Phe	Arg	Ala	Ser	Asn	Tyr	Gln	Ser	Thr	Thr
		100						105				110			
Arg	Val	Lys	Pro	Phe	Ile	Cys	Thr	Met	Pro	Met	Arg	Leu	Asp	Asp	Gly
		115					120					125			
Trp	Asn	Gln	Ile	Gln	Phe	Asn	Leu	Leu	Asp	Phe	Thr	Arg	Arg	Ala	Tyr
	130					135					140				
Gly	Thr	Asn	Tyr	Ile	Glu	Thr	Leu	Arg	Val	Gln	Ile	His	Ala	Asn	Cys
145				150						155				160	
Arg	Ile	Arg	Arg	Val	Tyr	Phe	Ser	Asp	Arg	Leu	Tyr	Ser	Glu	Asp	Glu
			165					170					175		
Leu	Pro	Ala	Glu	Phe	Lys	Leu	Tyr	Leu	Pro	Val	Gln	Asn	Lys	Ala	Lys
		180						185				190			
Gln															

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<210> 4151
<211> 1372
<212> DNA
<213> Homo sapiens
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<400> 4151
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 120
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 180
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 240
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 300
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 360
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 420
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 480
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 540
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 660
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 720
 acgcgaagct ggaccggcca ggttcagagc ccgcctcggg tgctcccaat cagaatctgc
 780
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 840
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 900
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 960
 agcaggatga ggctgggggt gcgcagctgc cggtagacct gtagcagcct ctgggcgggtg
 1020
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 1080
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 1140
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 1200
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 1260
 gcgctgctgg gcacaggctg gtcattggcca cctctcggac gatgagggtga acgttggcgc
 1320
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 1372

<210> 4152

<211> 97

<212> PRT

<213> Homo sapiens

<400> 4152

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 Gly Cys Pro Ala Val Arg Lys Ala Ser Ala Gly Ala Ala Ala Val

```

                20                25                30
Arg Glu Gly Thr Pro Ala Glu Asp Ala Lys Leu Asp Arg Pro Gly
    35                40                45
Ser Glu Pro Ala Ser Val Ala Pro Asn Gln Asn Leu Cys Ala Pro
    50                55                60
Arg Pro Pro Ser Thr Phe Met Ser Val Leu Leu Arg Gly Gln Val
    65                70                75                80
Leu Pro Ser Leu Thr Ala Leu Ala Arg Pro Ala Arg Phe Pro Ser Asn
    85                90                95
Pro

```

<210> 4153
 <211> 395
 <212> DNA
 <213> Homo sapiens

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<400> 4153
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120
tcattaattc ttccacttta tcatttacat ctaggctctc ttctgaggct tcaaaactgt
180
atgacctctg acccatgctg ttgcatgga agcgagttgg tgacatcttt ccattggatg
240
tagataatcg ctcattatto tcctcccat tttgattggt agtgcaggcg tgtggggaag
300
tatcataact gttgctaggt gacggggaca ttcccgaatg ctgcgtctgt gtggaagctg
360
tagctgtaga ggaagatgct gggacattgt tagtn
395

```

<210> 4154
 <211> 110
 <212> PRT
 <213> Homo sapiens

```

<400> 4154
Met Ser Pro Ser Pro Ser Asn Ser Tyr Asp Thr Ser Pro Gln Pro Cys
1      5      10      15
Thr Thr Asn Gln Asn Gly Arg Glu Asn Asn Glu Arg Leu Ser Thr Ser
    20      25      30
Asn Gly Lys Met Ser Pro Thr Arg Phe His Ala Asn Ser Met Gly Gln
    35      40      45
Arg Ser Tyr Ser Phe Glu Ala Ser Glu Glu Asp Leu Asp Val Asn Asp
    50      55      60
Lys Val Glu Glu Leu Met Arg Arg Asp Ser Ser Val Ile Lys Glu Glu
    65      70      75      80
Ile Lys Ala Phe Leu Ala Asn Arg Arg Ile Ser Gln Ala Val Asp Thr
    85      90      95
Ile Gly Lys Met Leu Phe Pro Ser Val His Ser Gly Leu Ile
    100     105     110

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<210> 4155

<211> 1191

<212> DNA

<213> Homo sapiens

<400> 4155

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120
ttgatggctc caagacgtgc accattgagg acgtgtctcg caaagccacg attgaggagc
180
tgcgcgagcg ggtgtgggcg ctgttcgacg tgcggcccg atgccagcgc ctcttctacc
240
ggggcaagca gttggaaaat ggatatacct tatttgatta tgatgttgga ctgaatgata
300
taattcagct gctagtctgc ccagaccctg atcatcttcc tggcacatct acacagattg
360
aggctaaacc ctgttctaata agtccaccta aagtaaagaa agctccgagg gtaggacctt
420
ccaatcagcc atctacatca gctcgtgccc gtcttattga tcctggcttt ggaatatata
480
agatacccg aaagcggtac tctagaaatg aatgtcaagg atcttagacc acgagctaga
540
accattttga aatggaatga actaaatgtt ggtgatgtgg taatggttaa ttataatgta
600
gaaagtcctg gacaaagagg attctggttt gatgcagaaa ttaccacatt gaagacaatc
660
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720
aatgactgca agataatata ttagatgaa atcttcaaga ttgagagacc tggagcccat
780
cccctttcat ttgcagatgg aaagttttta aggcgaaatg accctgaatg tgacctgtgt
840
ggtggagacc cagaaaagaa atgtcattct tgctcctgtc gtgtatgtgg tgggaaacat
900
gaaccaaca tgcagcttct gtgtgatgaa tgtaatgtgg cttatcatat ttactgtctg
960
aatccacctt tggataaagt ccagaagag gaatactggt attgtccttc ttgtaaaaat
1020
gattccagtg aagtgtgaaa ggctgggtgaa agactcaaga tgagtaaaaa gaaagcaaa
1080
atgccgtcag ctagtactga aagccgaaga gactgaggca ggggaggggg ggggaggggg
1140
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1191

<210> 4156

<211> 233

<212> PRT

<213> Homo sapiens

<400> 4156

Asp Leu Pro Ile Ser His Leu His Gln Leu Val Pro Val Leu Leu Ile

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Leu Ala Leu Glu Tyr Ile Arg Tyr Pro Glu Ser Gly Thr Leu Glu Met
20           25           30
Asn Val Lys Asp Leu Arg Pro Arg Ala Arg Thr Ile Leu Lys Trp Asn
35           40           45
Glu Leu Asn Val Gly Asp Val Val Met Val Asn Tyr Asn Val Glu Ser
50           55           60
Pro Gly Gln Arg Gly Phe Trp Phe Asp Ala Glu Ile Thr Thr Leu Lys
65           70           75           80
Thr Ile Ser Arg Thr Lys Lys Glu Leu Arg Val Lys Ile Phe Leu Gly
85           90           95
Gly Ser Glu Gly Thr Leu Asn Asp Cys Lys Ile Ile Ser Val Asp Glu
100          105          110
Ile Phe Lys Ile Glu Arg Pro Gly Ala His Pro Leu Ser Phe Ala Asp
115          120          125
Gly Lys Phe Leu Arg Arg Asn Asp Pro Glu Cys Asp Leu Cys Gly Gly
130          135          140
Asp Pro Glu Lys Lys Cys His Ser Cys Ser Cys Arg Val Cys Gly Gly
145          150          155          160
Lys His Glu Pro Asn Met Gln Leu Leu Cys Asp Glu Cys Asn Val Ala
165          170          175
Tyr His Ile Tyr Cys Leu Asn Pro Pro Leu Asp Lys Val Pro Glu Glu
180          185          190
Glu Tyr Trp Tyr Cys Pro Ser Cys Lys Thr Asp Ser Ser Glu Val Val
195          200          205
Lys Ala Gly Glu Arg Leu Lys Met Ser Lys Lys Lys Ala Lys Met Pro
210          215          220
Ser Ala Ser Thr Glu Ser Arg Arg Asp
225          230

```

<210> 4157

<211> 3460

<212> DNA

<213> Homo sapiens

<400> 4157

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120
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180
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240
gatatcgact atgctttgct cccaagggaa ataccaggaa agggggggcc ctgggaagtg
300
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420
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480
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540

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660
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720
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780
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840
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900
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960
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1020
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1680
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1860
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2040
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2100
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2160

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<213> Homo sapiens

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Leu	Pro	Met	Ala	Gly	Arg	Ser	Ser	Asn	Ile	Trp	Asn	Arg	Ile	Phe	Asn	Leu	Pro	Met	Ala	Gly	Arg	Ser	Ser	Asn	Ile	Trp	Asn	Arg	Ile	Phe	Asn		
575										580										585													
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Gly	Asp	Glu	Val	Val	Pro	Ser	Gln	Ser	Thr	Ser	Arg	Glu	Pro	Glu	Arg	Gly	Asp	Glu	Val	Val	Pro	Ser	Gln	Ser	Thr	Ser	Arg	Glu	Pro	Glu	Arg		
605										610										615													
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620										625										630													
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635										640										645													
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650										655										660													
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690	695	700
Ala Asp Asn Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser		
705	710	715
Pro Ala Arg His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly		720
	725	730
Leu Arg Trp Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln		735
	740	745
Asn Gln Ser Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu		750
	755	760
Asp Asp Asp Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser		765
	770	775
Asp Phe Asp Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser		780
	785	790
Asp Gln Gly Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly		795
		800
	805	810
Val Arg Pro Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val		815
	820	825
His Thr Ala Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn		830
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Glu Thr Ser Asp Asp Glu Ala Leu Leu Leu Cys		845
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<210> 4163

<211> 568

<212> DNA

<213> Homo sapiens

<400> 4163

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 180
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<210> 4164

<211> 187

<212> PRT

<213> Homo sapiens

<400> 4164

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      20              25              30
Cys Gly Leu Gln Asp Pro Ala Gly Ser Arg Pro Leu Ser Pro Pro Phe
      35              40              45
Ser Arg Leu Arg Ser Glu Gly Ser Lys Ser Val Leu Pro Gln Trp Leu
      50              55              60
Trp Gly Met Lys Gly Ile Pro Val Pro Ser Gly His Pro Gln Ala Asp
65              70              75              80
Gly Arg Arg Ala Leu Val Arg Ala Val Gly His Pro Gln Asp Leu Leu
      85              90              95
Thr Glu Ala Ser Pro Arg Cys Pro Ala Gly Pro Ser Pro Leu Arg Ser
      100              105              110
Thr Gly Arg Lys Pro Pro Gly Pro Pro Arg Gly Gly Asp Leu Ala Ala
      115              120              125
Pro Val Leu Phe Lys Ala Trp Ala Thr Ser Leu Ala Cys Pro Lys Trp
      130              135              140
Gln Ala Leu Arg Arg Ala Arg Met Val Pro Val Val Gln Gly Ser Pro
145              150              155              160
Pro Ala Trp Ala Ala Pro Val Pro Trp Asn Leu Leu Pro Trp Gly Pro
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Trp Thr Cys Arg His Met Ala Ile Glu Leu Gln
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<210> 4165

<211> 717

<212> DNA

<213> Homo sapiens

<400> 4165

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660

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<210> 4166

<211> 166

<212> PRT

<213> Homo sapiens

<400> 4166

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		20						25					30		
Arg	Arg	Thr	Gly	Gln	Tyr	Lys	Gly	Leu	Leu	Asp	Cys	Ala	Arg	Arg	Ile
		35					40					45			
Leu	Glu	Arg	Glu	Gly	Pro	Arg	Ala	Phe	Tyr	Arg	Gly	Tyr	Leu	Pro	Asn
	50					55					60				
Val	Leu	Gly	Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu
65					70				75					80	
Thr	Leu	Lys	Asn	Trp	Trp	Leu	Gln	Gln	Tyr	Ser	His	Asp	Ser	Ala	Asp
			85						90					95	
Pro	Gly	Ile	Leu	Val	Leu	Leu	Ala	Cys	Gly	Thr	Ile	Ser	Ser	Thr	Cys
			100						105					110	
Gly	Gln	Ile	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	Gln
		115					120						125		
Ala	Gln	Gly	Phe	His	His	Val	Ala	Gln	Ala	His	Leu	Glu	Leu	Val	Gly
		130					135				140				
Ser	Arg	Asn	Ser	Pro	Ala	Phe	Ser	Leu	Pro	Thr	Cys	Trp	Asp	Tyr	Arg
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Lys	Pro	Val	Val	Met	Pro										
					165										

<210> 4167

<211> 897

<212> DNA

<213> Homo sapiens

<400> 4167

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120
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180
ctgagttagct tggactacag atatggccgc gtggaaagtg tcaaaattct tcccaagagg
240
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300
gctcacaact cggtaacaa aatgggtgac agagacctac gcacggatta taatgaacca
360
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agagaggttt ctgggttcag aggaggtggt ggagggcctg cttatgggtc cccaccgtca
480

cttcacgacac gagaaggacg ttatgagcgg agacttgatg gggcttcaga taacagggag
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 780
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 897

<210> 4168

<211> 299

<212> PRT

<213> Homo sapiens

<400> 4168

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Gly	Gln	Phe	Thr	Arg	Glu	Arg	Ala	Gly	Arg	Glu	Asp	His	Arg	Ala	Phe
			20					25				30			
Gln	Thr	Ala	Gly	Val	Gln	Trp	Arg	Asp	Leu	Ser	Pro	Pro	Gln	Leu	Pro
			35				40				45				
Pro	Pro	Gly	Ile	Lys	Gln	Ser	Ser	Cys	Phe	Ser	Leu	Leu	Ser	Ser	Leu
	50				55					60					
Asp	Tyr	Arg	Tyr	Gly	Arg	Val	Glu	Ser	Val	Lys	Ile	Leu	Pro	Lys	Arg
65					70				75					80	
Gly	Ser	Glu	Gly	Gly	Val	Ala	Ala	Phe	Val	Asp	Phe	Val	Asp	Ile	Lys
			85					90						95	
Ser	Ala	Gln	Lys	Ala	His	Asn	Ser	Val	Asn	Lys	Met	Gly	Asp	Arg	Asp
			100				105					110			
Leu	Arg	Thr	Asp	Tyr	Asn	Glu	Pro	Gly	Thr	Ile	Pro	Ser	Ala	Ala	Arg
		115				120					125				
Gly	Leu	Asp	Asp	Thr	Val	Ser	Ile	Ala	Ser	Arg	Ser	Arg	Glu	Val	Ser
	130				135					140					
Gly	Phe	Arg	Gly	Gly	Gly	Gly	Pro	Ala	Tyr	Gly	Pro	Pro	Pro	Pro	Ser
145				150				155						160	
Leu	His	Ala	Arg	Glu	Gly	Arg	Tyr	Glu	Arg	Arg	Leu	Asp	Gly	Ala	Ser
			165					170					175		
Asp	Asn	Arg	Glu	Arg	Ala	Tyr	Glu	His	Ser	Ala	Tyr	Gly	His	His	Glu
		180					185					190			
Arg	Gly	Thr	Gly	Gly	Phe	Asp	Arg	Thr	Arg	His	Tyr	Asp	Gln	Asp	Tyr
		195				200						205			
Tyr	Arg	Asp	Pro	Arg	Glu	Arg	Thr	Leu	Gln	His	Gly	Leu	Tyr	Tyr	Ala
	210				215					220					
Ser	Arg	Ser	Arg	Ser	Pro	Asn	Arg	Phe	Asp	Ala	His	Asp	Pro	Arg	Tyr
225				230				235						240	
Glu	Pro	Arg	Ala	Arg	Glu	Gln	Phe	Thr	Leu	Pro	Ser	Val	Val	His	Arg
			245					250					255		
Asp	Ile	Tyr	Arg	Asp	Asp	Ile	Thr	Arg	Glu	Val	Arg	Gly	Arg	Arg	Pro

	260		265		270
Glu Arg Asn Tyr Gln His Ser Arg Ser Arg Ser	Pro His Ser Ser Gln				
275	280	285			
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<210> 4169

<211> 4743

<212> DNA

<213> Homo sapiens

<400> 4169

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1260

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<210> 4170

<211> 900

<212> PRT

<213> Homo sapiens

<400> 4170

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Ile	Cys	Phe	Pro	Asp	Ser	Leu	Leu	Gln	Asp	Glu	Glu	Arg	Ser	Phe	Phe
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Lys	Ala	Gly	Pro	Pro	Glu	Asp	Glu	Gly	Asp	Pro	Lys	Ala	Gly	Ala	Gly
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					230				235						240
Thr	Ser	Pro	Ile	Phe	Cys	Ser	Thr	Lys	Pro	Lys	Lys	Leu	Leu	Lys	Thr
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Lys	Lys	Leu	Tyr	Ala	Gln	Glu	Tyr	Glu	Phe	Glu	Ala	Asp	Glu	Asp	Lys
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Ala	Asp	Val	Pro	Ala	Asp	Ile	Arg	Leu	Asn	Pro	Arg	Arg	Leu	Pro	Asp

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<211> 889

<212> DNA

<213> Homo sapiens

<400> 4171

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 <213> Homo sapiens

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 Val Phe Ile Leu Pro Leu Asp Val Ser Thr Thr Ile Tyr Asn Arg Cys
 50 55 60
 Lys His Ala Ala Gln Ile Gln Ala Leu Leu Arg Ile Ala Thr Leu Gln
 65 70 75 80
 Asp Cys Ala Thr Ala Asn Pro Val Pro Ser Gln His Pro Cys Phe Lys
 85 90 95
 Pro Trp Ser Tyr Ile Pro Asp Gly Ile Met Pro Ile Phe Trp Arg Val
 100 105 110
 Val Tyr Trp Thr Ser Gln Phe Leu Thr Trp Ile Leu Leu Pro Phe Met
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 Gln Ser Tyr Ala Arg Ser Gly Gly Phe Ser Ile Thr Gly Lys Ile Lys
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 Thr Ala Leu Ile Glu Asn Ala Ile Tyr Tyr Gly Thr Tyr Leu Leu Ile
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 <212> DNA
 <213> Homo sapiens

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<211> 586

<212> PRT

<213> Homo sapiens

<400> 4176

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His	Thr	Ser	Val	His	Gly	Val	Gly	His	Ser	Phe	Val	Gln	Ser	Ala	Phe
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<211> 4763

<212> DNA

<213> Homo sapiens

<400> 4177

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<210> 4178

<211> 398

<212> PRT

<213> Homo sapiens

<400> 4178

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 35 40 45
 Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly Asp Gln His Glu
 50 55 60
 Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu Thr Val Phe Pro
 65 70 75 80
 His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys Thr Phe Ser Glu
 85 90 95
 Ala Cys Leu Met Val Arg Lys Pro Ala Leu Glu Leu Leu His Tyr Leu
 100 105 110
 Lys Asn Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly
 115 120 125
 Glu Lys Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Phe His Phe
 130 135 140
 Cys Ala Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu
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 Trp Val Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln
 165 170 175
 Arg Phe Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys
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 Thr Thr Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr
 195 200 205
 Val Trp Asn Lys Arg Glu Leu Thr Glu Lys Gly Ser Pro Leu Gly Glu
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 Val Val Glu Gln Gly Ile Thr Arg Val Arg Asn Ala Thr Asp Ala Val
 225 230 235 240
 Gly Ile Val Leu Lys Glu Leu Lys Arg Gln Ser Ser Leu Gly Met Phe
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 His Leu Leu Val Ala Val Asp Gly Ile Asn Ala Leu Trp Gly Arg Thr
 260 265 270
 Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala Pro Glu Glu Leu Ala
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 305 310 315 320
 Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu Gly Phe Asp Ala
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 Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn Trp Leu Gln His
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<210> 4179

<211> 2208

<212> DNA

<213> Homo sapiens

<400> 4179

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<210> 4180

<211> 257

<212> PRT

<213> Homo sapiens

<400> 4180

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 35 40 45
 Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
 50 55 60
 Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
 65 70 75 80
 Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
 85 90 95
 Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
 100 105 110
 Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
 115 120 125
 Phe Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
 130 135 140
 Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
 145 150 155 160
 Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
 165 170 175
 Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg

	180		185		190
Ile Leu	Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly				
	195		200		205
Leu Ser	Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val				
	210		215		220
Ala Asn	Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu				
225		230		235	240
Cys Arg	Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp				
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<210> 4181
 <211> 735
 <212> DNA
 <213> Homo sapiens

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<210> 4182
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 4182
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Val	Gly	Gly	Ile	Ile	Gly	Gly	Ile	Val	Ala	Gly	Leu	Val	Ser	Asp	Tyr				
50			55			60			65			70							
Thr	Asn	Gly	Arg	Ala	Thr	Thr	Cys	Cys	Val	Met	Leu	Ile	Leu	Ala	Ala				
65			70			75			80			85							
Pro	Met	Met	Phe	Leu	Tyr	Asn	Tyr	Ile	Gly	Gln	Asp	Gly	Ile	Ala	Ser				
85			90			95			100			105							
Ser	Ile	Val	Met	Leu	Ile	Ile	Cys	Gly	Gly	Leu	Val	Asn	Gly	Pro	Tyr				
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Ala	Xaa	Ile	Thr	Thr	Ala	Val	Ser	Ala	Asp	Leu	Gly	Thr	His	Lys	Ser				
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Leu	Lys	Gly	Asn	Ala	Lys	Ala	Leu	Ser	Thr	Val	Thr	Ala	Ile	Ile	Asp				
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<210> 4183

<211> 1129

<212> DNA

<213> Homo sapiens

<400> 4183

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<210> 4184

<211> 374

<212> PRT

<213> Homo sapiens

<400> 4184

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Arg	Phe	Met	Pro	Gln	Gln	Asn	Ser	Pro	Val	Pro	Ser	Pro	Tyr	Ala	Pro
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Gln	Ser	Pro	Ala	Gly	Tyr	Met	Pro	Tyr	Ser	His	Pro	Ser	Ser	Tyr	Thr
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Thr	His	Pro	Gln	Met	Gln	Gln	Ala	Ser	Val	Ser	Ser	Pro	Ile	Val	Ala
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Gly	Gly	Leu	Arg	Asn	Ile	His	Asp	Asn	Lys	Val	Ser	Gly	Pro	Leu	Ser
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Gly	Asn	Ser	Ala	Asn	His	His	Ala	Asp	Asn	Pro	Arg	His	Gly	Ser	Ser
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Glu	Asp	Tyr	Leu	His	Met	Val	His	Arg	Leu	Ser	Ser	Asp	Asp	Gly	Asp
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Pro	Pro	Leu	Ile	Leu	Gln	Ser	Gln	Ser	Leu	Pro	Cys	Ser	Ser	Pro	Arg
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Asp	Val	Pro	Pro	Asp	Ile	Leu	Leu	Asp	Ser	Pro	Glu	Arg	Lys	Gln	Lys
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Lys	Gln	Lys	Lys	Met	Lys	Leu	Gly	Lys	Asp	Glu	Lys	Glu	Gln	Ser	Glu
		195					200					205			
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		210				215					220				
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Gln	Glu	Asp	Met	Leu	Ser	Gly	Met	Glu	Asn	Ser	Asn	Val	Ser	Glu	Asn
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Val	Gln	Asn	Gln	Gln	Gln	Ile	Ser	Gln	Gln	Gly	Pro	Ile	Tyr	Asp	Glu
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Val	Glu	Leu	Asp	Ala	Leu	Ala	Glu	Ile	Glu	Arg	Ile	Glu	Arg	Glu	Ser
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Ala	Ile	Glu	Arg	Glu	Arg	Phe	Ser	Lys	Glu	Val	Gln	Asp	Lys	Asp	Lys
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<210> 4185

<211> 1481

<212> DNA

<213> Homo sapiens

<400> 4185

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<210> 4186
 <211> 385
 <212> PRT
 <213> Homo sapiens

<400> 4186
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 35 40 45
 Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu Leu His Pro Val
 50 55 60
 Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His Ser Thr Ile Phe
 65 70 75 80
 Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe Thr Val Glu Glu
 85 90 95
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 100 105 110
 Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp Arg Leu Lys Val
 115 120 125
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 130 135 140
 Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Arg Ser Leu Trp Arg
 145 150 155 160
 Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu Ser Ala Ile Lys
 165 170 175
 Phe Met Ala Tyr Glu Gln Ile Lys Arg Leu Val Gly Ser Asp Gln Glu
 180 185 190
 Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser Leu Ala Gly Ala
 195 200 205
 Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu Lys Thr Arg Met
 210 215 220
 Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu Asp Cys Ala Arg
 225 230 235 240
 Arg Ile Leu Ala Arg Glu Gly Val Ala Ala Phe Tyr Lys Gly Tyr Val


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Tyr Glu Thr Leu Lys Asn Ala Trp Leu Gln His Tyr Ala Val Asn Ser
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Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly Thr Met Ser Ser
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Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu Val Arg Thr Arg
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Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser
                320                325                330
Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu Tyr
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Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val Ser Ile
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<210> 4187

<211> 1087

<212> DNA

<213> Homo sapiens

<400> 4187

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<210> 4188

<211> 272

<212> PRT

<213> Homo sapiens

<400> 4188

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		20						25					30		
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Val	Asp	Ser	Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg
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Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala	Arg
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Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn
		115					120					125			
Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val
	130					135					140				
Ile	Thr	Tyr	Pro	Glu	Xaa	Gly	Cys	Thr	Arg	Gly	Ser	Arg	Asp	Ile	
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Cys	Ser	Ser	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly	Asn	Leu	Ser	Ala
			165						170				175		
Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile	Leu	Leu	Gly	Leu	Leu
		180						185					190		
Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile	Asn	His	Asn	Arg	Ala	Leu
	195						200					205			
Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu	Cys	Gly	Ile	Pro	Lys	His	Phe
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Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr	Ala	Leu	Met	Met	Glu	Gly	Leu	Leu
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Ser	Ala	Cys	Tyr	His	Val	Cys	Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Gly
			245					250					255		
Glu	Trp	Gly	Val	Leu	Leu	Phe	Trp	Leu	Asn	Leu	Gln	Gln	Gly	Pro	Ala
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<210> 4189

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 4189

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1570

<210> 4190

<211> 523

<212> PRT

<213> Homo sapiens

<400> 4190

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			20					25					30		
Met	Val	Ser	Thr	Val	Glu	Cys	Ala	Leu	Lys	His	Val	Ser	Asp	Trp	Leu
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Asp	Glu	Thr	Asn	Lys	Gly	Thr	Lys	Thr	Glu	Gly	Glu	Thr	Glu	Val	Lys
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Lys	Asp	Glu	Ala	Gly	Glu	Asn	Tyr	Ser	Lys	Asp	Gln	Gly	Gly	Arg	Thr
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				85					90					95	
Lys	Asp	Asp	Met	Asp	Leu	Glu	Leu	Val	Leu	Met	Cys	Lys	Asp	Lys	Pro
			100					105					110		
Thr	Glu	Thr	Leu	Leu	Asn	Thr	Val	Lys	Asp	Asn	Leu	Pro	Ile	Gln	Ile
			115				120					125			
Gln	Lys	Leu	Thr	Glu	Glu	Lys	Tyr	Gln	Val	Glu	Gln	Cys	Val	Asn	Glu
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Lys	Cys	Leu	Asn	Ala	Leu	Ala	Ser	Leu	Arg	His	Ala	Lys	Trp	Phe	Gln
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Asp	Pro	Thr	Asp	Ala	Leu	Ser	Tyr	Met	Thr	Ile	Gln	Gln	Lys	Glu	Asp
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Ile	Thr	His	Ser	Ala	Gln	His	Ala	Leu	Arg	Leu	Ser	Ala	Phe	Gly	Gln
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Ile	Tyr	Lys	Val	Leu	Glu	Met	Asp	Pro	Leu	Pro	Ser	Ser	Lys	Pro	Phe
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Gln	Lys	Tyr	Ser	Trp	Ser	Val	Thr	Asp	Lys	Glu	Gly	Ala	Gly	Ser	Ser

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 385 390 395 400
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 405 410 415
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 420 425 430
 Pro Ser Lys Lys Thr Ala Lys Leu His Val Ala Val Lys Val Leu Gln
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 Ala Met Gly Tyr Pro Thr Gly Phe Asp Ala Asp Ile Glu Cys Met Ser
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 Ser Asp Glu Lys Arg Arg Gly Leu Lys Tyr Glu Leu Ile Ser Glu Thr
 465 470 475 480
 Gly Gly Ser His Asp Lys Arg Phe Val Met Glu Val Glu Val Asp Gly
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<210> 4191

<211> 1661

<212> DNA

<213> Homo sapiens

<400> 4191

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<212> PRT

<213> Homo sapiens

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 35 40 45
 Ala Ser Ile Ala Thr Ala Ser Ala Ser Ala Gln Ala Arg Asn His Val
 50 55 60
 Asp Ala Gln Val Gln Thr Glu Ala Pro Val Pro Val Ser Val Gln Pro
 65 70 75 80
 Pro Ser Gln Tyr Asp Ile Pro Arg Leu Ala Ala Phe Leu Arg Arg Val
 85 90 95
 Glu Ala Met Val Ile Arg Glu Leu Asn Lys Asn Trp Gln Ser His Ala
 100 105 110
 Phe Asp Gly Phe Glu Val Asn Trp Thr Glu Gln Gln Gln Met Val Ser

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 Tyr Gly Arg Leu Asp His Gly Asp Trp Ser Thr Leu Lys Ser Phe Val
 165 170 175
 Cys Ala Trp Asn Leu Asp Arg Arg Asp Leu Arg Pro Gln Gln Pro Ser
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 Ala Val Val Glu Val Pro Ser Ala Val Leu Cys Leu Ala Phe His Pro
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 Thr Gln Pro Ser His Val Ala Gly Gly Leu Tyr Ser Gly Glu Val Leu
 210 215 220
 Val Trp Asp Leu Ser Arg Leu Glu Asp Pro Leu Leu Trp Arg Thr Gly
 225 230 235 240
 Leu Thr Asp Asp Thr His Thr Asp Pro Val Ser Gln Val Val Trp Leu
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 Pro Glu Pro Gly His Ser His Arg Phe Gln Val Leu Ser Val Ala Thr
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 Asp Gly Lys Val Leu Leu Trp Gln Gly Ile Gly Val Gly Gln Leu Gln
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 Leu Thr Glu Gly Phe Ala Leu Val Met Gln Gln Leu Pro Arg Ser Thr
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 Lys Leu Lys Lys His Pro Arg Gly Glu Thr Glu Val Gly Ala Thr Ala
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<210> 4193

<211> 6439

<212> DNA

<213> Homo sapiens

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<211> 519

<212> PRT

<213> Homo sapiens

<400> 4194

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Met Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly		
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<211> 1200

<212> DNA

<213> Homo sapiens

<400> 4195

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<213> Homo sapiens

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<211> 1769

<212> DNA

<213> Homo sapiens

<400> 4199

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 130 135 140
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 <212> PRT
 <213> Homo sapiens

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 50 55 60
 Leu Leu Ala Ser Gly Xaa Ala Ala Leu Ala Cys Val Phe Leu Gly Val

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Leu	Thr	Gly	Ile	Ala	Ser	Leu	Val	Leu	Leu	Gly	Leu	Trp	Asp	Tyr	Leu
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Asn	Glu	Ala	Ala	Ile	Thr	Thr	Phe	Ser	Val	Leu	Gly	Leu	Phe	Ser	Ser
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Gln	Ala	Ala	Ala	Ile	Leu	Ser	Thr	Leu	Leu	Ala	Ala	Glu	Val	Ile	Pro
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<211> 1368

<212> DNA

<213> Homo sapiens

<400> 4203

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<213> Homo sapiens

<400> 4204

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<213> Homo sapiens

<400> 4205

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<211> 829

<212> PRT

<213> Homo sapiens

<400> 4206

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Ser Val Ile Val Glu Val Arg Ser Asp Asp Asp Lys Asp Glu Asp Thr			
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His Ser Arg Lys Ser Thr Val Thr Asp Glu Ser Glu Met Gln Asp Met			
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Met Thr Arg Gly Asn Leu Gly Leu Leu Glu Gln Ala Ile Ala Leu Lys			
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Ala Glu Gln Val Arg Thr Val Cys Glu Pro Gly Cys Pro Pro Ala Glu			
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Gln Ser Gln Leu Gly Leu Gly Glu Pro Gly Lys Ala Ala Lys Pro Leu			
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Asp Thr Val Arg Lys Ser Tyr Tyr Ser Lys Asp Pro Ser Arg Ala Glu			
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Lys Arg Glu Ile Lys Cys Pro Thr Pro Gly Cys Asp Gly Thr Gly His			
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Val Thr Gly Leu Tyr Pro His His Arg Ser Leu Ser Gly Cys Pro His			
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Lys Asp Arg Ile Pro Pro Glu Ile Leu Ala Met His Glu Asn Val Leu			
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Lys Cys Pro Thr Pro Gly Cys Thr Gly Gln Gly His Val Asn Ser Asn			
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Ala Pro Ala Thr Pro Arg Ala Asn Leu Ala Lys Glu Leu Glu Lys Phe			
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Ser Lys Val Thr Phe Asp Tyr Ala Ser Phe Asp Ala Gln Val Phe Gly			
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<210> 4207

<211> 1016

<212> DNA

<213> Homo sapiens

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<211> 193

<212> PRT

<213> Homo sapiens

<400> 4208

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Ile	Asp	Arg	Arg	Thr	Ser	Thr	Pro	Asn	Ser	Arg	Ile	Gln	Arg	Ala	Thr
			35				40					45			
Thr	Val	Ser	Gln	Lys	Lys	Ser	Ser	Lys	Leu	Cys	Thr	Cys	Thr	Glu	Pro
			50				55				60				
Ile	Arg	Lys	Val	Pro	Val	Ser	Lys	Thr	Pro	Lys	Lys	Thr	His	Ser	Asp
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4200> 4209
ntctctctgta cctgggcctc cagaaaaatg gtggtgatgg cgcgacttcc gcggcccgag
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caattctctg tcaaatgctg gcttcgctac atcagagtca aacagggcgc cccgaagccc
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taccgatacc tgaagcgcgc tcgggcacag gtgaagcacc gctgtgtgac cgacctgtcc
300
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360
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420
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480
tatctgcgct tcctgcgctc acaccactg cctgagacag ctgtgcgagg ctatcgccgc
540
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600
cggctggatg aggcgcgcga gcgcctggcc accgtggtga acgacgagcg ttctgtgtct
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720
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840
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960

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1140
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1200
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1260
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1320
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1380
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1860
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1920
aacatctaca tcaagcggcg ggccgagatc tatggggcca cccacacccg cggcatctac
1980
cagaaggcca ttgaggtgct gtccgacgag cgcgcgcgtg agatgtgcct gcggtttgca
2040
gacatggagt gcaagctcgg ggagatcgac cgcgcccggg ctatctacag cttctgtctc
2100
cagatctgtg atccccggac aactggggca ttctggcaaa cgtggaagga ctttgaggtc
2160
cggcatggca acgaggacac catcaggagg atgctgagga tacggcggag tgtgcaggcc
2220
acgtacaaca ctacagtgca cttcatggcc tcgcagatgc tcaaggtgtc gggcagtgcc
2280
acggggcaccg tgtctgacct ggctcccggg cagagcgcca tggatgacat gaagtgtctg
2340
gaacagagag cagaacagct ggcggctgag gcggagcgtg accagccctt gcgcgcccag
2400
agcaagatcc tgttcgtgag gagtgcgcgc tcccgggagg agctggcaga gctggcacag
2460
caggtcaacc ccgaggagat ccagctgggc gaggacgagg acgaggacga gatggacctg
2520
gagcccaacg aggttcggct ggagcagcag agcgtgccag ccgcagtggt tgggagcctg
2580

aaggaagact gaccgcgtccc tcccccatcc cccctcccga cccctcccc aatacagcta
 2640
 cgtttgtaga tcaaaaaaaaa a
 2661

<210> 4210

<211> 863

<212> PRT

<213> Homo sapiens

<400> 4210

Xaa Ser Cys Thr Trp Ala Ser Arg Lys Met Val Val Met Ala Arg Leu
 1 5 10 15
 Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu Glu Asp Leu Pro
 20 25 30
 Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val Lys Cys Trp Leu
 35 40 45
 Arg Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro Arg Leu Asn Gln
 50 55 60
 Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser Tyr Lys Leu Trp
 65 70 75 80
 Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys His Arg Cys Val
 85 90 95
 Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His Glu Arg Ala Phe
 100 105 110
 Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp Tyr Cys Gln Phe
 115 120 125
 Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg Thr Phe Asp Arg
 130 135 140
 Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg Ile Trp Pro Leu
 145 150 155 160
 Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu Thr Ala Val Arg
 165 170 175
 Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser Ala Glu Glu Tyr
 180 185 190
 Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu Ala Ala Gln Arg
 195 200 205
 Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser Lys Ala Gly Lys
 210 215 220
 Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu Ile Ser Gln Asn
 225 230 235 240
 Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile Ile Arg Gly Gly
 245 250 255
 Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp Cys Ser Leu Ala
 260 265 270
 Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala Arg Asp Val Tyr
 275 280 285
 Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp Phe Thr Gln Val
 290 295 300
 Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile Ala Ala Lys Met
 305 310 315 320
 Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp Asp Val Asp Leu
 325 330 335
 Glu Leu Arg Leu Ala Arg Phe Glu His Leu Ile Ser Arg Arg Pro Leu

340 345 350
 His Leu Ser Ser Val Leu Leu Arg Gln Asn Pro His His Val His Glu
 355 360 365
 Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro Arg Glu Ile Ile
 370 375 380
 Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro Phe Lys Ala Thr
 385 390 395 400
 Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys Phe Tyr Glu Asp
 405 410 415
 Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu Lys Ala Thr Lys
 420 425 430
 Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val Trp Cys Gln Cys
 435 440 445
 Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu Ala Leu Arg Leu
 450 455 460
 Leu Arg Lys Ala Thr Ala Leu Pro Pro Gly Arg Val Phe Asp Gly
 465 470 475 480
 Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser Leu Lys Val Trp Ser
 485 490 495
 Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr Phe Gln Ser Thr Lys
 500 505 510
 Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile Ala Thr Pro Gln Ile
 515 520 525
 Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His Lys Tyr Phe Glu Glu
 530 535 540
 Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu Phe Lys Trp Pro Asn
 545 550 555 560
 Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys Phe Ile Ala Arg Tyr
 565 570 575
 Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu Phe Glu Gln Ala Leu
 580 585 590
 Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu Tyr Leu Leu Tyr Ala
 595 600 605
 Gln Leu Glu Glu Glu Trp Gly Leu Ala Arg His Ala Met Ala Val Tyr
 610 615 620
 Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln Gln Tyr Asp Met Phe
 625 630 635 640
 Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr Gly Val Thr His Thr
 645 650 655
 Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu Ser Asp Glu His Ala
 660 665 670
 Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu Cys Lys Leu Gly Glu
 675 680 685
 Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys Ser Gln Ile Cys Asp
 690 695 700
 Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp Lys Asp Phe Glu Val
 705 710 715 720
 Arg His Gly Asn Glu Asp Thr Ile Arg Glu Met Leu Arg Ile Arg Arg
 725 730 735
 Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn Phe Met Ala Ser Gln
 740 745 750
 Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr Val Ser Asp Leu Ala
 755 760 765
 Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu Leu Glu Gln Arg Ala

```

      770              775              780
Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln Pro Leu Arg Ala Gln
785              790              795              800
Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser Arg Glu Glu Leu Ala
      805              810              815
Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile Gln Leu Gly Glu Asp
      820              825              830
Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn Glu Val Arg Leu Glu
      835              840              845
Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser Leu Lys Glu Asp
      850              855              860

```

<210> 4211
 <211> 456
 <212> DNA
 <213> Homo sapiens

```

<400> 4211
ggggatcgct agcccccagc ttctcagaac taaatatgaa agctcttgct cgtctacgct
60
tagttacaac agactccctg ggcctactgt aggggtcaag agcagatttc cagactctca
120
agctggaaaa gagacgctcc acactgcgac gacaaccaac acatgggaca agctgagaaa
180
gtgcactcag gacttcgctg gatgtcacca ccatggcaat acttagatcc tgttgcttaa
240
gcataccatg tcgctgaaag agggaaagaa aatgaaagag cgtcctttaa aaagacgtaa
300
aattacactt tcactactac tggttcctat cttgtgagc taaagtacaa cctggccagg
360
gtttaccagc tctacctgca actgagtcag aaaggcaaag tagtcagctt tgtccatgct
420
gtacggaatt tgctccacaa acccccttgc tctaga
456

```

<210> 4212
 <211> 81
 <212> PRT
 <213> Homo sapiens

```

<400> 4212
Met Leu Lys Gln Gln Asp Leu Ser Ile Ala Met Val Val Thr Ser Arg
1      5      10      15
Glu Val Leu Ser Ala Leu Ser Gln Leu Val Pro Cys Val Gly Cys Arg
20      25      30
Arg Ser Val Glu Arg Leu Phe Ser Ser Leu Arg Val Trp Lys Ser Ala
35      40      45
Leu Asp Pro Tyr Ser Arg Pro Arg Glu Ser Val Val Thr Lys Arg Arg
50      55      60
Arg Ala Arg Ala Phe Ile Phe Ser Ser Glu Lys Leu Gly Ala Ser Asp
65      70      75      80
Pro

```


<210> 4213

<211> 383

<212> DNA

<213> Homo sapiens

<400> 4213

```

nacgcgtacc tgtgccagcg cgcgcgcttc ttcgcagaga acgagggcct agacgactac
60
atggaggcac gcgaggcat gcacctcaag aacgtggagt tccgtgagtt catggtggcc
120
ttcccggacc cggcccgccc gccctggtag gcctgctcgt cggccttctg ggccgcggcg
180
ctgctcacgc tgtcgtggcc gctgcgagtg ctggccgagt accgcacggc ctacgcgcac
240
taccacgtgg agaagctgtt tggcctggag ggcccgggct cggccagcag cgcaggcggt
300
ggcctcagcc ccagcgatga gctgctgccc ccgctcaccc accgcctgcc gcggttcaac
360
acagtagaca gcacggagct cgg
383

```

<210> 4214

<211> 127

<212> PRT

<213> Homo sapiens

<400> 4214

```

Xaa Ala Tyr      5  Gln Arg Ala Arg Phe Phe Ala Glu Asn Glu Gly
1              5              10              15
Leu Asp Asp Tyr Met Glu Ala Arg Glu Gly Met His Leu Lys Asn Val
20              25              30
Asp Phe Arg Glu Phe Met Val Ala Phe Pro Asp Pro Ala Arg Pro Pro
35              40              45
Trp Tyr Ala Cys Ser Ser Ala Phe Trp Ala Ala Ala Leu Leu Thr Leu
50              55              60
Ser Trp Pro Leu Arg Val Leu Ala Glu Tyr Arg Thr Ala Tyr Ala His
65              70              75              80
Tyr His Val Glu Lys Leu Phe Gly Leu Glu Gly Pro Gly Ser Ala Ser
85              90              95
Ser Ala Gly Gly Gly Leu Ser Pro Ser Asp Glu Leu Leu Pro Pro Leu
100             105             110
Thr His Arg Leu Pro Arg Val Asn Thr Val Asp Ser Thr Glu Leu
115             120             125

```

<210> 4215

<211> 939

<212> DNA

<213> Homo sapiens

<400> 4215

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nggtacctcg gctgaataaa aattcaaaaa aacagcaatg gacaggaact tgagaagacg
60
ctggaagaaa gcaaaagaaat ggatatcaaa cgtaaagaaa ataaaggcaa tgataccctt
120

```

ttggccctag agagtacaaa cactgaaaag gagacaagcc tggaggaaac aaaaatcggg
 180
 gagatccctga tccagggtt gacagaagat atggtgactg ttttaatccg ggctgcgtg
 240
 agcatgctgg gagtccctgt ggaccagat actttgcatg ccaccctttg tttctgttg
 300
 agggtcactc ggggccccca attagccatg atgtttgcag aactgaagaa taccgcgatg
 360
 atcttgaatt tgaccagag ctcagggttc aatgggttta ctcccctggt cacccttctc
 420
 ttaagacaca tcattgagga cccctgtacc ctctgcata ccatggaaaa ggtgtgtcgc
 480
 tcagcagcta caagtggagc tggtagcact acctctgggt ttgtgtctgg cagcctcggc
 540
 tctcgggaga tcaactacat cttctgtgtc ctggggccag cgcgatgccg caatccagac
 600
 atattcacag aagtggccaa ctgctgtatc cgcctgcgcc ttctgcgcc tggaggtca
 660
 ggaactgctt cagatgatga atttgagaat cttagaatta aaggccctaa tgctgtacag
 720
 ctggtgaaga ccacccttt gaagccctca cctctgcctg tcatccctga tactatcaag
 780
 gaagtgatct atgatatgct gaatgctctg gctgcatacc atgctccaga ggaagcagat
 840
 aaatctgata ctaaacctgg gggttatgacc caagaggttg gccagctcct gcaagacatg
 900
 ggtgatgatg tataaccagca gtaccggtca cttacgctg
 939

<210> 4216

<211> 287

<212> PRT

<213> Homo sapiens

<400> 4216

Met Asp Ile Lys Arg Lys Glu Asn Lys Gly Asn Asp Thr Pro Leu Ala
 1 5 10 15
 Leu Glu Ser Thr Asn Thr Glu Lys Glu Thr Ser Leu Glu Glu Thr Lys
 20 25 30
 Ile Gly Glu Ile Leu Ile Gln Gly Leu Thr Glu Asp Met Val Thr Val
 35 40 45
 Leu Ile Arg Ala Cys Val Ser Met Leu Gly Val Pro Val Asp Pro Asp
 50 55 60
 Thr Leu His Ala Thr Leu Cys Phe Cys Leu Arg Val Thr Arg Gly Pro
 65 70 75 80
 Gln Leu Ala Met Met Phe Ala Glu Leu Lys Asn Thr Arg Met Ile Leu
 85 90 95
 Asn Leu Thr Gln Ser Ser Gly Phe Asn Gly Phe Thr Pro Leu Val Thr
 100 105 110
 Leu Leu Leu Arg His Ile Ile Glu Asp Pro Cys Thr Leu Arg His Thr
 115 120 125
 Met Glu Lys Val Val Arg Ser Ala Ala Thr Ser Gly Ala Gly Ser Thr
 130 135 140
 Thr Ser Gly Val Val Ser Gly Ser Leu Gly Ser Arg Glu Ile Asn Tyr

```

145             150             155             160
Ile Leu Arg Val Leu Gly Pro Ala Ala Cys Arg Asn Pro Asp Ile Phe
             165             170             175
Thr Glu Val Ala Asn Cys Cys Ile Arg Ile Ala Leu Pro Ala Pro Arg
             180             185             190
Gly Ser Gly Thr Ala Ser Asp Asp Glu Phe Glu Asn Leu Arg Ile Lys
             195             200             205
Gly Pro Asn Ala Val Gln Leu Val Lys Thr Thr Pro Leu Lys Pro Ser
             210             215             220
Pro Leu Pro Val Ile Pro Asp Thr Ile Lys Glu Val Ile Tyr Asp Met
             225             230             235
Leu Asn Ala Leu Ala Ala Tyr His Ala Pro Glu Glu Ala Asp Lys Ser
             245             250             255
Asp Pro Lys Pro Gly Val Met Thr Gln Glu Val Gly Gln Leu Leu Gln
             260             265             270Met Gly Asp Asp
Val Tyr Gln Gln Tyr Arg Ser Leu Thr Arg
             275             280             285

```

<210> 4217

<211> 619

<212> DNA

<213> Homo sapiens

<400> 4217

```

acacacacac gcacacaaaa ctcagccaca ggctcaccag ggctctctctc aacatgcaca
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catacacaca cacacccctc agtcataggc tcacaagagt ctctcttgtc tctctctcat
120
acatacacac acacacacaa ccagccacag gccacacaaag gtgtctctctc ctttgtccct
180
gtctgtctctc tcgcactcac acacacacat ctcagccaca ggcccaccag agtctgtctg
240
tctctttgtc tctctcactc tctctcacac acatacacct cagccacagg ccacacaggg
300
tctctctctc tgtccctggc tcctctctctc cgcacactcc cacacacaca catacagctc
360
agccacaggc ccacgagggt gtctctctctc ctctctctctc ctcacacaca cacacacaca
420
cacacacgcc tgtgcagctc cacagggggc tggggcagga gacagatctg aatacacata
480
ccaccctgtg ctgtgagtgg ccaactccat ccaacaactg agactttctg ttactggggc
540
aaggttttct gccaaactca cttcccttat aatgaatgaa ttatccctca gaagggtcca
600
cagtcctccc ctggcgcg
619

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<210> 4218

<211> 155

<212> PRT

<213> Homo sapiens

<400> 4218

Met His Thr Tyr Thr His Thr Pro Leu Ser His Arg Leu Thr Arg Val

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      1             5             10             15
Ser Leu Val Ser Leu Ser Tyr Ile His Thr His Thr Gln Pro Ala Thr
      20             25             30
Gly Pro Gln Arg Cys Leu Ser Leu Cys Pro Cys Leu Leu Ser Arg Thr
      35             40             45
His Thr His Thr Ser Gln Pro Gln Ala His Gln Ser Leu Ser Val Ser
      50             55             60
Leu Ser Leu Ser Leu Ser Leu Thr His Ile His Leu Ser His Arg Pro
      65             70             75             80
Thr Arg Val Ser Leu Leu Val Pro Gly Ser Ser Leu Ser His Thr Pro
      85             90             95
Thr His Thr His Thr Ala Gln Pro Gln Ala His Glu Gly Val Ser Leu
      100            105            110
Ser Leu Ser Leu Ser His Thr His Thr His Thr His Thr Pro Val Gln
      115            120            125
Leu His Arg Gly Leu Gly Gln Glu Thr Asp Leu Asn Thr His Thr Thr
      130            135            140
Leu Cys Cys Glu Trp Pro Leu Pro Ser Asn Asn
      145            150            155

```

<210> 4219

<211> 774

<212> DNA

<213> Homo sapiens

<400> 4219

```

ngcggccgcg cacctgctcc cgtcgcccta cagcaagatc acgccccgcg ggaggcccca
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ccgctgcagc agcggccacg gcagcgacaa cagcagcgtg ctgagcgggg agctccccgc
120
ggccatgggg aagacggccc tgttctacca cagcggcggc agcagcggct acgagagcgt
180
gatgcgggac agcgaggcca ccggcagcgc gtcctcggcg caggactcca cgagcgagaa
240
cagcagctcc gtgggcggca ggtgccggag cctcaagacc cgaagaanaac gctccaatcc
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360
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420
aggggccttg gggaaacctt gagattaaa tctnatgaaa tcgatgacgt ggagcgcttg
480
cagcggcgac gagggggtgc cagcaaggag gccatgtgct tcaatgcaaa gctgaagatt
540
ctggaacacc gccagcagag gatcgccgag gtcgcgcgca agtacgagtg gctgatgaag
600
gagctggagg cgaccaaaaca gtatctgatg ctggatccca acaagtggct cagtgaattt
660
gacttgagc aggtttggga gctggattcc ctggagtacc tggaggcact ggagtgtgtg
720
acggagcgcc tggagagcgg tgtcaacttc tgcaaggccc atctcatgat gctc
774

```

<210> 4220

<211> 258
 <212> PRT
 <213> Homo sapiens

<400> 4220
 Xaa Gly Arg Ala Pro Val Ala Leu Gln Gln Asp His Ala Pro
 1 5 10 15
 Ala Glu Ala Pro Pro Leu Gln Gln Arg Pro Arg Gln Arg Gln Gln Gln
 20 25 30
 Arg Ala Glu Arg Gly Ala Pro Ala Gly His Gly Glu Asp Gly Pro Val
 35 40 45
 Leu Pro Gln Arg Arg Gln Gln Arg Leu Arg Glu Arg Asp Ala Gly Gln
 50 55 60
 Arg Gly His Arg Gln Arg Val Leu Gly Ala Gly Leu His Glu Arg Glu
 65 70 75 80
 Gln Gln Leu Arg Gly Arg Gln Val Pro Glu Pro Gln Asp Pro Glu Glu
 85 90 95
 Thr Leu Gln Ser Arg Phe Ser Glu Thr Glu Ala Tyr Pro Ser Thr Ile
 100 105 110
 Pro Gly His Leu Phe Pro Cys Glu Lys Thr Pro Gln Gln His Arg Arg
 115 120 125
 Pro Leu Gly Gly Trp Xaa Pro Leu Arg Ser Ser Pro Arg Gly Leu Gly
 130 135 140
 Glu Pro Leu Arg Leu Lys Ser Xaa Glu Ile Asp Asp Val Glu Arg Leu
 145 150 155 160
 Gln Arg Arg Arg Gly Gly Ala Ser Lys Glu Ala Met Cys Phe Asn Ala
 165 170 175
 Lys Leu Lys Ile Leu Glu His Arg Gln Gln Arg Ile Ala Glu Val Arg
 180 185 190
 Ala Lys Tyr Glu Trp Leu Met Lys Glu Leu Glu Ala Thr Lys Gln Tyr
 195 200 205
 Leu Met Leu Asp Pro Asn Lys Trp Leu Ser Glu Phe Asp Leu Glu Gln
 210 215 220
 Val Trp Glu Leu Asp Ser Leu Glu Tyr Leu Glu Ala Leu Glu Cys Val
 225 230 235 240
 Thr Glu Arg Leu Glu Ser Arg Val Asn Phe Cys Lys Ala His Leu Met
 245 250 255
 Met Leu

<210> 4221
 <211> 789
 <212> DNA
 <213> Homo sapiens

<400> 4221
 aatgtgaaga ggattaaaga ataaagaaaa aacaaaaaag tcttatacta aaataagaaa
 60
 tcagcccat cttggcacag ttctcatgca gaattattgca cccagtgtga actaacgcta
 120
 gaagcttcaa actgtataaa tttaaatgta ttgcatatt ataaaaataa agataaacat
 180
 atacatatatt tacactagtt atggaacagc aatgaacgtc agtcgatccc tctttcacat
 240

ttaacagaac tgaatctga gtgctctaaa tactgccacc tgtactgtaa ctatggctta
 300
 tatgtgcacg gaaaacaaaa tccctgagaa gccattcgac tttttttttt tttctttttt
 360
 tcaagttagcg cgctccttgg aggatcacag ttctgaggtt cagggtgttaa aacatttgct
 420
 ccatgtttct gtccatgctt cccccacaa cccctctccc acctcttccc cagtcttcca
 480
 aaaagcacc tgcaagcacg cgttgctact caagttcaca gaacacgctg ggggtgagtgc
 540
 agaggggtctg ccaggtgcaa aagatggctc aggtgttcag atgctctctt ttctccatgg
 600
 aaattccaca gccacaaacg tcaactggtt ctgtgctttt caccaacatt cttcccttaa
 660
 aaattgggtgc tcctaaagtc acagtttggg tacagtaaaa atgatggcat aaggaaaaga
 720
 agcactatct ttccactta attttccaag aaagtatgaa gatacttgga acaggggctg
 780
 atcacagtc
 789

<210> 4222

<211> 127

<212> PRT

<213> Homo sapiens

<400> 4222

Met	Ala	Tyr	Met	Cys	Thr	Glu	Asn	Lys	Ile	Pro	Glu	Lys	Pro	Phe	Asp
1				5				10					15		
Phe	Phe	Phe	Phe	Ser	Phe	Leu	Gln	Val	Ala	Arg	Ser	Leu	Glu	Asp	His
			20					25				30			
Ser	Ser	Glu	Val	Gln	Val	Val	Lys	His	Leu	Leu	His	Val	Leu	Val	His
			35				40					45			
Ala	Ser	Pro	His	His	Pro	Leu	Pro	Thr	Ser	Ser	Pro	Val	Val	Gln	Lys
			50			55					60				
Ala	Pro	Cys	Lys	His	Ala	Leu	Ser	Leu	Lys	Phe	Thr	Glu	His	Ala	Gly
65				70						75				80	
Val	Ser	Ala	Glu	Gly	Leu	Pro	Gly	Ala	Lys	Asp	Gly	Pro	Gly	Val	Gln
			85					90						95	
Met	Leu	Ser	Phe	Leu	His	Gly	Asn	Ser	Thr	Ala	Thr	Asn	Val	Thr	Gly
			100					105					110		
Phe	Cys	Ala	Phe	His	Gln	His	Ser	Ser	Leu	Lys	Asn	Trp	Cys	Ser	
			115				120						125		

<210> 4223

<211> 852

<212> DNA

<213> Homo sapiens

<400> 4223

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 60
 gaggccgtgg cctatttgca ctcaactcaag atcgtgcaca ggaatctcaa gctggagaac
 120

ctgggtttact acaaccggct gaagaactcg aagattgtca tcagtgaactt ccatctggct
 180
 aagctagaaa atggcctcat caaggagccc tgtgggagccc ccgaagattt tgccecccaa
 240
 ggggaaggcc ggcagcggta tggacgcctt gtggactgct gggccattgg agtcatcatg
 300
 tacatcctgc ttccaggcaa tccaccttcc tatgaggagg tggagaaga tgattatgag
 360
 aaccatgata agaattctctt ccgcaagatc ctggctgggtg actatgagtt tgactctcca
 420
 tattgggatg atatttcgca ggcagccaaa gacctgggtca caaggctgat ggagggtggg
 480
 caagaccagc ggatcactgc agaagaggcc atctcccatg agtggatttc tggcaatgct
 540
 gcttctgata agaacatcaa ggatgggtgct tbtgcccaga ttgaaaagaa ctttgccagg
 600
 gccaaagtga agaaggctgt ccgagtgtacc accctcatga aacggctccg ggcaccagag
 660
 cagtccagca cggctcgagc ccagtcggcc tcagccacag acactgccac ccccggggct
 720
 gcagaccgta gtgccacccc agccacagat ggaagtgtcca cccagccac tgatggcagt
 780
 gtcacccag ccaccgatgg aagcatcact ccagccattg atgggagtgt caccacagcc
 840
 actgacagga gc
 852

<210> 4224

<211> 284

<212> PRT

<213> Homo sapiens

<400> 4224

Ile	Leu	Asp	Gln	Gly	Tyr	Tyr	Ser	Glu	Arg	Asp	Thr	Ser	Asn	Val	Val
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Arg	Gln	Val	Leu	Glu	Ala	Val	Ala	Tyr	Leu	His	Ser	Leu	Lys	Ile	Val
			20					25					30		
His	Arg	Asn	Leu	Lys	Leu	Glu	Asn	Leu	Val	Tyr	Tyr	Asn	Arg	Leu	Lys
		35					40					45			
Asn	Ser	Lys	Ile	Val	Ile	Ser	Asp	Phe	His	Leu	Ala	Lys	Leu	Glu	Asn
		50				55					60				
Gly	Leu	Ile	Lys	Glu	Pro	Cys	Gly	Thr	Pro	Glu	Asp	Phe	Ala	Pro	Gln
65				70					75					80	
Gly	Glu	Gly	Arg	Gln	Arg	Tyr	Gly	Arg	Pro	Val	Asp	Cys	Trp	Ala	Ile
			85					90					95		
Gly	Val	Ile	Met	Tyr	Ile	Leu	Leu	Ser	Gly	Asn	Pro	Pro	Phe	Tyr	Glu
			100					105					110		
Glu	Val	Glu	Glu	Asp	Asp	Tyr	Glu	Asn	His	Asp	Lys	Asn	Leu	Phe	Arg
			115				120					125			
Lys	Ile	Leu	Ala	Gly	Asp	Tyr	Glu	Phe	Asp	Ser	Pro	Tyr	Trp	Asp	Asp
			130				135				140				
Ile	Ser	Gln	Ala	Ala	Lys	Asp	Leu	Val	Thr	Arg	Leu	Met	Glu	Val	Glu
145					150				155					160	
Gln	Asp	Gln	Arg	Ile	Thr	Ala	Glu	Glu	Ala	Ile	Ser	His	Glu	Trp	Ile

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                165                170                175
Ser Gly Asn Ala Ala Ser Asp Lys Asn Ile Lys Asp Gly Val Cys Ala
                180                185                190
Gln Ile Glu Lys Asn Phe Ala Arg Ala Lys Trp Lys Lys Ala Val Arg
                195                200                205
Val Thr Thr Leu Met Lys Arg Leu Arg Ala Pro Glu Gln Ser Ser Thr
                210                215                220
Ala Ala Ala Gln Ser Ala Ser Ala Thr Asp Thr Ala Thr Pro Gly Ala
225                230                235                240
Ala Asp Arg Ser Ala Thr Pro Ala Thr Asp Gly Ser Ala Thr Pro Ala
                245                250                255
Thr Asp Gly Ser Val Thr Pro Ala Thr Asp Gly Ser Ile Thr Pro Ala
                260                265                270
Ile Asp Gly Ser Val Thr Pro Ala Thr Asp Arg Ser
                275                280

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<210> 4225

<211> 470

<212> DNA

<213> Homo sapiens

<400> 4225

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nntgtacaag aaagtgagcc agtcatcgtc aatattcaag tgatggatgc aaatgataac
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acgccaaacct tccttgaaat atcctatgat gtgtatgttt atacagacat gagacctggg
120
gacagggttcc tacagttaac tgcagtcgac gcagacgaag ggtcaaatgg ggagatcaca
180
tatgaaatcc ttgttggggc tcaggggagac ttcatcatca ataaaacaac agggcttacc
240
accatcgctc caggggtgga aatgatagtc gggcggaact acgcactccc ggtccaagca
300
gcggataatg ctccctctgc aaagcaaagg actcccatct gcaactgtgta tattgaagtg
360
cttccaccaa ataatcaaag cctcctctgc tccccacagc tgatgtatag ccttgaaatt
420
agtgaagcca tgagggttgg tgctgtttta ttaaatctac aggcaactga
470

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<210> 4226

<211> 156

<212> PRT

<213> Homo sapiens

<400> 4226

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Xaa Val Gln Glu Ser Glu Pro Val Ile Val Asn Ile Gln Val Met Asp
1         5         10         15
Ala Asn Asp Asn Thr Pro Thr Phe Pro Glu Ile Ser Tyr Asp Val Tyr
20        25        30
Val Tyr Thr Asp Met Arg Pro Gly Asp Arg Val Leu Gln Leu Thr Ala
35        40        45
Val Asp Ala Asp Glu Gly Ser Asn Gly Glu Ile Thr Tyr Glu Ile Leu
50        55        60
Val Gly Ala Gln Gly Asp Phe Ile Ile Asn Lys Thr Thr Gly Leu Ile

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65		70		75		80									
Thr	Ile	Ala	Pro	Gly	Val	Glu	Met	Ile	Val	Gly	Arg	Thr	Tyr	Ala	Leu
				85					90					95	
Pro	Val	Gln	Ala	Ala	Asp	Asn	Ala	Pro	Pro	Ala	Lys	Gln	Arg	Thr	Pro
			100					105					110		
Ile	Cys	Thr	Val	Tyr	Ile	Glu	Val	Leu	Pro	Pro	Asn	Asn	Gln	Ser	Pro
			115				120					125			
Pro	Arg	Phe	Pro	Gln	Leu	Met	Tyr	Ser	Leu	Glu	Ile	Ser	Glu	Ala	Met
			130				135				140				
Arg	Val	Gly	Ala	Val	Leu	Leu	Asn	Leu	Gln	Ala	Thr				
145					150					155					

<210> 4227

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 4227

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120
cattcaaatg catcacaatc actttgtgaa attgttcgcc tgagcagaga ccagatgtta
180
caaattcaga acagtacaga gcccgacccc ctgcttgcca ctctagaaaa gcaagaaatt
240
atagagcagc ttctatcaaa tattttccac aaggagaaaa atgagtcagc catagtcagt
300
gcaatccaga tattgtctgac tttacttgag acacgacgac caacatttga aggccatata
360
gagatctgcc caccaggcat gagccattca gcttgttcag taaacaagag tgttctagaa
420
gccatcagag gaagacttgg atcttttcat gaactctctg tggagccacc caagaaaagt
480
gtgatgaaga ccacatgggg tgtgctggat cctcctgtgg ggaatacccg gttgaatgtc
540
attaggttga tatecagcct gcttcaaacc aataccagca gtataaatgg ggaccttatg
600
gagctgaata gcattggagt catattgaac atgttcttca agtatacatg gaataacttt
660
ttgcatacac aagtggaaat ttgtattgca ctgattcttg caagtctctt tgaacaacaa
720
gaaaatgcc caattaccga tcaagactcc actggtgata atttgttatt aaaacatctt
780
ttccaaaaat gtcaattaat agaacgaata cttgaagcct gggaaatgaa tgagaagaaa
840
caggctgagg gaggaagacg gcatggttac atgggacacc taacgaggat agctaactgt
900
atcgtgcaca gcactgacaa gggccccaac agtgcattag tgcagcagct tatcaaaggt
960
aagttatttg tgaaatttga attacatttt tgttggggtg caggaaggat ttaagggtca
1020
agtagaaatg catgtagcat ttttaatagt gatttgtggg acttctttat atttgacaaa
1080

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ttatgtattt gaatgaggtt cttgagaatg tgtttgaaca ggggtgtttt ttgggttgta
 1140
 tttttatgttc atgtagttac agaccattcc ataagcattg gcaggcttgg ctggattca
 1199

<210> 4228

<211> 298

<212> PRT

<213> Homo sapiens

<400> 4228

Arg His Ser Asn Ala Ser Gln Ser Leu Cys Glu Ile Val Arg Leu Ser
 1 5 10 15
 Arg Asp Gln Met Leu Gln Ile Gln Asn Ser Thr Glu Pro Asp Pro Leu
 20 25 30
 Leu Ala Thr Leu Glu Lys Gln Glu Ile Ile Glu Gln Leu Leu Ser Asn
 35 40 45
 Ile Phe His Lys Glu Lys Asn Glu Ser Ala Ile Val Ser Ala Ile Gln
 50 55 60
 Ile Leu Leu Thr Leu Leu Glu Thr Arg Arg Pro Thr Phe Glu Gly His
 65 70 75 80
 Ile Glu Ile Cys Pro Gly Met Ser His Ser Ala Cys Ser Val Asn
 85 90 95
 Lys Ser Val Leu Glu Ala Ile Arg Gly Arg Leu Gly Ser Phe His Glu
 100 105 110
 Leu Leu Leu Glu Pro Pro Lys Lys Ser Val Met Lys Thr Thr Trp Gly
 115 120 125
 Val Leu Asp Pro Pro Val Gly Asn Thr Arg Leu Asn Val Ile Arg Leu
 130 135 140
 Ile Ser Ser Leu Leu Gln Thr Asn Thr Ser Ser Ile Asn Gly Asp Leu
 145 150 155 160
 Met Glu Leu Asn Ser Ile Gly Val Ile Leu Asn Met Phe Phe Lys Tyr
 165 170 175
 Thr Trp Asn Asn Phe Leu His Thr Gln Val Glu Ile Cys Ile Ala Leu
 180 185 190
 Ile Leu Ala Ser Pro Phe Glu Asn Thr Glu Asn Ala Thr Ile Thr Asp
 195 200 205
 Gln Asp Ser Thr Gly Asp Asn Leu Leu Leu Lys His Leu Phe Gln Lys
 210 215 220
 Cys Gln Leu Ile Glu Arg Ile Leu Glu Ala Trp Glu Met Asn Glu Lys
 225 230 235 240
 Lys Gln Ala Glu Gly Gly Arg Arg His Gly Tyr Met Gly His Leu Thr
 245 250 255
 Arg Ile Ala Asn Cys Ile Val His Ser Thr Asp Lys Gly Pro Asn Ser
 260 265 270
 Ala Leu Val Gln Gln Leu Ile Lys Gly Lys Leu Phe Val Lys Phe Glu
 275 280 285
 Leu His Phe Cys Trp Val Ala Gly Arg Ile
 290 295

<210> 4229

<211> 1612

<212> DNA

<213> Homo sapiens

<400> 4229
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120
ggaacaatga agtcggtcct cacctggaag caccggaagg agcacgcat ccccaactg
180
gtttctgggc ggaacctccc cgggggagcc tggcactcca tcgaaggctc catggtgatc
240
ctgagccaag gccagtggat ggggctcccc gacctggagg tcaaggactg gatgcagaag
300
aagcgaagag gtcttcgcaa cagccgggccc actgccgggg acatgccca ctactacagg
360
gactacgttg tcaagaaggg tctggggcat aacttttgtt ccggtgtgtg agtcacagcc
420
gtggagtggg ggacccccga tcccagcagc tgtggggccc aggaactcag cccctcttc
480
caggtgagcg gcttctcgac caggaaccag gccacgagc ccttctcgct gtggggccgc
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600
gccctgccc tcatccacca tgagctgtct gccttgagg ccgccacaag ggtgggtgctg
660
gtgaccccg cctcagacct tgtcctcacc attggcgagg ggctgtcagc ggccgacgcc
720
gtcctctacg ccgccacta caacatcccg gtgatccatg ccttcgcgcg ggcggtggag
780
gacctgtggc tgggtgttaa ccagctgccc aagatgtctg accccagta ccacaagggt
840
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900
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960
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gacctctcct tctgcctgg ggcaggggct gactttgcag tggatcctga ccagccgctg
1080
agcgccaaga ggaaccccat tgacgtggac cccttcacct accagagcac ccgccaggag
1140
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1200
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1260
gccagacccc ctggctccca ggcctgaga ggacagagat gaccacatcc ctgctggatg
1320
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1380
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1440
agaccagtgt gtgaggtggt aacagcgccc gcagcagggg gttggcctag acctgggatt
1500
tgtggggaaa gctgctggtg tgaccagctg agcaccagc caggagacct gcagccctgc
1560

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1612

<210> 4230

<211> 417

<212> PRT

<213> Homo sapiens

<400> 4230

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Leu	Glu	Gly	Arg	Ser	Gln	Ser	Pro	Val	Ala	Leu	Leu	Phe	Asp	Ala	Leu
			20					25					30		
Leu	Arg	Pro	Asp	Thr	Asp	Phe	Gly	Gly	Asn	Met	Lys	Ser	Val	Leu	Thr
			35				40					45			
Trp	Lys	His	Arg	Lys	Glu	His	Ala	Ile	Pro	His	Val	Val	Leu	Gly	Arg
	50					55				60					
Asn	Leu	Pro	Gly	Gly	Ala	Trp	His	Ser	Ile	Glu	Gly	Ser	Met	Val	Ile
	65				70				75					80	
Leu	Ser	Gln	Gly	Gln	Trp	Met	Gly	Leu	Pro	Asp	Leu	Glu	Val	Lys	Asp
			85					90						95	
Trp	Met	Gln	Lys	Lys	Arg	Arg	Gly	Leu	Arg	Asn	Ser	Arg	Ala	Thr	Ala
			100					105					110		
Gly	Asp	Ile	Ala	His	Tyr	Tyr	Arg	Asp	Tyr	Val	Val	Lys	Lys	Gly	Leu
		115					120					125			
Gly	His	Asn	Phe	Val	Ser	Gly	Ala	Val	Val	Thr	Ala	Val	Glu	Trp	Gly
						135				140					
Thr	Pro	Asp	Pro	Ser	Ser	Cys	Gly	Ala	Gln	Asp	Ser	Ser	Pro	Leu	Phe
					150					155				160	
Gln	Val	Ser	Gly	Phe	Leu	Thr	Arg	Asn	Gln	Ala	Gln	Gln	Pro	Phe	Ser
				165					170					175	
Leu	Trp	Ala	Arg	Asn	Val	Val	Leu	Ala	Thr	Gly	Thr	Phe	Asp	Ser	Pro
			180					185					190		
Ala	Arg	Leu	Gly	Ile	Pro	Gly	Glu	Ala	Leu	Pro	Phe	Ile	His	His	Glu
			195				200					205			
Leu	Ser	Ala	Leu	Glu	Ala	Ala	Thr	Arg	Val	Gly	Ala	Val	Thr	Pro	Ala
			210			215					220				
Ser	Asp	Pro	Val	Leu	Ile	Ile	Gly	Ala	Gly	Leu	Ser	Ala	Ala	Asp	Ala
					230				235					240	
Val	Leu	Tyr	Ala	Arg	His	Tyr	Asn	Ile	Pro	Val	Ile	His	Ala	Phe	Arg
				245				250					255		
Arg	Ala	Val	Asp	Asp	Pro	Gly	Leu	Val	Phe	Asn	Gln	Leu	Pro	Lys	Met
			260					265					270		
Leu	Tyr	Pro	Glu	Tyr	His	Lys	Val	His	Gln	Met	Met	Arg	Glu	Gln	Ser
			275				280					285			
Ile	Leu	Ser	Pro	Ser	Pro	Tyr	Glu	Gly	Tyr	Arg	Ser	Leu	Pro	Arg	His
			290			295					300				
Gln	Leu	Leu	Cys	Phe	Lys	Glu	Asp	Cys	Gln	Ala	Val	Phe	Gln	Asp	Leu
					310					315				320	
Glu	Gly	Val	Glu	Lys	Val	Phe	Gly	Val	Ser	Leu	Val	Leu	Val	Leu	Ile
				325					330					335	
Gly	Ser	His	Pro	Asp	Leu	Ser	Phe	Leu	Pro	Gly	Ala	Gly	Ala	Asp	Phe
			340					345				350			
Ala	Val	Asp	Pro	Asp	Gln	Pro	Leu	Ser	Ala	Lys	Arg	Asn	Pro	Ile	Asp

	355		360		365										
Val	Asp	Pro	Phe	Thr	Tyr	Gln	Ser	Thr	Arg	Gln	Glu	Gly	Leu	Tyr	Ala
	370					375				380					
Met	Gly	Pro	Leu	Ala	Gly	Asp	Asn	Phe	Val	Arg	Phe	Val	Gln	Gly	Gly
385					390					395				400	
Ala	Leu	Ala	Val	Ala	Ser	Ser	Leu	Leu	Arg	Lys	Glu	Thr	Arg	Lys	Pro
			405						410					415	

Pro

<210> 4231
 <211> 1588
 <212> DNA
 <213> Homo sapiens

<400> 4231
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 120
 gagctggaaa atctcaagag caaactcgta gaagtaattg aagaagtaaa taaagttaaa
 180
 caagaaaaga ctgttttaaa ttcagaagtt cttgaacaga gaaaagtctt agaaaaatgc
 240
 aatagagtgt ccatgttagc tgtagaagag tatgaggaga tgcaagtaaa cctggagctg
 300
 gagaaggacc ttcgaaagaa agcagagtca ttgcccag agatgttctc tgagccaaac
 360
 cagggtaaaa agacaaagcc cccctttggg cggcagagtt ccatccttga tcagcagtta
 420
 gcttttagacg aaaatgcaaa actcaccag caacttgaag aagagagaat tcagcatcaa
 480
 caaaaggtca aagaattaga agagcaacta gaaaatgaaa cactccacaa agaaatacac
 540
 aacctcaaac agcaactgga gcttctagag gaagataaaa aggaattgga attgaaatat
 600
 cagaattctg aagagaaagc cagaaattta aagcactctg ttgatgaact ccagaaacga
 660
 gtgaaccagt ctgagaattc agtacctcca ccacctctc ctccaccacc acttccccct
 720
 ccacctccca atcctatccg atccctcatg tccatgatcc ggaaacgac ccaccccagt
 780
 ggcagtgggt ctaagaaaaa aaaggcaact caaccagaaa caactgaaga agtcacagat
 840
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 900
 cccgttaatc agacagccag accgaagaca aagccagaat cttcgaaagg ctgcgaaagt
 960
 gcagtggatg aactaaaagg aatactgggg aacttaaca aatccactag ttcaagaagc
 1020
 ttaaaaatccc ttgacctga aaacagtga actgagttag aaaggatttt gcgtgcgaga
 1080
 aaggtagacag cagaagcaga tagcagtagt ccaactggga tattagccac ctacagatgc
 1140

aaatccatgc cagtgttggg ttctgtatcc agtgtaacaa aaacagcctt gaacaagaaa
 1200
 actctggagg cagaattcaa cagcccgctc cccccaacac ctgagccagg tgaagggccc
 1260
 cgtaaatgg aaggatgcac aagttccaag gttacgttcc agtaagtaac gatgctcttt
 1320
 actaagtggg gtatagaaga atctgtaatg actaacttgt gtgtttcttt gattgttttc
 1380
 ctttagagag attttgattg gctcgccggt aaattctctt cttcttttca tttgatgggc
 1440
 cagctttttc attctagcct cctagataag agatctaatt aagatccaaa gcaagtacca
 1500
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 1560
 attgatctgg atgatacaga ctctgcag
 1588

<210> 4232

<211> 434

<212> PRT

<213> Homo sapiens

<400> 4232

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Cys	Gln	Lys	Gln	Ile	Lys	Glu	Leu	Arg	Asp	Gln	Ile	Val	Ser	Val	Gln
			20					25				30			
Glu	Glu	Lys	Lys	Ile	Leu	Ala	Ile	Glu	Leu	Glu	Asn	Leu	Lys	Ser	Lys
		35				40					45				
Leu	Val	Glu	Val	Ile	Glu	Glu	Val	Asn	Lys	Val	Lys	Gln	Glu	Lys	Thr
		50				55				60					
Val	Leu	Asn	Ser	Glu	Val	Leu	Glu	Gln	Arg	Lys	Val	Leu	Glu	Lys	Cys
65				70						75				80	
Asn	Arg	Val	Ser	Met	Leu	Ala	Val	Glu	Glu	Tyr	Glu	Glu	Met	Gln	Val
				85				90						95	
Asn	Leu	Glu	Leu	Glu	Lys	Asp	Leu	Arg	Lys	Lys	Ala	Glu	Ser	Phe	Ala
				100				105						110	
Gln	Glu	Met	Phe	Leu	Glu	Pro	Asn	Gln	Gly	Lys	Lys	Thr	Lys	Pro	Pro
				115				120						125	
Phe	Gly	Arg	Gln	Ser	Ser	Ile	Leu	Asp	Gln	Gln	Leu	Ala	Leu	Asp	Glu
				130				135						140	
Asn	Ala	Lys	Leu	Thr	Gln	Gln	Leu	Glu	Glu	Glu	Arg	Ile	Gln	His	Gln
145				150						155				160	
Gln	Lys	Val	Lys	Glu	Leu	Glu	Glu	Gln	Leu	Glu	Asn	Glu	Thr	Leu	His
				165				170						175	
Lys	Glu	Ile	His	Asn	Leu	Lys	Gln	Gln	Leu	Glu	Leu	Leu	Glu	Glu	Asp
				180				185						190	
Lys	Lys	Glu	Glu	Glu	Leu	Lys	Tyr	Gln	Asn	Ser	Glu	Glu	Lys	Ala	Arg
				195				200						205	
Asn	Leu	Lys	His	Ser	Val	Asp	Glu	Leu	Gln	Lys	Arg	Val	Asn	Gln	Ser
				210				215						220	
Glu	Asn	Ser	Val	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro
225				230							235			240	
Pro	Pro	Pro	Asn	Pro	Ile	Arg	Ser	Leu	Met	Ser	Met	Ile	Arg	Lys	Arg

[illegible]

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<210> 4233
<211> 2827
<212> DNA
<213> Homo sapiens
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180	cctatgtact	ctctggatcg	aatatttgtc	ggatttcgaa	cacgaagtc	gatgctgtg
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<211> 833

<212> PRT

<213> Homo sapiens

<400> 4234

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Gln	Cys	Asp	Arg	Arg	Leu	Thr	Leu	Gln	Gln	Lys	Glu	His	Glu	Gln	Lys
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Ile His Ser Ser Leu Ala Pro Pro Ser Gly His Met Leu Gly Asn Glu
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        770                775                780
Val Thr Pro Val Lys Leu Cys Arg Lys Glu Leu Arg Gln Ile Ser Ala
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<210> 4235

<211> 971

<212> DNA

<213> Homo sapiens

<400> 4235

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<211> 198

<212> PRT

<213> Homo sapiens

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 Ser Arg Gly Phe Glu Asn Leu Val Pro Tyr Thr Ser Thr Val Ser Val
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 130 135 140
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<211> 560

<212> DNA

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<211> 860

<212> PRT

<213> Homo sapiens

<400> 4240

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Pro	Arg	Pro	Ser	Ile	Lys	Lys	Ala	Gln	Asn	Ser	Gln	Ala	Ala	Arg	Gln
				85					90					95	
Ala	Gln	Glu	Ala	Gly	Pro	Lys	Pro	Asn	Leu	Val	Pro	Gly	Gly	Val	Pro
				100				105						110	
Asp	Pro	Pro	Gly	Leu	Glu	Ala	Ala	Lys	Glu	Val	Met	Val	Lys	Ala	Thr
		115					120					125			
Gly	Pro	Leu	Glu	Asp	Thr	Pro	Ala	Met	Glu	Pro	Asn	Pro	Ser	Ala	Val
		130				135						140			
Glu	Val	Asp	Pro	Ile	Arg	Lys	Pro	Glu	Val	Pro	Thr	Gly	Asp	Val	Glu
145					150					155					160
Glu	Glu	Arg	Pro	Pro	Arg	Asp	Val	His	Ser	Glu	Arg	Ala	Ala	Gly	Glu
				165					170					175	
Pro	Glu	Ala	Gly	Ser	Asp	Tyr	Val	Lys	Phe	Ser	Lys	Glu	Lys	Tyr	Ile
			180					185					190		
Leu	Asp	Ser	Ser	Pro	Glu	Lys	Leu	His	Lys	Glu	Leu	Glu	Glu	Glu	Leu
		195					200					205			
Lys	Leu	Ser	Ser	Thr	Asp	Leu	Arg	Ser	His	Ala	Trp	Tyr	His	Gly	Arg
		210				215					220				
Ile	Pro	Arg	Glu	Val	Ser	Glu	Thr	Leu	Val	Gln	Arg	Asn	Gly	Asp	Phe
225					230					235					240
Leu	Ile	Arg	Asp	Ser	Leu	Thr	Ser	Leu	Gly	Asp	Tyr	Val	Leu	Thr	Cys
				245					250					255	
Arg	Trp	Arg	Asn	Gln	Ala	Leu	His	Phe	Lys	Ile	Asn	Lys	Val	Val	Val
			260					265					270		
Lys	Ala	Gly	Glu	Ser	Tyr	Thr	His	Ile	Gln	Tyr	Leu	Phe	Glu	Gln	Glu
		275					280					285			
Ser	Phe	Asp	His	Val	Pro	Ala	Leu	Val	Arg	Tyr	His	Val	Gly	Ser	Arg
		290				295					300				
Lys	Ala	Val	Ser	Glu	Gln	Ser	Gly	Ala	Ile	Ile	Tyr	Cys	Pro	Val	Asn
305				310						315					320
Arg	Thr	Phe	Pro	Leu	Arg	Tyr	Leu	Glu	Ala	Ser	Tyr	Gly	Leu	Gly	Gln
			325						330					335	
Gly	Ser	Ser	Lys	Pro	Ala	Ser	Pro	Val	Ser	Pro	Ser	Gly	Pro	Lys	Gly
			340					345					350		
Ser	His	Met	Lys	Arg	Arg	Ser	Val	Thr	Met	Thr	Asp	Gly	Leu	Thr	Ala
		355													

435 440 445
 Pro Gln Leu Cys Pro Gly Ser Ala Pro Lys Thr His Gly Glu Ser Asp
 450 455 460
 Lys Gly Pro His Thr Ser Pro Ser His Thr Leu Gly Lys Ala Ser Pro
 465 470 475 480
 Ser Pro Ser Leu Ser Ser Tyr Ser Asp Pro Asp Ser Gly His Tyr Cys
 485 490 495
 Gln Leu Gln Pro Pro Val Arg Gly Ser Arg Glu Trp Ala Ala Thr Glu
 500 505 510
 Thr Ser Ser Gln Gln Ala Arg Ser Tyr Gly Glu Arg Leu Lys Glu Leu
 515 520 525
 Ser Glu Asn Gly Ala Pro Glu Gly Asp Trp Gly Lys Thr Phe Thr Val
 530 535 540
 Pro Ile Val Glu Val Thr Ser Ser Phe Asn Pro Ala Thr Phe Gln Ser
 545 550 555 560
 Leu Leu Ile Pro Arg Asp Asn Arg Pro Leu Glu Val Gly Leu Leu Arg
 565 570 575
 Lys Val Lys Glu Leu Leu Ala Glu Val Asp Ala Arg Thr Leu Ala Arg
 580 585 590
 His Val Thr Lys Val Asp Cys Leu Val Ala Arg Ile Leu Gly Val Thr
 595 600 605
 Lys Glu Met Gln Thr Leu Met Gly Val Arg Trp Gly Met Glu Leu Leu
 610 615 620
 Thr Leu Pro His Gly Arg Gln Leu Arg Leu Asp Leu Leu Glu Arg Phe
 625 630 635 640
 His Thr Met Ser Ile Met Leu Ala Val Asp Ile Leu Gly Cys Thr Gly
 645 650 655
 Ser Ala Glu Glu Arg Ala Ala Leu Leu His Lys Thr Ile Gln Leu Ala
 660 665 670
 Ala Glu Leu Arg Gly Thr Met Gly Asn Met Phe Ser Phe Ala Ala Val
 675 680 685
 Met Gly Ala Leu Asp Met Ala Gln Ile Ser Arg Leu Glu Gln Thr Trp
 690 695 700
 Val Thr Leu Arg Gln Arg His Thr Glu Gly Ala Ile Leu Tyr Glu Lys
 705 710 715 720
 Lys Leu Lys Pro Phe Leu Lys Ser Leu Asn Glu Gly Lys Glu Gly Pro
 725 730 735
 Pro Leu Ser Asn Thr Thr Phe Pro His Val Leu Pro Leu Ile Thr Leu
 740 745 750
 Leu Glu Cys Asp Ser Ala Pro Pro Glu Gly Pro Glu Pro Trp Gly Ser
 755 760 765
 Thr Glu His Gly Val Glu Val Val Leu Ala His Leu Glu Ala Ala Arg
 770 775 780
 Thr Val Ala His His Gly Gly Leu Tyr His Thr Asn Ala Glu Val Lys
 785 790 795 800
 Leu Gln Gly Phe Gln Ala Arg Pro Glu Leu Leu Glu Val Phe Ser Thr
 805 810 815
 Glu Phe Gln Met Arg Leu Leu Trp Gly Ser Gln Gly Ala Ser Ser Ser
 820 825 830
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 835 840 845
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<210> 4241
 <211> 479
 <212> DNA
 <213> Homo sapiens

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 aagatggacc tgttgcaagt gatccaaagc aaaactcaga gcgacggctc caccctgcag
 180
 cagggtctct tggagttctt cagctgcttg tacgagatcc aggaggagga gtttatccag
 240
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 300
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 360
 gccacctaca gcgcggacgg ggaagaccgc gcgaggtgct cgcaggagcg cacacgtgtg
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<210> 4242
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 4242
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 Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu Gln Trp Ile
 35 40 45
 Gln Ser Lys Thr Gln Ser Asp Gly Ser Thr Leu Gln Gln Gly Ser Leu
 50 55 60
 Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu Phe Ile Gln
 65 70 75 80
 Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn Ile Ala Ser
 85 90 95
 Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg Cys Arg Ser
 100 105 110
 Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala Asp Gly Glu
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 Asp Arg Ala Arg Cys Pro Gln Glu Arg Thr Arg Cys Trp Cys Ser Tyr
 130 135 140
 Gln Arg Gly Pro Phe Cys Trp Thr Pro Thr Val Asn Ile Trp Gln
 145 150 155

<210> 4243
 <211> 3159
 <212> DNA
 <213> Homo sapiens

<400> 4243
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tgccactgcc gccctgccgg ggccatgttc gctctgggct tgcctctctt ggtgtcttgg
120
gtggcctcgg tegagagcca tctgggggtt ctggggccca agaacgtctc gcagaaagac
180
gccgagtttg agcgcaccta cgtggagcag gtcaacagcg agctgggtcaa catctacacc
240
ttcaaccata ctgtgacccg caacaggaca gaggcggtgc gtgtgtctgt gaacgtcctg
300
aacaagcaga agggggcgcc gttgtgttt gtggtccgc agaaggaggc tgtgtgttcc
360
ttccagggtc ccctaattct gcgagggatg ttccagcgca agtacctcta caaaaagtg
420
gaacgaacc tgtgtcagcc cccaccaag aatgagtcgg agattcagtt cttctacgtg
480
gatgtgtcca cctgtcacc agtcaacacc acataccagc tcggggtcag ccgcatggac
540
gattttgtgc tcaggactgg ggagcagttc agcttcaata ccacagcagc acagccccag
600
tacttcaagt atgagttccc tgaaggcgtg gactcggtaa ttgtcaaggt gacctccaac
660
aaggccttcc cctgtcagt catctccatt caggatgtgc tgtgtcctgt ctatgacctg
720
gacaacaacg tagccttcac cggcatgtac cagacgatga ccaagaaggc ggccatcacc
780
gtacagcgca aagacttccc cagcaacagc ttttatgtgg tgggtggtgg gaagaccgaa
840
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900
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1020
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1080
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1140
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1200
accgatggtc tgggtgacag cgctggcact ggggacctct cttacgggta ccaggggcac
1260
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1320
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1380
gatgactacg acacattgac cgacatcgat tccgacaaga atgtcattcg caccaagcaa
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1500
atctacttct ggaacattgc caccattgct gtcttctatg cccttctctg ggtgcagctg
1560

gtgatcacct accagacggt ggtgaatgtc acaggggaatc aggacatctg ctactacaac
1620
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1860
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1920
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1980
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2040
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2100
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2160
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2220
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2700
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2760
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2820
ttcaggcaag ttctgtgtta gtcatgcaca cacataccta tgaaaccttg aagtttacia
2880
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2940
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3000
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3060
gtgggtctgg atcttttctc agagcgtctc catgctatgg ttgcatttcc gttttctatg
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3159

<210> 4244
 <211> 849
 <212> PRT
 <213> Homo sapiens

<400> 4244
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 35 40 45
 Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
 50 55 60
 Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
 65 70 75 80
 Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
 85 90 95
 Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
 100 105 110
 Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
 115 120 125
 Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
 130 135 140
 Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
 145 150 155 160
 Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
 165 170 175
 Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
 180 185 190
 Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
 195 200 205
 Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
 210 215 220
 Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 225 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
 245 250 255
 Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
 260 265 270
 Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
 275 280 285
 Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
 290 295 300
 Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
 305 310 315 320
 Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
 325 330 335
 Glu Ser Ala Ser Leu Leu Gly His Pro Arg Val Leu Ala Asp Ser Phe
 340 345 350
 Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn
 355 360 365
 Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp

370	375	380
Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro		
385	390	395
Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu		
	405	410
Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu		
	420	425
Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile		
	435	440
Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys		
	450	455
Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr		
	465	470
Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr		
	485	490
Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn		
	500	505
Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile		
	515	520
Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile		
	530	535
Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp		
	545	550
Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr		
	565	570
Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr		
	580	585
His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met		
	595	600
Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His		
	610	615
Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile		
	625	630
Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr		
	645	650
Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu		
	660	665
Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly		
	675	680
Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln		
	690	695
Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly		
	705	710
Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro		
	725	730
Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu		
	740	745
Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg		
	755	760
Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp		
	770	775
Gly Phe Ala Leu Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys		
	785	790
Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp		
	795	800

[illegible]

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<210> 4245
<211> 909
<212> DNA
<213> Homo sapiens
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120						
ctcagggggcc	agcttgaggga	gcaaggcccg	cagctgcagg	ctgctgaggga	agctgtggag	
180						
aaagctgaagg	ccaccaagc	agacatggga	gagaagctga	gctgcactag	caaccatctt	
240						
gcagagtgtcc	aggcgcccat	gctgaggaag	gacaaggagg	gggctgccct	gcgtgaagac	
300						
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360						
aaactctctgc	aggaggtgac	aaatcgtgag	aggaatgacc	agaagatgct	tctgtgacctg	
420						
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480						
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540						
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<210> 4246
<211> 303
<212> PRT
<213> Homo sapiens
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<400> 4246
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Asn Ala Gly Glu Glu Cys Lys Ser Leu Arg Gly Gln Leu Glu Glu Gln			
35		40	45
Gly Arg Gln Leu Gln Ala Ala Glu Glu Ala Val Glu Lys Leu Lys Ala			
50		55	60
Thr Gln Ala Asp Met Gly Glu Lys Leu Ser Cys Thr Ser Asn His Leu			
65		70	75
Ala Glu Cys Gln Ala Ala Met Leu Arg Lys Asp Lys Glu Gly Ala Ala			
85		90	95
Leu Arg Glu Asp Leu Glu Arg Thr Gln Lys Glu Leu Glu Lys Ala Thr			
100		105	110
Thr Lys Ile Gln Glu Tyr Tyr Asn Lys Leu Cys Gln Glu Val Thr Asn			
115		120	125
Arg Glu Arg Asn Asp Gln Lys Met Leu Ala Asp Leu Asp Asp Leu Asn			
130		135	140
Arg Thr Lys Lys Tyr Leu Glu Glu Arg Leu Ile Glu Leu Leu Arg Asp			
145		150	155
Lys Asp Ala Leu Trp Gln Lys Ser Asp Ala Leu Glu Phe Gln Gln Lys			
165		170	175
Leu Ser Ala Glu Glu Arg Trp Leu Gly Asp Thr Glu Ala Asn His Cys			
180		185	190
Leu Asp Cys Lys Arg Glu Phe Ser Trp Met Val Arg Arg His His Cys			
195		200	205
Arg Ile Cys Gly Arg Ile Phe Cys Tyr Tyr Cys Cys Asn Asn Tyr Val			
210		215	220
Leu Ser Lys His Gly Gly Lys Lys Glu Arg Cys Cys Arg Ala Cys Phe			
225		230	235
Gln Lys Leu Ser Glu Gly Pro Gly Ser Pro Asp Ser Ser Gly Ser Gly			
245		250	255
Thr Ser Gln Gly Glu Leu Ser Pro Ala Leu Ser Pro Ala Ser Pro Gly			
260		265	270
Pro Gln Ala Thr Gly Gly Gln Gly Ala Asn Thr Asp Tyr Arg Pro Pro			
275		280	285
Asp Asp Ala Val Phe Asp Ile Ile Thr Asp Glu Glu Leu Cys Gln			
290		295	300

<210> 4247

<211> 5755

<212> DNA

<213> Homo sapiens

<400> 4247

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180
gggcgccaca cactcggcag ccgagccgc ggtagccgca gcgggatgga ggcggcgcg
240
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300

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360
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540
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660
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720
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1320
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<210> 4248

<211> 1297

<212> PRT

<213> Homo sapiens

<400> 4248

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Thr	Glu	Arg	Pro	Ala	Gly	Arg	Pro	Gly	Ala	Pro	Leu	Val	Arg	Thr	Gly
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Leu	Leu	Leu	Leu	Ser	Thr	Trp	Val	Leu	Ala	Gly	Ala	Glu	Ile	Thr	Trp
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Asp	Ala	Thr	Gly	Gly	Pro	Gly	Arg	Pro	Ala	Ala	Pro	Ala	Ser	Arg	Pro
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Pro	Ala	Leu	Ser	Pro	Leu	Ser	Pro	Arg	Ala	Val	Ala	Ser	Gln	Trp	Pro
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Glu	Glu	Leu	Ala	Ser	Ala	Arg	Arg	Ala	Ala	Val	Leu	Gly	Arg	Arg	Ala
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Gly	Pro	Glu	Leu	Leu	Pro	Gln	Gln	Gly	Gly	Gly	Arg	Gly	Gly	Glu	Met
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Gln	Val	Glu	Ala	Gly	Gly	Thr	Ser	Pro	Ala	Gly	Glu	Arg	Arg	Gly	Arg
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Gly	Ile	Pro	Ala	Pro	Ala	Lys	Leu	Gly	Gly	Ala	Arg	Arg	Ser	Arg	Arg
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Glu Glu Val Lys Ala	Pro Arg Ala Gly Gly	Ser Ala Ala Glu Asp Leu
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Arg Leu Pro Ser Thr	Ser Phe Ala Leu Thr	Gly Asp Ser Ala His Asn
260	265	270
Gln Ala Met Val His	Trp Ser Gly His Asn Ser	Ser Val Ile Leu Ile
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Leu Thr Lys Leu Tyr	Asp Phe Asn Leu Gly	Ser Val Thr Glu Ser Ser
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Leu Trp Arg Ser Thr	Asp Tyr Gly Thr Thr	Tyr Glu Lys Leu Asn Asp
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Lys Val Gly Leu Lys	Thr Val Leu Ser Tyr	Leu Tyr Val Asn Pro Thr
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Asn Lys Arg Lys Ile	Met Leu Leu Ser Asp	Pro Glu Met Glu Ser Ser
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Ile Leu Ile Ser Ser	Asp Glu Gly Ala Thr	Tyr Gln Lys Tyr Arg Leu
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Thr Phe Tyr Ile Gln	Ser Leu Leu Phe His	Pro Lys Gln Glu Asp Trp
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Val Leu Ala Tyr Ser	Leu Asp Gln Lys Leu Tyr	Ser Ser Met Asp Phe
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Gly Arg Arg Trp Gln	Leu Met His Glu Arg	Ile Thr Pro Asn Arg Phe
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Glu Val Arg Thr Thr	Asp Gly Tyr Ala His	Tyr Leu Thr Cys Arg Ile
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Gln Glu Cys Ala Glu	Thr Thr Arg Ser Gly	Pro Phe Ala Arg Ser Ile
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Thr Thr Ser Gly Arg	Ala Ser Tyr Tyr Val	Ser Tyr Arg Arg Glu Ala
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Phe Ala Gln Ile Lys	Leu Pro Lys Tyr Ser	Leu Pro Lys Asp Met His
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Ile Ile Ser Thr Asp	Glu Asn Gln Val Phe	Ala Val Gln Glu Trp
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Asn Gln Asn Asp Thr	Tyr Asn Leu Tyr Ile	Ser Asp Thr Arg Gly Ile
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Tyr Phe Thr Leu Ala	Met Glu Asn Ile Lys	Ser Ser Arg Gly Leu Met
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Gly Asn Ile Ile Ile	Glu Leu Tyr Glu Val	Ala Gly Ile Lys Gly Ile
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Phe Leu Ala Asn Lys	Lys Val Asp Asp Gln	Val Lys Thr Tyr Ile Thr
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Tyr Asn Lys Gly Arg	Asp Trp Arg Leu Leu	Gln Ala Pro Asp Val Asp
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Ser Lys Glu Thr Ala	Pro Gly Leu Val Val	Ala Thr Gly Asn Ile Gly

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Pro Pro Lys Asn Leu Thr Glu Arg Arg Lys Gly Asn Glu Gly Asp Leu
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<211> 553

<212> DNA

<213> Homo sapiens

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<400> 4250

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<212> DNA

<213> Homo sapiens

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 agacagcctc tggg
 1574

<210> 4252

<211> 352

<212> PRT

<213> Homo sapiens

<400> 4252

Met Gly Val Gly Arg Gly Pro Val Glu Pro Ile Thr Ser Leu His Ile
 1 5 10 15
 Thr Asp Pro Asp Pro Glu Ser Gln Glu Leu Gln Ile Gly Gly Thr Cys
 20 25 30
 Pro Asp Ile Thr Lys Arg Tyr Leu Arg Leu Thr Cys Ala Pro Asp Pro
 35 40 45
 Ser Thr Val Arg Pro Val Ala Val Leu Lys Lys Ser Leu Cys Met Val
 50 55 60
 Lys Cys His Trp Lys Glu Lys Gln Asp Tyr Ala Phe Ala Cys Glu Gln

```

65              70              75              80
Met Lys Ser Ile Arg Gln Asp Leu Thr Val Gln Gly Ile Arg Thr Glu
              85              90              95
Phe Thr Val Glu Val Tyr Glu Thr His Ala Arg Ile Ala Leu Glu Lys
              100              105              110
Gly Asp His Glu Glu Phe Asn Gln Cys Gln Thr Gln Leu Lys Ser Leu
              115              120              125
Tyr Ala Glu Asn Leu Pro Gly Asn Val Gly Glu Phe Thr Ala Tyr Arg
              130              135              140
Ile Leu Tyr Tyr Ile Phe Thr Lys Asn Ser Gly Asp Ile Thr Thr Glu
              145              150              155              160
Leu Ala Tyr Leu Thr Arg Glu Leu Lys Ala Asp Pro Cys Val Ala His
              165              170              175
Ala Leu Ala Leu Arg Thr Ala Trp Ala Leu Gly Asn Tyr His Arg Phe
              180              185              190
Phe Arg Leu Tyr Cys His Ala Pro Cys Met Ser Gly Tyr Leu Val Asp
              195              200              205
Lys Phe Ala Asp Arg Glu Arg Lys Val Ala Leu Lys Ala Met Ile Lys
              210              215              220
Thr Tyr Val Val Pro Ser Ser Leu Leu Pro Leu Leu Phe Pro Ser Phe
              225              230              235              240
Arg Leu Ala Pro Pro Leu Arg Pro Ala Pro Gly Arg Arg Pro Pro Pro
              245              250              255
Ala Pro Asn Pro Cys Pro Gly Pro Cys Phe Pro Ile Ile Phe Leu His
              260              265              270
Ser Ala Leu Pro Ser Pro Val Pro Leu Ala Leu Leu Val Gly His Leu
              275              280              285
Cys Val Pro Gly His Ser Ser Pro Ser Pro His Cys Ser Gln Leu Thr
              290              295              300
Ala Ser Gly Ala Ser Ser Pro Pro His Leu Cys Val Ser Ser Ser Cys
              305              310              315              320
Ser Leu Leu Pro Gly Pro Pro Ser Ser Leu Leu Ala Leu Gly Phe Leu
              325              330              335
Arg Thr Leu Arg Ser Leu Leu Ser Gln Leu Val Ala Val Leu Pro Pro
              340              345              350

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<210> 4253

<211> 1287

<212> DNA

<213> Homo sapiens

<400> 4253

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nntacggctg cgagaagaca cagactgtgc aacccccaaa gcaggtctcc tcaactcaccg
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ggatagatag aactatcggc cccaattcct cagccctacc tgcaaccacc gcttgccatg
120
gtttccttgt ggggtgaggg tactttcccg cccctgtgtt tcgggcttgc ccacgtggct
180
tgctctggcc atggaatgaa gcagaaacga aagcctgccca gttctgagcc tatgcggaa
240
gacgccttgg ggggttccgc ggtccctgtg cgcttccacc ttcaccaga aggacttctc
300
tggtgcagcc gctgcttctt cagccacggc ccaaaaggat cggagccccc tggccgatcc
360

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gcaggctctgc agggagccac agagcgcagc ggccggccca gcgttcaagc ccaagcacag
 420
 gccctgcgaga accttgttcc agccaccgtt tgggatggtt gattaggact tgttgcatgtg
 480
 gcggtagctc accaatccag tgcgtgcacc cgctccttta ttaggtata gagccagtgg
 540
 ctccacaggg gacctgatac aacagtgcgt taaataagga gcatattgag ctctcatgtc
 600
 gtaagccagt ggagaagtcc agggctagt tgggggctcc ggcgggggct gtggccccc
 660
 tccgcatgga gcctcccat ggttcacagg tctcagctct cgagaccctt gccctgcga
 720
 gcccgaaagg tccacagggc ggccgagac cctctttcga acgccatcct cttaaaggcg
 780
 tggaacaagg ttcttgccag cctgtgcttg ggcttgaacg ctggggccgg cgctgcgct
 840
 ctgtggctcc ctgtaggcct gcggatcggc cagggggctc cgttctttt gggcgaggc
 900
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 960
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 1020
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 1080
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 1140
 tctatcccg tgagtggga gacctgttt gagggttgca caactggat ctgcttttac
 1200
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 1260
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 1287

<210> 4254

<211> 114

<212> PRT

<213> Homo sapiens

<400> 4254

Met Val Ser Leu Trp Val Glu Gly Thr Phe Pro Pro Pro Gly Phe Gly
 1 5 10 15
 Leu Ala His Val Ala Cys Ser Gly His Gly Met Lys Gln Lys Arg Lys
 20 25 30
 Pro Ala Ser Ser Glu Pro Met Pro Glu Asp Ala Leu Gly Gly Ser Ala
 35 40 45
 Val Pro Val Arg Phe His Leu His Pro Glu Gly Leu Leu Trp Cys Ser
 50 55 60
 Arg Cys Phe Phe Ser His Gly Pro Lys Gly Ser Glu Pro Pro Gly Arg
 65 70 75 80
 Ser Ala Gly Leu Gln Gly Ala Thr Glu Arg Ser Gly Arg Pro Ser Val
 85 90 95
 Gln Ala Gln Ala Gln Ala Cys Glu Asn Leu Val Pro Ala Thr Val Trp
 100 105 110
 Asp Gly

<210> 4255

<211> 2205

<212> DNA

<213> Homo sapiens

<400> 4255

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120
aacacccaat ggcgctcctca gaattttattc tgggtccctc atgggacaag cattggatcc
180
cactaggaaa caatgggtatc tccatgcagt agctaatacca ggggtgattt ctttgactgg
240
tccttactta gatgttgag gagctgggta tgttgtagaca atcagtcaca caattcattc
300
atccagtaca cagctgtctt ctgggcacac tgtggctgtg atgggcattg acttcacact
360
cagatacttc taaaaagttc tgatggacct attacctgtc tgtaaccaag atgggtggca
420
caaaaataagg tgcttcataa tggaggacag ggggttatctg gtggcgacac cgactctcat
480
cgaccccaaa ggacatgcac ctgtggagca gcagcacatc acccacaagg agccccctgt
540
agcaaatgat atcctcaacc accccaactt tgtaaaagaaa aacctgtgca acagcttcag
600
tgacagaacg gtcagaggt ttataaatt caacaccagc ctgcgggggg atttgacgaa
660
ccttggtgat ggcagccact gttccaaata cagattagca aggatcccg gaaccaacgc
720
gtttgttgcc attgtcaacg aaacctgcga ctctcttgcc ttctgtgcct gcagcatggt
780
ggaccgactc tgtctcaact gtcaccgaat ggaacaaaat gaatgtgaat gtccttgtga
840
gtgcctctca gaggtcaatg agtgcactgg caacctcacc aatgcagaga accgaaccc
900
cagctgcgag gtccaccagg agccggtgac atacacagct attgacctg gcctgcaaga
960
tgctcttcac cagtgtgtca acagcaggtg cagtcagagg ctggaaagtg gggactgttt
1020
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1080
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1140
cgttgatgac atgggagcaa taggtgatga ggtgatcaca taaaatgat taaaagcgcc
1200
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1260
gtatgcctac cgccaccaga ttcacgccc gagccatcag catatgtctc ctcttgctgc
1320
ccaagaaatg tcagtgcgta tgtccaacct ggagaatgac agagatgaaa gggacgacga
1380

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 1440
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 1500
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 1560
 ccccttgta cccggggctg atgtgggaaa ccatgatgag gacttagacc tggatacccc
 1620
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 1680
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 1740
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 1800
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 1860
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 1920
 cagtcacatt tgtgaagatg tgaggctggt tctgaaatgg aggggaaata agcctgatga
 1980
 acagacctgc cataacacta atggaaggta acagaaggcg aacctccaaa cacagagacg
 2040
 gaacctgcaa gtgaagctga gccagaggaa tgttccaaag agccagaagc attcagctct
 2100
 ccttaactgg aagagagaaa aatctgctca cccagagact ggaatgtggc acatgcagat
 2160
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 2205

<210> 4256

<211> 384

<212> PRT

<213> Homo sapiens

<400> 4256

Met	Ala	Thr	Ser	His	Val	Thr	Asp	Glu	Trp	Met	Thr	Gln	Met	Glu	Met
1				5					10				15		
Ser	Ser	Leu	Asn	Thr	Tyr	Ile	Val	Arg	Cys	Ile	Ala	Thr	Pro	Asn	
			20					25				30			
Gly	Val	Leu	Arg	Ile	Tyr	Ser	Gly	Ser	Leu	Met	Gly	Gln	Ala	Leu	Asp
			35				40				45				
Pro	Thr	Arg	Lys	Gln	Trp	Tyr	Leu	His	Ala	Val	Ala	Asn	Pro	Gly	Leu
			50			55					60				
Ile	Ser	Leu	Thr	Gly	Pro	Tyr	Leu	Asp	Val	Gly	Gly	Ala	Gly	Tyr	Val
					70				75					80	
Val	Thr	Ile	Ser	His	Thr	Ile	His	Ser	Ser	Thr	Gln	Leu	Ser	Ser	
				85					90				95		
Gly	His	Thr	Val	Ala	Val	Met	Gly	Ile	Asp	Phe	Thr	Leu	Arg	Tyr	Phe
				100			105					110			
Tyr	Lys	Val	Leu	Met	Asp	Leu	Leu	Pro	Val	Cys	Asn	Gln	Asp	Gly	Gly
			115				120					125			
Asn	Lys	Ile	Arg	Cys	Phe	Ile	Met	Glu	Asp	Arg	Gly	Tyr	Leu	Val	Ala
				130			135				140				
His	Pro	Thr	Leu	Ile	Asp	Pro	Lys	Gly	His	Ala	Pro	Val	Glu	Gln	Gln

145 150 155 160
 His Ile Thr His Lys Glu Pro Leu Val Ala Asn Asp Ile Leu Asn His
 165 170 175
 Pro Asn Phe Val Lys Lys Asn Leu Cys Asn Ser Phe Ser Asp Arg Thr
 180 185 190
 Val Gln Arg Phe Tyr Lys Phe Asn Thr Ser Leu Ala Gly Asp Leu Thr
 195 200 205
 Asn Leu Val His Gly Ser His Cys Ser Lys Tyr Arg Leu Ala Arg Ile
 210 215 220
 Pro Gly Thr Asn Ala Phe Val Gly Ile Val Asn Glu Thr Cys Asp Ser
 225 230 235 240
 Leu Ala Phe Cys Ala Cys Ser Met Val Asp Arg Leu Cys Leu Asn Cys
 245 250 255
 His Arg Met Glu Gln Asn Glu Cys Glu Cys Pro Cys Glu Cys Pro Leu
 260 265 270
 Glu Val Asn Glu Cys Thr Gly Asn Leu Thr Asn Ala Glu Asn Arg Asn
 275 280 285
 Pro Ser Cys Glu Val His Gln Glu Pro Val Thr Tyr Thr Ala Ile Asp
 290 295 300
 Pro Gly Leu Gln Asp Ala Leu His Gln Cys Val Asn Ser Arg Cys Ser
 305 310 315 320
 Gln Arg Leu Glu Ser Gly Asp Cys Phe Gly Val Leu Asp Cys Glu Trp
 325 330 335
 Cys Met Val Asp Ser Asp Gly Lys Thr His Leu Asp Lys Pro Tyr Cys
 340 345 350
 Ala Pro Gln Lys Glu Cys Phe Gly Gly Ile Val Gly Ala Lys Ser Pro
 355 360 365
 Tyr Val Asp Asp Met Gly Ala Ile Gly Asp Glu Val Ile Thr Leu Lys
 370 375 380

<210> 4257

<211> 1541

<212> DNA

<213> Homo sapiens

<400> 4257

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 120
 tgagtgccct gaggagtgc acagagcctg ggatggatct tggggagttc tgcagcgaaa
 180
 ctttccaaag accttaccag tatttaagac gattcaatcc aaaccagac ctttaaccgg
 240
 ttcaagattc agaaagggtt tgccgaaggc cccccggagg aatgcctcca gcatctctg
 300
 ttctactggg gggtaataaa cccatcctgg ccaaacctcc ggaactttgc tgggttctg
 360
 aattatcagc tcagagattg tgaggcctct ctcttctgca atccagattt tattggcgac
 420
 acactgagg gcttcaagaa gtctgtgtg accttcatga tctttatggc aagagatttt
 480
 gccacacat cactccacac ctctgaccaa agccccggga agcacatggt caccatggat
 540

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gggggttaggg aagaagatct agcgcccttc tccctccgga agaggtggga gtcggagcct
600
caccatacag ttttcttcaa tgacgaccac acaacctga cattcatcg cttccatctg
660
cagcccaaca tcaacggcag tgtcgatgcc atcagtcact tgactgggaa ggtcatcaag
720
agagacgtca tgaccaggga cctgtaccag ggctgtgctg tccagagggg gcccttcaat
780
gtcgactttg ataaactgcc cagacacaag aaacttgaga ggctctgcct gaccttaggg
840
atcccccagg ccaccgaccc cgacaaaacg tatgagctca caaccgacaa tatgcttaaa
900
atccttgcca tcgagatgcg gttccggtgt gggatccccg ttatcatcat gggagaaact
960
ggctgtggga aaaccaggct tattaaattc cttagcgacc tgcggcggtg tggtagcaat
1020
gctgacacca taaagctggg caaggtgcac ggaggaacaa ctgcagacat gatctactcc
1080
agagtcaggg aggctgaaaa tgtggccttc gccaaataag accaactca gttggacacc
1140
atcttgtttt ttgatgaagc caacacaacg gaagctataa gctgtatcaa agaagctctg
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tgtgatcata tgggtgatgg ccagcctctg gctgaggact ctggcctgca tattatagct
1260
gcctgcaatc catacccgga gaactctgag gagatgatct gccgtttgga gtcagctggg
1320
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1380
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1440
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1500
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1541

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<210> 4258

<211> 314

<212> PRT

<213> Homo sapiens

<400> 4258

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Met Ile Phe Met Ala Arg Asp Phe Ala Thr Pro Ser Leu His Thr Ser
1      5      10      15
Asp Gln Ser Pro Gly Lys His Met Val Thr Met Asp Gly Val Arg Glu
20      25      30
Glu Asp Leu Ala Pro Phe Ser Leu Arg Lys Arg Trp Glu Ser Glu Pro
35      40      45
His Pro Tyr Val Phe Phe Asn Asp Asp His Thr Thr Met Thr Phe Ile
50      55      60
Gly Phe His Leu Gln Pro Asn Ile Asn Gly Ser Val Asp Ala Ile Ser
65      70      75      80
His Leu Thr Gly Lys Val Ile Lys Arg Asp Val Met Thr Arg Asp Leu
85      90      95
Tyr Gln Gly Leu Leu Leu Gln Arg Val Pro Phe Asn Val Asp Phe Asp

```

```

          100          105          110
Lys Leu Pro Arg His Lys Lys Leu Glu Arg Leu Cys Leu Thr Leu Gly
      115          120          125
Ile Pro Gln Ala Thr Asp Pro Asp Lys Thr Tyr Glu Leu Thr Thr Asp
      130          135          140
Asn Met Leu Lys Ile Leu Ala Ile Glu Met Arg Phe Arg Cys Gly Ile
      145          150          155          160
Pro Val Ile Ile Met Gly Glu Thr Gly Cys Gly Lys Thr Arg Leu Ile
      165          170          175
Lys Phe Leu Ser Asp Leu Arg Arg Gly Gly Thr Asn Ala Asp Thr Ile
      180          185          190
Lys Leu Val Lys Val His Gly Gly Thr Thr Ala Asp Met Ile Tyr Ser
      195          200          205
Arg Val Arg Glu Ala Glu Asn Val Ala Phe Ala Asn Lys Asp Gln His
      210          215          220
Gln Leu Asp Thr Ile Leu Phe Phe Asp Glu Ala Asn Thr Thr Glu Ala
      225          230          235          240
Ile Ser Cys Ile Lys Glu Val Leu Cys Asp His Met Val Asp Gly Gln
      245          250          255
Pro Leu Ala Glu Asp Ser Gly Leu His Ile Ala Ala Cys Asn Pro
      260          265          270
Tyr Pro Glu Asn Ser Glu Glu Met Ile Cys Arg Leu Glu Ser Ala Gly
      275          280          285
Leu Gly Tyr Arg Val Ser Met Glu Glu Thr Ala Asp Arg Leu Gly Ser
      290          295          300
Ile Pro Leu Gly Tyr Thr Cys Thr Gln Arg
      305          310

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<210> 4259

<211> 377

<212> DNA

<213> Homo sapiens

<400> 4259

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tctgcgacgg gacccggcgt gcccatgtgt caggtgggcg aggactacgg ggagccggcg
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cctgaggagc cgccccggc gcccgggccc agccgtgagc agaagtgtgt gaagtgcagg
120
gaagcgcagc ccgttgttgt gatacgagcc ggagatgcct tctgcaggga ctgtttcaag
180
gccttctacg tccacaagtt cagagccatg ctgggcaaga accggctcat ctttcaggc
240
gagaaggtgc tcttgcggtg gtctgggggg ccttcgtcca gctccatggt ctggcaggtt
300
cttgagggcc tgagccaaga ttctgccaaa agactgcgtt ttgtggcagg agtcatcttt
360
gttgacgagg gagcagc
377

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<210> 4260

<211> 125

<212> PRT

<213> Homo sapiens

<400> 4260

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Ser Ala Thr Gly Pro Gly Val Pro Met Cys Gln Val Gly Glu Asp Tyr
 1              5              10              15
Gly Glu Pro Ala Pro Glu Glu Pro Pro Ala Pro Arg Pro Ser Arg
      20              25              30
Glu Gln Lys Cys Val Lys Cys Lys Glu Ala Gln Pro Val Val Val Ile
 35              40              45
Arg Ala Gly Asp Ala Phe Cys Arg Asp Cys Phe Lys Ala Phe Tyr Val
 50              55              60
His Lys Phe Arg Ala Met Leu Gly Lys Asn Arg Leu Ile Phe Pro Gly
 65              70              75              80
Glu Lys Val Leu Leu Ala Trp Ser Gly Gly Pro Ser Ser Ser Ser Met
      85              90              95
Val Trp Gln Val Leu Glu Gly Leu Ser Gln Asp Ser Ala Lys Arg Leu
      100              105              110
Arg Phe Val Ala Gly Val Ile Phe Val Asp Glu Gly Ala
      115              120              125

```

<210> 4261

<211> 592

<212> DNA

<213> Homo sapiens

<400> 4261

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60
atactcttga cttaaatatg ttgttttata aagacaaatg gagaaatcaa tttttttccc
120
tgaattctta ggagcacttt agtgaataaa gaacctgaca gtatgctggc ccacatgttt
180
aaggacaaag gtgtctgggg aaataagcaa gatcatagag gagctttctt aattgaccga
240
agtcctgagt acttogaacc cattttgaac tacttgcgtc atggacagct cattgtaaat
300
gatggcatta atttattggg tgtgttagaa gaagcaagat tttttgggat tgactcattg
360
attgaacacc tagaagtggc aataaagaat tctcaaccac cggaggatca ttcaccaata
420
tcccgaaagg aatttgtccg atttttgeta gcaactccaa ccaagtcaga actgcatgac
480
cagggtttga acttcagtgg tgctgatctt tctcgtttgg accttcgata cattaacttc
540
aaaatggcca atttaagccg ctgtaatctt gcacatgcaa atctttgctg tg
592

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<210> 4262

<211> 156

<212> PRT

<213> Homo sapiens

<400> 4262

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Ile Leu Arg Ser Thr Leu Val Asn Lys Glu Pro Asp Ser Met Leu Ala
 1              5              10              15
His Met Phe Lys Asp Lys Gly Val Trp Gly Asn Lys Gln Asp His Arg

```

	20		25		30										
Gly	Ala	Phe	Leu	Ile	Asp	Arg	Ser	Pro	Glu	Tyr	Phe	Glu	Pro	Ile	Leu
	35						40					45			
Asn	Tyr	Leu	Arg	His	Gly	Gln	Leu	Ile	Val	Asn	Asp	Gly	Ile	Asn	Leu
	50					55					60				
Leu	Gly	Val	Leu	Glu	Glu	Ala	Arg	Phe	Phe	Gly	Ile	Asp	Ser	Leu	Ile
65					70					75				80	
Glu	His	Leu	Glu	Val	Ala	Ile	Lys	Asn	Ser	Gln	Pro	Pro	Glu	Asp	His
			85						90					95	
Ser	Pro	Ile	Ser	Arg	Lys	Glu	Phe	Val	Arg	Phe	Leu	Leu	Ala	Thr	Pro
	100							105					110		
Thr	Lys	Ser	Glu	Leu	Arg	Cys	Gln	Gly	Leu	Asn	Phe	Ser	Gly	Ala	Asp
	115					120						125			
Leu	Ser	Arg	Leu	Asp	Leu	Arg	Tyr	Ile	Asn	Phe	Lys	Met	Ala	Asn	Leu
	130					135					140				
Ser	Arg	Cys	Asn	Leu	Ala	His	Ala	Asn	Leu	Cys	Cys				
145					150						155				

<210> 4263

<211> 7710

<212> DNA

<213> Homo sapiens

<400> 4263

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 tacatcatcc ctgtgtccat gtacgtcacg gtcgagatgc agaagttcct cggctcttac
 120
 ttcatcacct gggacgaaga catgtttgac gaggagactg gcgagggggc tctggtgaac
 180
 acgtcggacc tcaatgaaga gctgggacag gtggagtaca tcttcacaga caagaccggc
 240
 accctcacgg aaaacaacat ggagttcaag gagtgtctga tcgaaggcca tgtctacgtg
 300
 cccacagtca tctgcaacgg gcaggtcctc ccagagtctg caggaatcga catgattgac
 360
 tcgtccccc cgcgtcaacgg gaggggagcgc gaggagctgt ttttcggggc cctctgtctc
 420
 tgccacacgg tccagtgtaa agacgatgac agcgtagacg gccccaggaa atcgccggac
 480
 ggggggaaat cctgtgtgta catctcatcc tcgcccagcg aggtggcgct ggctgaagggt
 540
 gtccagagac ttggctttac ctacctaaagg ctgaaggaca attacatgga gatattaaac
 600
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 660
 aggagaatga gtgtaattgt aaaatctgct acaggagaaa tttatctgtt ttgcaaagga
 720
 gcagattctt cgatattccc ccgagtgata gaaggcaaaag ttgaccagat ccgagccaga
 780
 gtggagcgtg acgcagtgga ggggctccga actttgtgtg ttgcttataa aaggctgac
 840
 caagaagaat atgaaggcat ttgtaagctg ctgcaggctg ccaaagtggt ctttcaagat
 900

cgagagaaaa agttagcaga agcctatgag caaatagaga aagatcttac tctgcttggt
960
gctacagctg ttgaggaccg gctgcaggag aaagctgcag acaccatcga ggccctgcag
1020
aaggccggga tcaaatctct ggttctcacg ggagacaaga tggagacggc cgcggccacg
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<211> 797

<212> PRT

<213> Homo sapiens

<400> 4264

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<212> DNA

<213> Homo sapiens

<400> 4265

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<212> PRT

<213> Homo sapiens

<400> 4266

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<210> 4267

<211> 2230

<212> DNA

<213> Homo sapiens

<400> 4267

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<211> 2081

<212> DNA

<213> Homo sapiens

<400> 4273
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 2081

<210> 4274

<211> 235

<212> PRT

<213> Homo sapiens

<400> 4274

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			20					25					30		
Glu	Glu	Ser	Ile	Arg	Ala	His	Val	Met	Ala	Ser	His	His	Ser	Lys	Arg
		35					40					45			
Arg	Gly	Arg	Ala	Ser	Ser	Glu	Ser	Gln	Gly	Leu	Gly	Ala	Gly	Val	Arg
	50					55				60					
Thr	Glu	Xaa	Asp	Val	Glu	Glu	Glu	Ala	Leu	Arg	Arg	Lys	Leu	Glu	Glu
65				70					75				80		
Leu	Thr	Ser	Asn	Val	Ser	Asp	Gln	Glu	Thr	Phe	Val	Arg	Gly	Gly	Gly
			85						90				95		
Ser	Gln	Gly	Arg	Lys	Cys	Arg	Ala	Gln	Gln	Gly	Gln	Ile	Ser	Trp	Ala
		100					105					110			
Ser	Pro	Pro	Gly	Gly	Pro	Gly	Arg	Trp	His	Gly	Cys	Pro	Ser	Asn	Gln
		115					120					125			
Gln	Thr	Gly	Lys	Lys	Pro	Gln	Asp	Pro	Gly	Asp	Pro	Val	Gln	Tyr	Asn
		130				135					140				
Arg	Thr	Thr	Asp	Glu	Glu	Leu	Ser	Glu	Leu	Glu	Asp	Arg	Val	Ala	Val
145				150					155				160		
Thr	Ala	Ser	Glu	Val	Gln	Gln	Ala	Glu	Ser	Glu	Val	Ser	Asp	Ile	Glu
			165					170					175		
Ser	Arg	Ile	Ala	Ala	Leu	Arg	Ala	Ala	Gly	Leu	Thr	Val	Lys	Pro	Ser
		180					185					190			
Gly	Lys	Pro	Arg	Arg	Lys	Ser	Asn	Leu	Pro	Ile	Phe	Leu	Pro	Arg	Val
		195					200				205				
Ala	Gly	Lys	Leu	Gly	Lys	Arg	Pro	Glu	Asp	Pro	Asn	Ala	Asp	Pro	Ser
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Ser	Glu	Ala	Lys	Ala	Met	Ala	Val	Pro	Ile	Phe					

225

230

235

<210> 4275
 <211> 874
 <212> DNA
 <213> Homo sapiens

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 180
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 720
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 780
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<210> 4276
 <211> 264
 <212> PRT
 <213> Homo sapiens

<400> 4276
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 Gly Lys Ser Ser Leu Val Asn Leu Leu Ser Arg Lys Pro Val Ser Ile
 35 40 45
 Val Ser Pro Glu Pro Gly Thr Thr Arg Asp Val Leu Glu Thr Pro Val
 50 55 60
 Asp Leu Ala Gly Phe Pro Val Leu Leu Ser Asp Thr Ala Gly Leu Arg


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65          70          75          80
Glu Gly Val Gly Pro Val Glu Gln Glu Gly Val Arg Arg Ala Arg Glu
      85          90          95
Arg Leu Glu Gln Ala Asp Leu Ile Leu Ala Met Leu Asp Ala Ser Asp
      100          105          110
Leu Ala Ser Pro Ser Ser Cys Asn Phe Leu Ala Thr Val Val Ala Ser
      115          120          125
Val Gly Ala Gln Ser Pro Ser Asp Ser Ser Gln Arg Leu Leu Leu Val
      130          135          140
Leu Asn Lys Ser Asp Leu Leu Ser Pro Glu Gly Pro Gly Pro Gly Pro
145          150          155          160
Asp Leu Pro Pro His Leu Leu Leu Ser Cys Leu Thr Gly Glu Gly Leu
      165          170          175
Asp Gly Leu Leu Glu Ala Leu Arg Lys Glu Leu Ala Val Cys Gly
      180          185          190
Asp Pro Ser Thr Asp Pro Pro Leu Leu Thr Arg Ala Arg His Gln His
      195          200          205
His Leu Gln Gly Cys Leu Asp Ala Leu Gly His Tyr Lys Gln Ser Lys
      210          215          220
Asp Leu Ala Leu Ala Ala Glu Ala Leu Arg Val Ala Arg Gly His Leu
225          230          235          240
Thr Arg Leu Thr Gly Gly Gly Thr Glu Glu Ile Leu Asp Ile Ile
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<210> 4277

<211> 1070

<212> DNA

<213> Homo sapiens

<400> 4277

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180
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240
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300
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360
gaccggggacc gagagagaga gaaaagagac aaagcaagag agagtggaaa ttcaaggcca
420
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480
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540
aaaccaccga aaaaaaagtc tcgttatgaa aggacagata ccggtgagat aacatcctac
600
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660

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 960
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<210> 4278

<211> 253

<212> PRT

<213> Homo sapiens

<400> 4278

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Glu	Asn	Ser	Arg	Pro	Arg	Arg	Ser	Cys	Thr	Leu	Glu	Gly	Gly	Ala	Lys	40	45	50	55
Asn	Tyr	Ala	Glu	Ser	Asp	His	Ser	Glu	Asp	Glu	Asp	Asn	Asp	Asn	Asn	60	65	70	75
Ser	Ala	Thr	Ala	Glu	Glu	Ser	Thr	Lys	Lys	Asn	Lys	Lys	Lys	Pro	Pro	80	85	90	95
Lys	Lys	Lys	Ser	Arg	Tyr	Glu	Arg	Thr	Asp	Thr	Gly	Glu	Ile	Thr	Ser	100	105	110	115
Tyr	Ile	Thr	Glu	Asp	Asp	Val	Val	Tyr	Arg	Pro	Gly	Asp	Cys	Val	Tyr	120	125	130	135
Ile	Glu	Ser	Arg	Arg	Pro	Asn	Thr	Pro	Tyr	Phe	Ile	Cys	Ser	Ile	Gln	140	145	150	155
Asp	Phe	Lys	Leu	Val	His	Asn	Ser	Gln	Ala	Cys	Cys	Arg	Ser	Pro	Thr	160	165	170	175
Pro	Ala	Leu	Cys	Asp	Pro	Pro	Ala	Cys	Ser	Leu	Pro	Val	Ala	Ser	Gln	180	185	190	195
Arg	Asp	His	Leu	Leu	Met	Asn	Val	Lys	Trp	Tyr	Tyr	Arg	Gln	Ser	Glu	200	205	210	215
Val	Pro	Asp	Ser	Val	Tyr	Gln	His	Leu	Val	Gln	Asp	Arg	His	Asn	Glu	220	225	230	235
Asn	Asp	Ser	Gly	Arg	Glu	Leu	Val	Ile	Thr	Asp	Pro	Val	Ile	Lys	Asn	240	245	250	
Arg	Glu	Leu	Phe	Ile	Ser	Asp	Tyr	Val	Asp	Thr	Tyr	His	Ala	Ala	Ala				
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<210> 4279

<211> 1963

<212> DNA

<213> Homo sapiens

<400> 4279

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 240
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 1963

<210> 4280

<211> 575

<212> PRT

<213> Homo sapiens

<400> 4280

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		20					25					30			
Val	Ser	Asp	Asp	Val	Asn	Glu	Tyr	Ala	Met	Ala	Leu	Arg	Asp	Thr	Glu
	35					40					45				
Asp	Lys	Leu	Arg	Arg	Cys	Pro	Lys	Arg	Arg	Lys	Asp	Ile	Leu	Ala	Glu
	50				55					60					
Leu	Thr	Lys	Ser	Gln	Lys	Val	Phe	Ser	Glu	Lys	Leu	Asp	His	Leu	Ser
65				70					75					80	
Arg	Arg	Leu	Ala	Trp	Val	His	Ala	Thr	Val	Tyr	Ser	Gln	Glu	Lys	Met
		85						90					95		
Leu	Asp	Ile	Tyr	Trp	Leu	Leu	Arg	Val	Cys	Leu	Arg	Thr	Ile	Glu	His
	100						105						110		
Gly	Asp	Arg	Thr	Gly	Ser	Leu	Phe	Ala	Phe	Met	Pro	Glu	Phe	Tyr	Leu
	115					120						125			
Ser	Val	Ala	Ile	Asn	Ser	Tyr	Ser	Ala	Leu	Lys	Asn	Tyr	Phe	Gly	Pro
	130				135						140				
Val	His	Ser	Met	Glu	Glu	Leu	Pro	Gly	Tyr	Glu	Glu	Thr	Leu	Thr	Arg
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Leu	Ala	Ala	Ile	Leu	Ala	Lys	His	Phe	Ala	Asp	Ala	Arg	Ile	Val	Gly
		165						170					175		
Thr	Asp	Ile	Arg	Asp	Ser	Leu	Met	Gln	Ala	Leu	Ala	Ser	Tyr	Val	Cys
	180						185						190		
Tyr	Pro	His	Ser	Leu	Arg	Ala	Val	Glu	Arg	Ile	Pro	Glu	Glu	Gln	Arg
	195					200						205			
Ile	Ala	Met	Val	Arg	Asn	Leu	Leu	Ala	Pro	Tyr	Glu	Gln	Arg	Pro	Trp
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Gln	Gln	His	Met	Ala	Asp	Leu	Leu	Gln	Gln	Gly	Pro	Asp	Val	Ala	Pro														
275										280										285									
Ser	Phe	Leu	Asn	Ser	Val	Leu	Asn	Gln	Leu	Asn	Trp	Ala	Phe	Ser	Glu														
290										295										300									
Phe	Ile	Gly	Met	Ile	Gln	Glu	Ile	Gln	Gln	Ala	Ala	Glu	Arg	Leu	Glu														
305					310					315					320														
Arg	Asn	Phe	Val	Asp	Ser	Arg	Gln	Leu	Lys	Val	Cys	Ala	Thr	Cys	Phe														
325										330										335									
Asp	Leu	Ser	Val	Ser	Leu	Leu	Arg	Val	Leu	Glu	Met	Thr	Ile	Thr	Leu														
340										345										350									
Val	Pro	Glu	Ile	Phe	Leu	Asp	Trp	Thr	Arg	Pro	Thr	Ser	Glu	Met	Leu														
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Leu	Arg	Arg	Leu	Ala	Gln	Leu	Leu	Asn	Gln	Val	Leu	Asn	Arg	Val	Thr														
370										375										380									
Ala	Glu	Arg	Asn	Leu	Phe	Asp	Arg	Val	Val	Thr	Leu	Arg	Leu	Pro	Gly														
385					390					395					400														
Leu	Glu	Ser	Val	Asp	His	Tyr	Pro	Ile	Leu	Val	Ala	Val	Thr	Gly	Ile														
405										410										415									
Leu	Val	Gln	Leu	Leu	Val	Arg	Gly	Pro	Ala	Ser	Glu	Arg	Glu	Gln	Ala														
420										425										430									
Thr	Ser	Val	Leu	Leu	Ala	Asp	Pro	Cys	Phe	Gln	Leu	Arg	Ser	Ile	Cys														
435										440										445									
Tyr	Leu	Leu	Gly	Gln	Pro	Glu	Pro	Pro	Ala	Pro	Gly	Thr	Ala	Leu	Pro														
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Ala	Pro	Asp	Arg	Lys	Arg	Phe	Ser	Leu	Gln	Ser	Tyr	Ala	Asp	Tyr	Ile														
465					470					475					480														
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Ser	Ala	Ser	Ala	Gln	Ala	Ala	Ala	Ala	Ser	Leu	Pro	Thr	Ser	Glu	Glu														
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Asp	Leu	Cys	Pro	Ile	Cys	Tyr	Ala	His	Pro	Ile	Ser	Ala	Val	Phe	Gln														
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545					550					555					560														
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<210> 4281

<211> 507

<212> DNA

<213> Homo sapiens

<400> 4281

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120

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180

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 420
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 480
 acacccattc ccaagggcac aggatcc
 507

<210> 4282

<211> 106

<212> PRT

<213> Homo sapiens

<400> 4282

Met	Asn	Ala	Leu	Thr	Asp	Pro	Leu	Ser	Phe	Pro	Pro	Ala	Ser	Met	Pro
1				5					10					15	
Asp	Leu	Leu	Lys	Cys	Leu	Trp	Leu	Pro	Ala	Ser	Gln	Pro	Ala	Pro	Pro
			20				25						30		
Leu	Ile	Thr	Met	Gly	Gly	Val	Lys	Cys	Gln	Val	Asp	Met	Arg	Gly	Cys
			35				40					45			
Leu	Leu	Thr	Ser	Gly	Leu	Ile	Asn	Gln	Pro	Tyr	Lys	Cys	Asp	Arg	Gly
	50				55						60				
Arg	Cys	Trp	Arg	Glu	Ala	His	Cys	Leu	Ser	Glu	Ser	Ala	Gln	Arg	Thr
	65				70					75				80	
Glu	Ser	Gly	Asp	Ser	Trp	Gln	Lys	Arg	Gly	Gly	Leu	Arg	Leu	Trp	Gly
			85						90					95	
Ile	Trp	Pro	Ile	Gly	Gln	Leu	Trp	Gly	Ser						
			100					105							

<210> 4283

<211> 315

<212> DNA

<213> Homo sapiens

<400> 4283

gaattctcaa ccagaacagc ccagcaggaa aggagccggc atgggggtgcc cctctgcagc
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 120
 gggagaaacc gagtccccgc cgggtcccca ccgtgtggcg ccgaccgaaa taactccagt
 180
 ccagctgcaa aaacctctcc gaaaacccaa gcttgtccgg cacaacttcg gtctctccag
 240
 cctcattcct gcccgactc cgccaaaactg etcgccctgc ccagcgcagc ggaatgcagc
 300
 ctcccgccc nacgg
 315

<210> 4284

<211> 91
 <212> PRT
 <213> Homo sapiens

<400> 4284
 Met Gly Cys Pro Ser Ala Ala Asp Arg Phe Pro Arg Arg Pro Asn Arg
 1 5 10 15
 Ser Asn Gly Gln Gly Arg Gly Ala Gly Gly Pro Gly Glu Thr Glu Ser
 20 25 30
 Pro Pro Gly Pro His Arg Val Ala Pro Thr Glu Ile Thr Pro Val Gln
 35 40 45
 Leu Gln Lys Pro Ser Arg Lys Pro Lys Leu Val Arg His Asn Phe Gly
 50 55 60
 Leu Ser Ser Leu Ile Pro Ala Arg Thr Pro Pro Asn Cys Ser Pro Cys
 65 70 75 80
 Pro Ala Gln Arg Met Gln Arg Ser Arg Pro Xaa
 85 90

<210> 4285
 <211> 591
 <212> DNA
 <213> Homo sapiens

<400> 4285
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 120
 gagataccgc agggagccag tggctgctgg aaggatgacc tcagaagga actgagtgat
 180
 atatgggtgat gccagcctg cagtctgacc cctgaccctc ctctgaaccc gtccccccaa
 240
 cgggatctgg cagtgaccac cagaacctgg agcccacctg agtcacagact tcctcacc
 300
 cctaggactc acccccaccac ggcccccaac cttagctgta ctgctgtcta caccctgagc
 360
 agtgtggagt ctcccagcgc cccagctccc ttgtcttctt gcagggtctgc tgtgcacgtg
 420
 ctgcaggact ccatagacag cctcactttg tgcctggggg cctgtcccaa ggcctcgagc
 480
 ctaagaggcc acaagggcac cagtgcctga gccctccact cccctcctgg gactctgact
 540
 ccgactgtga ccaggacctc tcccagccac ctttcagcaa ggcggccgc a
 591

<210> 4286
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 4286
 Cys Pro Ala Cys Ser Leu Thr Pro Asp Pro Pro Leu Asn Pro Phe Pro
 1 5 10 15
 Gln Arg Asp Leu Ala Val Thr Thr Arg Thr Trp Ser Pro Pro Glu Ser

<400> 4288

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Met Arg Val Ala Thr Lys Ser Gly Arg Lys Arg Trp Leu Lys Ala Thr
 1              5              10              15
Thr Met Lys Asn Ser Val Arg Leu Val Ala Met Ala Pro Ser Pro Ala
 20              25              30
Leu Thr Ser Ile Ser Ser Glu Pro Ser Glu Ala Trp Val Gln Ala Phe
 35              40              45
Ala Ser Tyr Arg Met Ser Pro Gly Asn Trp Lys Thr Xaa Val Leu Ala
 50              55              60
Gln Thr Leu Val Glu Ala Leu Gln Leu Asp Pro Glu Thr Leu Ala Asn
 65              70              75
Glu Thr Ala Ala Arg Ala Ala Asn Val Ala Arg Ala Ala Ser Asn
 85              90              95
Arg Ala Ala Arg Ala Ala Ala Ala Arg Thr Ala Phe Ser Gln
100              105              110
Val Val Ala Ser His Arg Val Ala Thr Pro Gln Val Ser Gly Glu Asp
115              120              125
Thr Gln Pro Thr Thr Tyr Ala Ala Glu Ala Gln Gly Pro Thr Pro Glu
130              135              140
Pro Pro Leu Ala Ser Pro Gln Thr Ser Gln Met Leu Val Thr Ser Lys
145              150              155
Met Ala Ala Pro Glu Ala Pro Ala Thr Ser Ala Gln Ser Gln Thr Gly
165              170              175
Ser Pro Ala Gln Glu Ala Ala Thr Glu Gly Pro Ser Ser Ala Cys Ala
180              185              190
Phe Ser Gln Ala Pro Cys Ala Arg Glu Val Asp Ala Asn Arg Pro Ser
195              200              205
Thr Ala Phe Leu Gly Gln Asn Asp Val Phe Asp Phe Thr Gln Pro Ala
210              215              220
Val Ser Val Ala Trp Leu Pro Ala Pro Lys Arg Pro Ala Gln Pro Arg
225              230              235

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<210> 4289

<211> 353

<212> DNA

<213> Homo sapiens

<400> 4289

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120
caaagagcct tttgggaaca gttttcttat tgaacatac tcagtgttta aacctgcagg
180
tgtgggttgg tggcagtcca catggcatcc ttgctctgt cctgtttctc ctgtctctgg
240
ctattcagg tcccgtagg atactgtcac cttgaataa tggagcttgc ggaagaccaa
300
gccctgttt ttggagtcct tgtgctgagg ccgctgtaac ttgcggagag ttg
353

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<210> 4290

<211> 113

<212> PRT

<213> Homo sapiens

<400> 4290

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Met Thr Thr Leu Pro Val Arg Asp Met Arg Glu Lys Tyr Gly Ser Leu
 1              5              10              15
Leu Thr Ser Gly Val Thr Ala Gln His Ile Ser Arg Leu Cys Phe His
 20              25              30
Ile Gly Leu Ala Lys Ser Leu Leu Gly Thr Val Phe Leu Leu Lys His
 35              40              45
Thr Gln Cys Leu Asn Leu Gln Val Trp Val Gly Gly Ser Pro His Gly
 50              55              60
Ile Leu Cys Ser Val Pro Val Leu Leu Ser Leu Ala Ile Gln Val Pro
 65              70              75              80
Val Arg Ile Leu Ser Pro Leu Asn Asn Gly Ala Cys Gly Arg Pro Ser
 85              90              95
Pro Cys Phe Trp Ser Pro Cys Ala Glu Ala Ala Val Thr Cys Gly Glu
 100              105              110
Leu

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<210> 4291

<211> 517

<212> DNA

<213> Homo sapiens

<400> 4291

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nnaaatttgc caagccaaga gttaccccag gaagattctc tcttacatgg ccaattttca
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caagcagtc a cccccctagc ccatcatcac acagattatt caaagcccac cgatatctca
 120
tggagagaca cactttctca gaagtttgga tcctcagatc acttgaggaa actattttaag
 180
atggatgaag caagtgccca gtccttgct tataaggaaa aaggccattc tcagagttca
 240
caattttcct ctgatcaaga aatagctcat ctgctgctg aaaatgtgag tgcgtcccca
 300
gctacgggtg cagttgcttc tccacatacc acctcggtca ctccaaagcc cgccaccctt
 360
ctaccaccca atgcttcagt gacaccttct gggacttccc agccacagct ggcaccaca
 420
gctccacctg taaccactgt cacttctcag cctccacga cctcatttc tacagttttt
 480
acacgggctg tggctacact ccaagcaatg gctacaa
 517

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<210> 4292

<211> 172

<212> PRT

<213> Homo sapiens

<400> 4292

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Xaa Asn Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His
 1              5              10              15
Gly Gln Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp

```



```

1           5           10           15
Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser Gly
20           25           30
Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val
35           40           45
Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp
50           55           60
Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu
65           70           75           80
Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile
85           90           95
Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys
100          105          110
Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Val
115          120          125
Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn Ile
130          135          140
Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met Phe Ser
145          150          155          160
Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala Gly Val
165          170          175
Asp Gln Asn His Pro Arg
180

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<210> 4295

<211> 431

<212> DNA

<213> Homo sapiens

<400> 4295

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nntctagaaa atcactgtct cttctaccc tgccatctct acaccagggt tacaacaag
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agcccaactgc tggctccttg tttgtaaat aagatttgtt ggactacagc tatgccgtta
120
catgtacatt ttgtgtatgg ctgcttttgt gccacaacag cagggttgag tattgcgaca
180
gagaccccca ttgccacaa gcctaaaaca ttgcatcg agccctttaa gaaagagttt
240
gctggccctg cgcggtggcc gtggctcccg cctgtaatcc cagcactttg gaaggctgag
300
gcaggcggtg aggtctggag ttcgaaacca gcctggccag cgtggcgaaa cctgtctcc
360
ccctccaga ttcacgtgat tatcccacct cagcctcctg agtacctggg actataggcg
420
cgtgcccaacc a
431

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<210> 4296

<211> 138

<212> PRT

<213> Homo sapiens

<400> 4296

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Xaa Leu Glu Asn His Cys Leu Leu Leu Pro Cys His Leu Tyr Thr Arg

```

1	5	10	15
Val Thr Asn Lys Ser Pro Leu Leu Ala Pro Cys Phe Val Asn Lys Ile			
	20	25	30
Cys Trp Thr Thr Ala Met Pro Val His Val His Phe Val Tyr Gly Cys			
	35	40	45
Phe Cys Ala Thr Thr Ala Gly Leu Ser Ile Ala Thr Glu Thr Pro Ile			
	50	55	60
Ala His Lys Pro Lys Thr Phe Ala Ile Glu Pro Phe Lys Lys Glu Phe			
	65	70	75
Ala Gly Arg Ala Arg Trp Pro Trp Leu Pro Pro Val Ile Pro Ala Leu			
	85	90	95
Trp Lys Ala Glu Ala Gly Gly Glu Val Trp Ser Ser Lys Pro Ala Trp			
	100	105	110
Pro Ala Trp Arg Asn Pro Val Ser Pro Ser Gln Ile His Val Ile Ile			
	115	120	125
Pro Pro Gln Pro Pro Glu Tyr Leu Gly Leu			
	130	135	

<210> 4297

<211> 1668

<212> DNA

<213> Homo sapiens

<400> 4297

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 gattttaccg tgattccatc taaactgatt cagtttgacc caggaatgac aactaagatg
 120
 tggaatatag caattacccta tgacggatta gaggaagatg atgaggtcct tgaagtaatt
 180
 ctgaactccc ctgtgaatgc agttcttggc acaaagacaa aagctgcagt gaaaattttg
 240
 gactcaaaag gaggacaatg ccatccttca tattctctcca accaaagcaa gcacagcaca
 300
 tgggagaagg gcatttggca tctgctgccc ccagggtctt cctcatccac cacttctggt
 360
 tcctttcatc tggaaagaag acctcttcca tcttccatgc agctagcagt catcagggga
 420
 gacacctgc ggggctttga ttctacagat cttttctcaa ggaagcttag gacctgtggg
 480
 aatggcaaaa cagttcgtcc atcctctggt tatagaaatg gaacagacat catctataat
 540
 tatcatggga tagtttccctt gaaactggag gatgacagtt tcccaactca caaaagggaag
 600
 gccaaagtat ccattcattag tcagccacaa aagacaatca aagtggcaga actgcctcaa
 660
 gcagataagg tggaatccac aactgactca cacttcccca gacaggacca gttgccctca
 720
 ttccaaaga actgcactct ggaattaaag ggactcttcc attttgaaga aggcattccag
 780
 aagctgtatc agtgcaatgg gatcgcttgg aaagcctgga gtccccaac caaggatgtg
 840
 gaagacaaat cctgtccagc cgggtggcac cagcactcag gctactgtca catcttgatc
 900

acagagcaga aaggcacctg gaatgcggct gcccaagctt gcagggaaca atacctgggc
 960
 aaccttgtaa ctgtattctc caggcagcac atgcggctggc tctgggacat tgggtgggaga
 1020
 aagtcctttt ggtataggttt gaacgaccaa gtgcatgctg gccactggga gtggatcgggt
 1080
 ggtgaacctg ttgccttcac caatgggaga agagggccct ctccacgctc caagcttggga
 1140
 aagagctgtg ttttggttca aagacaaggg aaatggcaaa caaaagactg taggagagcc
 1200
 aaacctcata attatgtgtg ttccagaaaa ctctaaatat aacagacctt acagggggcc
 1260
 acctggagtt tgtcacctat ttattcacag gatctgtgaa tattgtctca tagaaaacaa
 1320
 attgttatga ttgagtgggt atacctttgt gattctgtct agtgaaaatg ggacattttt
 1380
 aatagtgcga gaaagattga taaataaata ttttttacia gataagatag aatttttcta
 1440
 tctcaataacc ttttaaaaaa atgcccagca gtattaaaaa gtgtaagggt tgtttatccc
 1500
 agaagacctt cacccttacc ccattccaaa tctcaggagg caccagtctc atagtccctg
 1560
 gatttttttt aaaaaaaatt tttggtcocg ttacctctaa tgaatttatt ctgaaatatg
 1620
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 1668

<210> 4298

<211> 411

<212> PRT

<213> Homo sapiens

<400> 4298

Xaa Met Asp Ser Ala Phe Val Gly Ile Lys Val Asn Gln Val Ser Ala
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 Ala Val Gly Lys Asp Phe Thr Val Ile Pro Ser Lys Leu Ile Gln Phe
 20 25 30
 Asp Pro Gly Met Ser Thr Lys Met Trp Asn Ile Ala Ile Thr Tyr Asp
 35 40 45
 Gly Leu Glu Glu Asp Asp Glu Val Phe Glu Val Ile Leu Asn Ser Pro
 50 55 60
 Val Asn Ala Val Leu Gly Thr Lys Thr Lys Ala Ala Val Lys Ile Leu
 65 70 75 80
 Asp Ser Lys Gly Gly Gln Cys His Pro Ser Tyr Ser Ser Asn Gln Ser
 85 90 95
 Lys His Ser Thr Trp Glu Lys Gly Ile Trp His Leu Leu Pro Gly
 100 105 110
 Ser Ser Ser Ser Thr Thr Ser Gly Ser Phe His Leu Glu Arg Arg Pro
 115 120 125
 Leu Pro Ser Ser Met Gln Leu Ala Val Ile Arg Gly Asp Thr Leu Arg
 130 135 140
 Gly Phe Asp Ser Thr Asp Leu Ser Gln Arg Lys Leu Arg Thr Arg Gly
 145 150 155 160
 Asn Gly Lys Thr Val Arg Pro Ser Ser Val Tyr Arg Asn Gly Thr Asp

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165          170          175
Ile Ile Tyr Asn Tyr His Gly Ile Val Ser Leu Lys Leu Glu Asp Asp
180          185          190
Ser Phe Pro Thr His Lys Arg Lys Ala Lys Val Ser Ile Ile Ser Gln
195          200          205
Pro Gln Lys Thr Ile Lys Val Ala Glu Leu Pro Gln Ala Asp Lys Val
210          215          220
Glu Ser Thr Thr Asp Ser His Phe Pro Arg Gln Asp Gln Leu Pro Ser
225          230          235          240
Phe Pro Lys Asn Cys Thr Leu Glu Leu Lys Gly Leu Phe His Phe Glu
245          250          255
Glu Gly Ile Gln Lys Leu Tyr Gln Cys Asn Gly Ile Ala Trp Lys Ala
260          265          270
Trp Ser Pro Gln Thr Lys Asp Val Glu Asp Lys Ser Cys Pro Ala Gly
275          280          285
Trp His Gln His Ser Gly Tyr Cys His Ile Leu Ile Thr Glu Gln Lys
290          295          300
Gly Thr Trp Asn Ala Ala Ala Gln Ala Cys Arg Glu Gln Tyr Leu Gly
305          310          315          320
Asn Leu Val Thr Val Phe Ser Arg Gln His Met Arg Trp Leu Trp Asp
325          330          335
Ile Gly Gly Arg Lys Ser Phe Trp Ile Gly Leu Asn Asp Gln Val His
340          345          350
Ala Gly His Trp Glu Trp Ile Gly Gly Glu Pro Val Ala Phe Thr Asn
355          360          365
Gly Arg Arg Gly Pro Ser Pro Arg Ser Lys Leu Gly Lys Ser Cys Val
370          375          380
Leu Val Gln Arg Gln Gly Lys Trp Gln Thr Lys Asp Cys Arg Arg Ala
385          390          395          400
Lys Pro His Asn Tyr Val Cys Ser Arg Lys Leu
405          410

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<210> 4299
<211> 988
<212> DNA
<213> Homo sapiens

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<400> 4299
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120
cctggggaca ggcccccgag cacaaagtga ggctgtctat ggagttctgc agcacgtgca
180
cagcagacca tatatcactc agttccttct ggaggtcctc ctccagcag ccactggctc
240
cctgcggtat ctcttcagtc tccggacagg cggctgtctc atgacctgc tgcttcctct
300
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360
tctctgagat ctcctctcc tgcgcttgga gcttctgata gatgaaggtc acctcctccc
420
gcaccagttc cagctcctcc cacaggaaact tcttgctgtc ccggtatctc tgggccagca
480

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gctgcaggca gcgagtggg cgggcccgct gcatctcctc actgtcacgc aggggtcttct
 540
 ccagcccctg aaggccttgg gtcagggccc catacagctc ctgccggccc tgctccatgc
 600
 cccacttggt ctcctccttc tctccatggc ggccctgtggg gctcagcacc tcttcaagct
 660
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 720
 ggaactcgaa agccttgggc tgggcctgta actggctctt gagtgactca agttcacatc
 780
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 900
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 cagagactga gtcacagaga ggggtgtc
 988

<210> 4300

<211> 84

<212> PRT

<213> Homo sapiens

<400> 4300

Gly	Cys	Leu	Trp	Ser	Ser	Ala	Ala	Arg	Ala	Gln	Gln	Thr	Ile	Tyr	His
1				5					10					15	
Ser	Val	Pro	Ser	Gly	Gly	His	Pro	Ser	Ser	His	Trp	Leu	Pro	Ala	
			20				25					30			
Val	Ser	Leu	Gln	Ser	Pro	Asp	Arg	Arg	Leu	Ser	His	Asp	Pro	Ala	Ala
			35				40				45				
Ser	Ser	Trp	Ser	Gly	Phe	Cys	Gly	Ile	Ser	Pro	Ala	Phe	Ser	Ala	Phe
			50			55				60					
Ser	Glu	Cys	Ser	Pro	Ser	Ser	Leu	Arg	Ser	His	Pro	Pro	Ala	Leu	Gly
65					70				75					80	
Ala	Ser	Asp	Arg												

<210> 4301

<211> 2429

<212> DNA

<213> Homo sapiens

<400> 4301

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 120
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 180
 ggattgtcgt tcagttctcg ctttgattca gggaatctag cccacgtgga gaaggtgaa
 240
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 300

gcctcttccc ctgactatga attcaacgtg tggacccgac cagactgtgc tgaacggaa
360
tttgagaatg ggaacaggtc atgggtctac ttcagcgtcc ggggaggaat gccaggaaaa
420
ctcatcaaga tcaacattat gaacatgaac aagcagagca agctgtatc ccagggcatg
480
gcccccttgg tgcgcacact gccaccocgg ccacgctggg aacgcattcg agaccggccc
540
acctttgaga tgacagagac gcagtttggg ttatcctttg ttcacgttt cgtggagggc
600
cgtggggcca ccaccttctt cgcttctgc taccctctct cctacagtga ctgccaggaa
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720
gataccatct attaccatcg ggagctcctt tgctattctc tggatggact tcgtgtagat
780
ctgctgacga tcaacttctg ccatgggctt cgagaagatc gagagccccg tctagagcag
840
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900
ttaagcagta gactacacc aggggagact ccatctagct ttgtcttcaa tggctttctg
960
gacttcatcc tccgacctga tgatccccg gcccaaaccc tccgtcgctt ctctgtcttt
1020
aagctgatto ccatgttgaa ccccgatggg gtgggtccgg gacactaccg cacagactca
1080
cgtggagtga atctgaacgg tcagtacctg aagcctgatg ccgtcctgca cccggccatc
1140
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1200
tcctctgagc accagcccag ttctgtctc cctcctgatg ctctgtttc tgacctggag
1260
aaagccaaca atctccaaaa tgaagctcag tgtgggacct cagctgacag gcataacgct
1320
gaagcctgga aacaaacaga gccagcagaa cagaagctca acagtgtgtg gattatgcc
1380
caacagctcg cggggcttga agagtcagcc cctgatacca tccccccaa agagagtggc
1440
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1500
aacagcttta gtgatgagag caccaggtg gaaacatcg tatatccaaa gctcatctcc
1560
ttgaattcag cccacttcga cttccagggc tgcaatttct cagagaagaa tatgtatgcc
1620
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1740
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1800
ccctccagat acactgtgga actatttgag cagggtgggac gagctatggc cattgcagcc
1860
ctggacatgg cggaatgtaa tccgtggccc cgaattgtac tgcagagca cagcagcctt
1920

actaatctac gggcctggat gctgaacat gtacgaaca gccgaggcct aagcagcact
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 ctgaatgttg gtgtcaaca gaagaggggc ctctgaactc caccacaaag tcacaatggg
 2040
 ttgcctgtct cctgctccga aaacaccttg agtcgggcac gaagtttttag caccggcaca
 2100
 agtgccgggtg gtacgacgag cagccaacaa aattctccac agatgaagaa ttccccagc
 2160
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 2220
 gtcaccaccc ggggtgctggg ccccgtcaga ggtaagccag tctgggagcc cctgcaacat
 2280
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 2340
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 2400
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 2429

<210> 4302

<211> 717

<212> PRT

<213> Homo sapiens

<400> 4302

Met	Glu	Leu	Arg	Cys	Gly	Gly	Leu	Leu	Phe	Ser	Ser	Arg	Phe	Asp	Ser
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Gly	Asn	Leu	Ala	His	Val	Glu	Lys	Val	Glu	Ser	Leu	Ser	Ser	Asp	Gly
			20					25					30		
Glu	Gly	Val	Gly	Gly	Gly	Ala	Ser	Ala	Leu	Thr	Ser	Gly	Ile	Ala	Ser
		35					40					45			
Ser	Pro	Asp	Tyr	Glu	Phe	Asn	Val	Trp	Thr	Arg	Pro	Asp	Cys	Ala	Glu
						55					60				
Thr	Glu	Phe	Glu	Asn	Gly	Asn	Arg	Ser	Trp	Phe	Tyr	Phe	Ser	Val	Arg
65					70					75					80
Gly	Gly	Met	Pro	Gly	Lys	Leu	Ile	Lys	Ile	Asn	Ile	Met	Asn	Met	Asn
				85					90				95		
Lys	Gln	Ser	Lys	Leu	Tyr	Ser	Gln	Gly	Met	Ala	Pro	Phe	Val	Arg	Thr
			100					105					110		
Leu	Pro	Thr	Arg	Pro	Arg	Trp	Glu	Arg	Ile	Arg	Asp	Arg	Pro	Thr	Phe
			115					120				125			
Glu	Met	Thr	Glu	Thr	Gln	Phe	Val	Leu	Ser	Phe	Val	His	Arg	Phe	Val
			130			135					140				
Glu	Gly	Arg	Gly	Ala	Thr	Thr	Phe	Phe	Ala	Phe	Cys	Tyr	Pro	Phe	Ser
145					150				155						160
Tyr	Ser	Asp	Cys	Gln	Glu	Leu	Leu	Asn	Gln	Leu	Asp	Gln	Arg	Phe	Pro
			165					170					175		
Glu	Asn	His	Pro	Thr	His	Ser	Ser	Pro	Leu	Asp	Thr	Ile	Tyr	Tyr	His
			180					185					190		
Arg	Glu	Leu	Leu	Cys	Tyr	Ser	Leu	Asp	Gly	Leu	Arg	Val	Asp	Leu	Leu
			195					200				205			
Thr	Ile	Thr	Ser	Cys	His	Gly	Leu	Arg	Glu	Asp	Arg	Glu	Pro	Arg	Leu
			210			215					220				
Glu	Gln	Leu	Phe	Pro	Asp	Thr	Ser	Thr	Pro	Arg	Pro	Phe	Arg	Phe	Ala

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225          230          235          240
Gly Lys Arg Ile Phe Phe Leu Ser Ser Arg Val His Pro Gly Glu Thr
                245          250          255
Pro Ser Ser Phe Val Phe Asn Gly Phe Leu Asp Phe Ile Leu Arg Pro
                260          265          270
Asp Asp Pro Arg Ala Gln Thr Leu Arg Arg Leu Phe Val Phe Lys Leu
                275          280          285
Ile Pro Met Leu Asn Pro Asp Gly Val Val Arg Gly His Tyr Arg Thr
                290          295          300
Asp Ser Arg Gly Val Asn Leu Asn Arg Gln Tyr Leu Lys Pro Asp Ala
305          310          315          320
Val Leu His Pro Ala Ile Tyr Gly Ala Lys Ala Val Leu Leu Tyr His
                325          330          335
His Val His Ser Arg Leu Asn Ser Gln Ser Ser Ser Glu His Gln Pro
                340          345          350
Ser Ser Cys Leu Pro Pro Asp Ala Pro Val Ser Asp Leu Glu Lys Ala
355          360          365
Asn Asn Leu Gln Asn Glu Ala Gln Cys Gly His Ser Ala Asp Arg His
370          375          380
Asn Ala Glu Ala Trp Lys Gln Thr Glu Pro Ala Glu Gln Lys Leu Asn
385          390          395          400
Ser Val Trp Ile Met Pro Gln Gln Ser Ala Gly Leu Glu Glu Ser Ala
                405          410          415
Pro Asp Thr Ile Pro Pro Lys Glu Ser Gly Val Ala Tyr Tyr Val Asp
                420          425          430
Leu His Gly His Ala Ser Lys Arg Gly Cys Phe Met Tyr Gly Asn Ser
435          440          445
Phe Ser Asp Glu Ser Thr Gln Val Glu Asn Met Leu Tyr Pro Lys Leu
450          455          460
Ile Ser Leu Asn Ser Ala His Phe Asp Phe Gln Gly Cys Asn Phe Ser
465          470          475          480
Glu Lys Asn Met Tyr Ala Arg Asp Arg Arg Asp Gly Gln Ser Lys Glu
                485          490          495
Gly Ser Gly Arg Val Ala Ile Tyr Lys Ala Ser Gly Ile Ile His Ser
500          505          510
Tyr Thr Leu Glu Cys Asn Tyr Asn Thr Gly Arg Ser Val Asn Ser Ile
515          520          525
Pro Ala Ala Cys His Asp Asn Gly Arg Ala Ser Pro Pro Pro Pro
530          535          540
Ala Phe Pro Ser Arg Tyr Thr Val Glu Leu Phe Glu Gln Val Gly Arg
545          550          555          560
Ala Met Ala Ile Ala Ala Leu Asp Met Ala Glu Cys Asn Pro Trp Pro
565          570          575
Arg Ile Val Leu Ser Glu His Ser Ser Leu Thr Asn Leu Arg Ala Trp
580          585          590
Met Leu Lys His Val Arg Asn Ser Arg Gly Leu Ser Ser Thr Leu Asn
595          600          605
Val Gly Val Asn Lys Lys Arg Gly Leu Arg Thr Pro Pro Lys Ser His
610          615          620
Asn Gly Leu Pro Val Ser Cys Ser Glu Asn Thr Leu Ser Arg Ala Arg
625          630          635          640
Ser Phe Ser Thr Gly Thr Ser Ala Gly Gly Ser Ser Ser Ser Gln Gln
                645          650          655
Asn Ser Pro Gln Met Lys Asn Ser Pro Ser Phe Pro Phe His Gly Ser

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	660		665		670										
Arg	Pro	Ala	Gly	Leu	Pro	Gly	Leu	Gly	Ser	Ser	Thr	Gln	Lys	Val	Thr
	675		680		685										
His	Arg	Val	Leu	Gly	Pro	Val	Arg	Gly	Lys	Pro	Val	Trp	Glu	Pro	Leu
	690		695		700										
Gln	His	Val	Phe	Gly	Cys	Leu	Gly	His	Cys	Trp	Gly	Lys			
705			710						715						

<210> 4303

<211> 768

<212> DNA

<213> Homo sapiens

<400> 4303

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120
ggtgtgtgcc ggacaggaac agttaatagt gttggaagta atcaatccat tcccagcatg
180
tccatcagtg ccagcagcca aagcagtagt gttaacagtc ttccagatgt ctcagatgac
240
aagactgagc tagacatgat ggagggagac cacacagtga tgtctaacag ttctgtttac
300
catttaaaac cagaggaaga aaattacaga gaagagggag atcctagaac aagagcatca
360
gatccacaat ctccacccca agtatctcgt cacaatcac actatcgtaa tcgagaacac
420
tttgcacta tacggacagc atcactgggtt acgaggcaaa tgcaagaaca tgagcaggac
480
tctgagctta gagaacaaat gtctggctat aagcgaatga ggcgacaaca tcaaaagcaa
540
ctgatgactc tggaaaaaaa gctaaaggct gagatggatg aacatcgctt cagattagac
600
aaagatcttg aaactcagcg taacaatttt gctgcagaaa tggagaaact tatcaagaaa
660
caccaggctg ctatggagaa agaggctaaa gtgatgtcca atgaagagaa aaaatttcag
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768

<210> 4304

<211> 256

<212> PRT

<213> Homo sapiens

<400> 4304

Thr	Arg	Ala	Ala	Arg	Glu	Leu	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys
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Lys	Leu	Leu	Phe	Gln	Glu	Ala	His	Asn	Gly	Pro	Ala	Val	Glu	Ala	Gln
			20					25					30		
Glu	Glu	Glu	Glu	Glu	Gln	Asp	His	Gly	Val	Gly	Arg	Thr	Gly	Thr	Val
			35				40					45			
Asn	Ser	Val	Gly	Ser	Asn	Gln	Ser	Ile	Pro	Ser	Met	Ser	Ile	Ser	Ala

50					55					60					
Ser	Ser	Gln	Ser	Ser	Ser	Val	Asn	Ser	Leu	Pro	Asp	Val	Ser	Asp	Asp
65					70					75				80	
Lys	Ser	Glu	Leu	Asp	Met	Met	Glu	Gly	Asp	His	Thr	Val	Met	Ser	Asn
			85						90					95	
Ser	Ser	Val	Ile	His	Leu	Lys	Pro	Glu	Glu	Asn	Tyr	Arg	Glu	Glu	Glu
			100					105					110		
Gly	Asp	Pro	Arg	Thr	Arg	Ala	Ser	Asp	Pro	Gln	Ser	Pro	Pro	Gln	Val
		115					120					125			
Ser	Arg	His	Lys	Ser	His	Tyr	Arg	Asn	Arg	Glu	His	Phe	Ala	Thr	Ile
	130				135						140				
Arg	Thr	Ala	Ser	Leu	Val	Thr	Arg	Gln	Met	Gln	Glu	His	Glu	Gln	Asp
145					150					155					160
Ser	Glu	Leu	Arg	Glu	Gln	Met	Ser	Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln
			165						170					175	
His	Gln	Lys	Gln	Leu	Met	Thr	Leu	Glu	Asn	Lys	Leu	Lys	Ala	Glu	Met
		180					185						190		
Asp	Glu	His	Arg	Leu	Arg	Leu	Asp	Lys	Asp	Leu	Glu	Thr	Gln	Arg	Asn
	195					200						205			
Asn	Phe	Ala	Ala	Glu	Met	Glu	Lys	Leu	Ile	Lys	Lys	His	Gln	Ala	Ala
	210				215					220					
Met	Glu	Lys	Glu	Ala	Lys	Val	Met	Ser	Asn	Glu	Glu	Lys	Lys	Phe	Gln
225					230					235					240
Gln	His	Ile	Gln	Ala	Gln	Gln	Lys	Lys	Glu	Leu	Asn	Ser	Phe	Leu	Glu
			245						250					255	

<210> 4305

<211> 3400

<212> DNA

<213> Homo sapiens

<400> 4305

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 120
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 180
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 240
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 300
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 360
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 420
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 480
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 540
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 600
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 660

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720
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780
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2100
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2280

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2340
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3180
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3240
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<210> 4306

<211> 1052

<212> PRT

<213> Homo sapiens

<400> 4306

Met	Ala	Gly	Met	Asp	Ser	Gly	Asn	Leu	Lys	Thr	Ala	Arg	Leu	Trp	Arg
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Asp	Ala	Ala	Leu	Arg	Ala	Arg	Lys	Leu	Arg	Ser	Asn	Leu	Arg	Gln	Leu
			20						25				30		
Thr	Leu	Thr	Ala	Ala	Gly	Ala	Cys	Pro	Gly	Ala	Gly	Ala	Asp	Ala	Leu
			35				40					45			
Glu	Ser	Pro	Ala	Ser	Pro	Gln	Leu	Val	Leu	Pro	Ala	Asn	Leu	Gly	Asp
	50					55					60				
Ile	Glu	Ala	Leu	Asn	Leu	Gly	Asn	Asn	Gly	Leu	Glu	Glu	Val	Pro	Glu

65					70					75					80
Gly	Leu	Gly	Ser	Ala	Leu	Gly	Ser	Leu	Arg	Val	Leu	Val	Leu	Arg	Arg
			85						90					95	
Asn	Arg	Phe	Ala	Arg	Leu	Pro	Pro	Ala	Val	Ala	Glu	Leu	Gly	His	His
			100					105					110		
Leu	Thr	Glu	Leu	Asp	Val	Ser	His	Asn	Arg	Leu	Thr	Ala	Leu	Gly	Ala
		115					120					125			
Glu	Val	Val	Ser	Ala	Leu	Arg	Glu	Leu	Arg	Lys	Leu	Asn	Leu	Ser	His
	130					135					140				
Asn	Gln	Leu	Pro	Ala	Leu	Pro	Ala	Gln	Leu	Gly	Ala	Leu	Ala	His	Leu
145					150					155					160
Glu	Glu	Leu	Asp	Val	Ser	Phe	Asn	Arg	Leu	Ala	His	Leu	Pro	Asp	Ser
			165					170						175	
Leu	Ser	Cys	Leu	Ser	Arg	Leu	Arg	Thr	Leu	Asp	Val	Asp	His	Asn	Gln
		180						185					190		
Leu	Thr	Ala	Phe	Pro	Arg	Gln	Leu	Gln	Leu	Val	Ala	Leu	Glu	Glu	
	195					200					205				
Leu	Asp	Val	Ser	Ser	Asn	Arg	Leu	Arg	Gly	Leu	Pro	Glu	Asp	Ile	Ser
	210					215					220				
Ala	Leu	Arg	Ala	Leu	Lys	Ile	Leu	Trp	Leu	Ser	Gly	Ala	Glu	Leu	Gly
225					230					235					240
Thr	Leu	Pro	Ala	Gly	Phe	Cys	Glu	Leu	Ala	Ser	Leu	Glu	Ser	Leu	Met
			245					250						255	
Leu	Asp	Asn	Asn	Gly	Leu	Gln	Ala	Leu	Pro	Ala	Gln	Phe	Ser	Cys	Leu
		260					265					270			
Gln	Arg	Leu	Lys	Met	Leu	Asn	Leu	Ser	Ser	Asn	Leu	Phe	Glu	Glu	Phe
	275					280						285			
Pro	Ala	Ala	Leu	Leu	Pro	Leu	Ala	Gly	Leu	Glu	Glu	Leu	Tyr	Leu	Ser
	290				295					300					
Arg	Asn	Gln	Leu	Thr	Ser	Val	Pro	Ser	Leu	Ile	Ser	Gly	Leu	Gly	Arg
305					310					315					320
Leu	Leu	Thr	Leu	Trp	Leu	Asp	Asn	Asn	Arg	Ile	Arg	Tyr	Leu	Pro	Asp
			325					330						335	
Ser	Ile	Val	Glu	Leu	Thr	Gly	Leu	Glu	Glu	Leu	Val	Leu	Gln	Gly	Asn
		340					345						350		
Gln	Ile	Ala	Val	Leu	Pro	Asp	His	Phe	Gly	Gln	Leu	Ser	Arg	Val	Gly
	355					360						365			
Leu	Trp	Lys	Ile	Lys	Asp	Asn	Pro	Leu	Ile	Gln	Pro	Pro	Tyr	Glu	Val
	370					375				380					
Cys	Met	Lys	Gly	Ile	Pro	Tyr	Ile	Ala	Ala	Tyr	Gln	Lys	Glu	Leu	Ala
385					390					395					400
His	Ser	Gln	Pro	Ala	Val	Gln	Pro	Arg	Leu	Lys	Leu	Leu	Leu	Met	Gly
			405					410						415	
His	Lys	Ala	Ala	Gly	Lys	Thr	Leu	Leu	Arg	His	Cys	Leu	Thr	Glu	Glu
		420						425					430		
Arg	Val	Glu	Gly	Cys	Pro	Gly	Gly	Gly	Asp	Lys	Glu	Lys	Cys	Tyr	Pro
		435				440					445				
Pro	Ser	Pro	Pro	Pro	Val	Ser	Lys	Gly	Ile	Glu	Val	Thr	Ser	Trp	Thr
	450					455				460					
Ala	Asp	Ala	Ser	Arg	Gly	Leu	Arg	Phe	Ile	Val	Tyr	Asp	Leu	Ala	Gly
465					470					475					480
Asp	Glu	Ser	Tyr	Glu	Val	Ile	Gln	Pro	Phe	Phe	Leu	Ser	Pro	Gly	Ala
				485				490					495		
Leu	Tyr	Val	Leu	Val	Val	Asn	Leu	Ala	Thr	Tyr	Glu	Pro	Arg	His	Phe

[illegible]

930		935		940
Ser His Ala Ser Leu Pro Asn Ile Trp Thr Ala Trp Gln Ala Ile Thr				
945		950		955
Pro Leu Val Glu Glu Leu Asn Val Leu Leu Gln Glu Trp Pro Gly Leu				960
	965		970	975
His Tyr Thr Val His Ile Leu Cys Ser Lys Cys Leu Lys Arg Gly Ser				990
	980		985	
Pro Asn Pro His Ala Phe Pro Gly Glu Leu Leu Ser Gln Pro Arg Pro				
	995	1000	1005	
Glu Gly Val Ala Glu Ile Ile Cys Pro Lys Asn Gly Ser Glu Arg Val				
	1010	1015	1020	
Asn Val Ala Leu Val Tyr Pro Pro Thr Pro Thr Val Ile Ser Pro Cys				
1025		1030	1035	1040
Ser Lys Lys Asn Val Gly Glu Lys His Arg Asn Gln				
	1045	1050		

<210> 4307

<211> 947

<212> DNA

<213> Homo sapiens

<400> 4307

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 300
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 360
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 420
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 720
 aactgccctc gccagtgcgc acagcttctt ttctagtggg gctgacttcc cagaggccat
 780
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 947

<210> 4308
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 4308
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 Ala Pro Gly Ala Arg Cys His Gly Asp Ala Pro Gly Ser Leu Ala Ala
 35 40 45
 Arg Cys Gly Cys Gly Val Gln Gly Val Gln Gly Thr Ala Arg Cys Ala
 50 55 60
 Ser Cys Ser Cys Cys His Ala Ser Leu Cys Pro Ala Gly Gly Cys Gly
 65 70 75 80
 Trp Gly Cys Ser Phe Leu Thr Gly Xaa Cys Gly Gly Ser Gly Ala Xaa
 85 90 95
 Cys Gly Asp Cys Glu Gly Phe Asp Val His Ile Met Asp Asp Met Ile
 100 105 110
 Lys Val Gly Arg Ala Thr Leu Cys Ile Val Pro Pro Thr Cys Ser Cys
 115 120 125
 Ile Ala Gly Leu Ser Gln Gly Pro Ser Leu Gly Ser Thr Gly Ser Ser
 130 135 140
 Val Gly Gly Ser Glu Val Arg Cys Cys His Phe Val Trp Phe Asn Met
 145 150 155 160
 Ser Ile Ala Trp Tyr Gln Pro Cys Ser Trp Leu Arg Ala Val Thr Leu
 165 170 175
 Cys Gln Asn Leu His Trp Ala Cys Thr Ser Cys His Cys Asn Cys Pro
 180 185 190
 Cys Gln Cys Pro Gln Leu Leu Phe
 195 200

<210> 4309
 <211> 1928
 <212> DNA
 <213> Homo sapiens

<400> 4309
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 180
 tccatttgaa atctcaacct tttcagggtc actatcacct tcaatgacat tcacagaagt
 240
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 300
 aagatttggt tcatcattca cctgttgaat tataaccctt tctgaatgct ttgatttata
 360
 ataggcatg aaaaattcag ttggtgaagg gaatatctgc ttctcatcct ttggtgcga
 420

caataacata tccaaagcct tttggtattg ttgacgttcc tgetgaattg ttacttccat
480
ttcatttttt aattcatttg gttctgaatt cccagccttt tcaaaatcaa atacattcaa
540
catatcaaca tcattttgct ttacogagtt ttccctccgat gtgcagccta agtctacttt
600
caggacatgc agcagggtgc gcattttttc ctctccaaa tgtttatttt gttttatatg
660
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720
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1080
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1140
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1260
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1440
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1500
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1680
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1740
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1800
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1920
tggaggac
1928

<210> 4310

<211> 599
 <212> PRT
 <213> Homo sapiens

<400> 4310

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Gly Pro Pro Cys Leu Phe Lys Gly His Leu Ser Thr Lys Ser Asn Ala
      20              25              30
Phe Cys Thr Asp Ser Ser Ser Leu Arg Leu Ser Thr Leu Gln Leu Val
      35              40              45
Lys Asn His Met Ala Val His Tyr Asn Lys Ile Leu Ser Ala Lys Ala
      50              55              60
Ala Val Asp Cys Ser Val Pro Val Ser Val Ser Thr Ser Ile Lys Tyr
      65              70              75              80
Ala Asp Gln Gln Arg Arg Glu Lys Leu Lys Lys Glu Leu Ala Gln Cys
      85              90              95
Glu Lys Glu Phe Lys Leu Thr Lys Thr Ala Met Arg Ala Asn Tyr Lys
      100             105             110
Asn Asn Ser Lys Ser Leu Phe Asn Thr Leu Gln Lys Pro Ser Gly Glu
      115             120             125
Pro Gln Ile Glu Asp Asp Met Leu Lys Glu Glu Met Asn Gly Phe Ser
      130             135             140
Ser Phe Ala Arg Ser Leu Val Pro Ser Ser Glu Arg Leu His Leu Ser
      145             150             155             160
Leu His Lys Ser Ser Lys Val Ile Thr Asn Gly Pro Glu Lys Asn Ser
      165             170             175
Ser Ser Ser Pro Ser Ser Val Asp Tyr Ala Ala Ser Gly Pro Arg Lys
      180             185             190
Leu Ser Ser Gly Ala Leu Tyr Gly Arg Arg Pro Arg Ser Thr Phe Pro
      195             200             205
Asn Ser His Arg Phe Gln Leu Val Ile Ser Lys Ala Pro Ser Gly Asp
      210             215             220
Leu Leu Asp Lys His Ser Glu Leu Phe Ser Asn Lys Gln Leu Pro Phe
      225             230             235             240
Thr Pro Arg Thr Leu Lys Thr Glu Ala Lys Ser Phe Leu Ser Gln Tyr
      245             250             255
Arg Tyr Tyr Thr Pro Ala Lys Arg Lys Lys Asp Phe Thr Asp Gln Arg
      260             265             270
Ile Glu Ala Glu Thr Gln Thr Glu Leu Ser Phe Lys Ser Glu Leu Gly
      275             280             285
Thr Ala Glu Thr Lys Asn Met Thr Asp Ser Glu Met Asn Ile Lys Gln
      290             295             300
Ala Ser Asn Cys Val Thr Tyr Asp Ala Lys Glu Lys Ile Ala Pro Leu
      305             310             315             320
Pro Leu Glu Gly His Asp Ser Thr Trp Asp Glu Ile Lys Asp Asp Ala
      325             330             335
Leu Gln His Ser Ser Pro Arg Ala Met Cys Gln Tyr Ser Leu Lys Pro
      340             345             350
Pro Ser Thr Arg Lys Ile Tyr Ser Asp Glu Glu Glu Leu Leu Tyr Leu
      355             360             365
Ser Phe Ile Glu Asp Val Thr Asp Glu Ile Leu Lys Leu Gly Leu Phe
      370             375             380
Ser Asn Arg Phe Leu Glu Arg Leu Phe Glu Arg His Ile Lys Gln Asn

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385          390          395          400
Lys His Leu Glu Glu Glu Lys Met Arg His Leu Leu His Val Leu Lys
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Val Asp Leu Gly Cys Thr Ser Glu Glu Asn Ser Val Lys Gln Asn Asp
          420          425          430
Val Asp Met Leu Asn Val Phe Asp Phe Glu Lys Ala Gly Asn Ser Glu
          435          440          445
Pro Asn Glu Leu Lys Asn Glu Ser Glu Val Thr Ile Gln Gln Glu Arg
          450          455          460
Gln Gln Tyr Gln Lys Ala Leu Asp Met Leu Leu Ser Ala Pro Lys Asp
          465          470          475          480
Glu Asn Glu Ile Phe Pro Ser Pro Thr Glu Phe Phe Met Pro Ile Tyr
          485          490          495
Lys Ser Lys His Ser Glu Gly Val Ile Ile Gln Gln Val Asn Asp Glu
          500          505          510
Thr Asn Leu Glu Thr Ser Thr Leu Asp Glu Asn His Pro Ser Ile Ser
          515          520          525
Asp Ser Leu Thr Asp Arg Glu Thr Ser Val Asn Val Ile Glu Gly Asp
          530          535          540
Ser Asp Pro Glu Lys Val Glu Ile Ser Asn Gly Leu Cys Gly Leu Asn
          545          550          555          560
Thr Ser Pro Ser Gln Ser Val Gln Phe Ser Ser Val Lys Gly Asp Asn
          565          570          575
Asn His Asp Met Glu Leu Ser Thr Leu Lys Ile Met Glu Met Ser Ile
          580          585          590
Glu Asp Cys Pro Leu Asp Val
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<210> 4311

<211> 432

<212> DNA

<213> Homo sapiens

<400> 4311

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120
aaaaacataa ccaactgggc atctgcagca tcccagactc agatgcctac gggccagaca
180
ggcaactgtg agtccccctt agggagcaag gaggacctca actccaaaga gaacctggat
240
gccgatgagg gagatgggaa aagtaacgac ctgcctctta gttgtcctta ctttagaaat
300
gagactggag gggaaggcga caggcggatt gcgctctctc gagccaactc atcctctttc
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<210> 4312

<211> 144

<212> PRT

<213> Homo sapiens

<400> 4312

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Xaa Arg Val Lys Gly Ile Arg Pro Trp Asn Cys Gln Arg Cys Phe Ala
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His Tyr Asp Val Gln Ser Ile Leu Phe Asn Ile Asn Glu Ala Met Ala
           20           25           30
Thr Arg Ala Asn Val Gly Lys Arg Lys Asn Ile Thr Thr Gly Ala Ser
           35           40           45
Ala Ala Ser Gln Thr Gln Met Pro Thr Gly Gln Thr Gly Asn Cys Glu
           50           55           60
Ser Pro Leu Gly Ser Lys Glu Asp Leu Asn Ser Lys Glu Asn Leu Asp
65           70           75           80
Ala Asp Glu Gly Asp Gly Lys Ser Asn Asp Leu Val Leu Ser Cys Pro
           85           90           95
Tyr Phe Arg Asn Glu Thr Gly Gly Glu Gly Asp Arg Arg Ile Ala Leu
           100          105          110
Ser Arg Ala Asn Ser Ser Ser Phe Ser Ser Gly Glu Ser Cys Ser Phe
           115          120          125
Glu Ser Ser Leu Ser Ser His Cys Thr Asn Ala Gly Val Ser Val Leu
130          135          140

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<210> 4313

<211> 936

<212> DNA

<213> Homo sapiens

<400> 4313

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120
attcagtatc caaccatcct ctccattctc ctctggacct caccactctc agagctgctt
180
gtcctggcag aatctacagt tcaccccaac tctatgcctt acccctccca acccaacagc
240
atttgacagt tgcaaaatat acagacccaa gtcctgaggg gactgaggac atgatgctgg
300
gccaagtct cctgctcagg gcttctctcc aatgccagcc ctgccactcc ttctcacc
360
tccttgagc ctctctgct gcttgtctat cccaacggcc ctgctccct ccttctctgc
420
ccttcaccag ctttctggga caccatgccc tgaggaaggg acctttgggt ttctctaaac
480
atctttgaag ggctgaggca gtcagggtg gctgccttgt cactctttat ttggaagcca
540
ctcaaaccat tccaagaag agggacctca gctggcaatc tggaaacctg gcccagggtc
600
gggcagatgt cttcacttct cctaccttcc cagtcttgtg atcctgtgat gagoaccagg
660
atggccctgt ggtccctaga gcacccctca tgcgtgtaggg tctcgagcc ccataccttc
720
tctaactggc cctggatatc tggctcctct ctcagctctg ccaactgatct ctgtgcctta
780

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gtttacttct ctgcacgggg gactcaccac aagaccattt ccagcagctt cccagggtgat
 840
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 900
 caccaggctg ctccagaatga ggtgactgcg ggcaac
 936

<210> 4314
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 4314
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 Thr Arg Met Ala Leu Trp Ser Leu Glu His Pro Ser Cys Cys Arg Val
 20 25 30
 Leu Gln Pro His Pro Phe Ser Thr Gly Pro Trp Tyr Pro Gly Ser Ser
 35 40 45
 Leu Ser Ser Ala Thr Asp Leu Cys Ala Leu Val Tyr Phe Ser Ala Arg
 50 55 60
 Gly Thr His Pro Lys Thr Ile Ser Ser Ser Phe Pro Gly Asp Val Val
 65 70 75 80
 Pro Gln Gly Trp Ala Leu Gln Leu Trp Pro Ser Ser Leu Val Leu Pro
 85 90 95
 Arg Arg His Gln Ala Ala Gln Asn Glu Val Thr Ala Gly Asn
 100 105 110

<210> 4315
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 4315
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 120
 cacctaccat ccaagccatg gtcaccttca ccaagccaca gtcacttacc atccaaggca
 180
 ccgtcaccta ccatccaagc catggccacc tacctgccaa gccatggcca cctaccggcc
 240
 aagccatggt cacctaccca ccaagtcagt gtcgcctacc atccaaggag caggcctgga
 300
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 360
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 420
 tctcttgatc cagttgcatt agccagttaa cctaccgggg cccttctgca gtcgcctggc
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 573

<210> 4316
 <211> 169
 <212> PRT
 <213> Homo sapiens

<400> 4316
 Xaa Leu Ile Gln Tyr Asp Trp Cys Pro Tyr Lys Lys Arg Lys Leu Gly
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 His Arg Gln Ala Gln Ser Asp Asp His Val Lys Thr Gln Gly Arg Asp
 20 25 30
 Gly His Leu Pro Pro Arg His Gly His Leu Pro Ser Lys Pro Trp Ser
 35 40 45
 Pro Ser Pro Ser His Ser His Leu Pro Ser Lys Pro Pro Ser Pro Thr
 50 55 60
 Ile Gln Ala Met Ala Thr Tyr Leu Pro Ser His Gly His Leu Pro Ala
 65 70 75 80
 Lys Pro Trp Ser Pro Thr His Gln Val Met Val Ala Tyr His Pro Arg
 85 90 95
 Ser Arg Pro Gly Thr Asp Pro Ser Pro Glu Pro Ser Val Gly Ala Asn
 100 105 110
 Pro Ala Asp Thr Leu Ile Ser Asp Phe Lys Pro Pro Glu Leu Trp Asp
 115 120 125
 Asn Pro Ser Leu Ser Phe Asn Pro Pro Ser Met Trp Ser Leu Val Thr
 130 135 140
 Val Ala Leu Ala Ser Glu Pro Thr Arg Ala Leu Leu Gln Ser Pro Gly
 145 150 155 160
 Ser Gly Val Val Leu Val Arg Lys Phe
 165

<210> 4317
 <211> 744
 <212> DNA
 <213> Homo sapiens

<400> 4317
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 120
 gatgttatca ttgggtgga aggaaaagaa ttctcttgcc atagagctgt gctctcagcc
 180
 ttagcagcgt acttcagagc tatgttttgt aatgaccaca gggaaagccg agaaatgttg
 240
 gttgagatca atggtatttt agctgaagct atggaatggt ttttgacagta tggtttatact
 300
 ggaaagggtga agatcactac agagaatgta cagtatctct ttgagacatc aagcctcttt
 360
 cagattagtg ttctccgtga tgcacgtgcc aagttcttgg aggagcaact tgatccttgt
 420
 aattgcttag gaatccagcg ctttgctgat acccattcac tcaaaacact cttcacaaaa
 480
 tgcaaaaatt ttgcgttaca gacttttgag gatgtatccc agcacgaaga atttcttgag
 540

cttgacaaag atgaacttat tgattatatt tgtagtgatg aacttggtat tggtaaagag
 600
 gagatgggtt ttgaagccgt catgcgttgg gtctatcggt ccgttgatct gagaagacca
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 720
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 744

<210> 4318

<211> 239

<212> PRT

<213> Homo sapiens

<400> 4318

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Ile	Leu	Gln	Ile	Phe	Asn	Glu	Phe	Arg	Asp	Ser	Arg	Leu	Phe	Thr	Asp
		20						25					30		
Val	Ile	Ile	Trp	Val	Glu	Gly	Lys	Glu	Phe	Pro	Cys	His	Arg	Ala	Val
		35					40					45			
Leu	Ser	Ala	Cys	Ser	Ser	Tyr	Phe	Arg	Ala	Met	Phe	Cys	Asn	Asp	His
	50				55						60				
Arg	Glu	Ser	Arg	Glu	Met	Leu	Val	Glu	Ile	Asn	Gly	Ile	Leu	Ala	Glu
65					70					75					80
Ala	Met	Glu	Cys	Phe	Leu	Gln	Tyr	Val	Tyr	Thr	Gly	Lys	Val	Lys	Ile
			85						90				95		
Thr	Thr	Glu	Asn	Val	Gln	Tyr	Leu	Phe	Glu	Thr	Ser	Ser	Leu	Phe	Gln
			100					105					110		
Ile	Ser	Val	Leu	Arg	Asp	Ala	Cys	Ala	Lys	Phe	Leu	Glu	Gln	Leu	
		115				120						125			
Asp	Pro	Cys	Asn	Cys	Leu	Gly	Ile	Gln	Arg	Phe	Ala	Asp	Thr	His	Ser
	130					135					140				
Leu	Lys	Thr	Leu	Phe	Thr	Lys	Cys	Lys	Asn	Phe	Ala	Leu	Gln	Thr	Phe
			145			150				155					160
Glu	Asp	Val	Ser	Gln	His	Glu	Glu	Phe	Leu	Glu	Leu	Asp	Lys	Asp	Glu
			165					170					175		
Leu	Ile	Asp	Tyr	Ile	Cys	Ser	Asp	Glu	Leu	Val	Ile	Gly	Lys	Glu	Glu
		180					185						190		
Met	Val	Phe	Glu	Ala	Val	Met	Arg	Trp	Val	Tyr	Arg	Ala	Val	Asp	Leu
		195					200					205			
Arg	Arg	Pro	Leu	Leu	His	Glu	Leu	Leu	Thr	His	Val	Arg	Leu	Pro	Leu
		210				215					220				
Leu	His	Pro	Asn	Tyr	Phe	Val	Gln	Thr	Val	Glu	Val	Asp	Gln	Leu	
225					230					235					

<210> 4319

<211> 388

<212> DNA

<213> Homo sapiens

<400> 4319

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 120
 gcagtcgcaa gtgactcttg caataatagc atctcactcc tatctgaaaa gttgacaagc
 180
 agctgttccc cccatcatat caagagaagt gtagtggaag ctatgcaacg ccaagctcgg
 240
 aaaatgtgca attacgacaa aatcttggcc acaaagaaaa acctagacca tgtcaataaa
 300
 atcttaaaag ccaaaaaaact tcaaaggcag gccaggacag ggaataaact tgtgaaacgt
 360
 aggccaggtc gaccgcggtc ggagagag
 388

<210> 4320

<211> 129

<212> PRT

<213> Homo sapiens

<400> 4320

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Pro	Ser	Ser	Ser	Pro	Gly	Arg	Ser	His	Ser	Lys	Asp	Arg	Thr	Leu	Gly
			20				25						30		
Lys	Pro	Asp	Ser	Leu	Leu	Val	Pro	Ala	Val	Ala	Ser	Asp	Ser	Cys	Asn
		35					40					45			
Asn	Ser	Ile	Ser	Leu	Leu	Ser	Glu	Lys	Leu	Thr	Ser	Ser	Cys	Ser	Pro
		50				55					60				
His	His	Ile	Lys	Arg	Ser	Val	Val	Glu	Ala	Met	Gln	Arg	Gln	Ala	Arg
65					70				75					80	
Lys	Met	Cys	Asn	Tyr	Asp	Lys	Ile	Leu	Ala	Thr	Lys	Lys	Asn	Leu	Asp
			85						90					95	
His	Val	Asn	Lys	Ile	Leu	Lys	Ala	Lys	Lys	Leu	Gln	Arg	Gln	Ala	Arg
		100						105					110		
Thr	Gly	Asn	Asn	Phe	Val	Lys	Arg	Arg	Pro	Gly	Arg	Pro	Arg	Ser	Glu
		115					120					125			

Arg

<210> 4321

<211> 278

<212> DNA

<213> Homo sapiens

<400> 4321

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 120
 cgtcccgggtg gaaggcagcc ctgggcggaa cccaggcggt taacggctca ctaggcagcc
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 240
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 278

<210> 4322
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 4322
 Met Gly Ala Gly Gly His Lys Thr Ser Ala Gln Leu Thr Pro Ala Pro
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 His Val Leu Ile Cys Ser Pro Asp Leu Gly Leu Pro Ser Glu Pro Leu
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 Asn Ala Trp Val Pro Pro Arg Ala Ala Phe His Arg Asp Ala Gly Pro
 35 40 45
 Ala Val Ala Gly Pro Cys Arg Cys Gly Gly Leu Leu Thr Lys Glu Pro
 50 55 60
 Gly Leu Ala Ala Trp Asn Asn Leu Gln Val Gly Val Leu Arg Gly Leu
 65 70 75 80
 Trp Gln Val Leu Gly
 85

<210> 4323
 <211> 1542
 <212> DNA
 <213> Homo sapiens

<400> 4323
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 120
 gacgagaaga ttgaggtgga tgacccccct gacaaggagg acatgcgac aagcttcagg
 180
 tcgaatgtgt tgacgggggtc ggctccccag caggactacg ataagctgaa ggcaactcga
 240
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 300
 gttaagagag aaacagaagc cagttctata aacctgagtg tttatgaacc ttttaaagtc
 360
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 420
 gatgggaagc tgagctccga gaagaatgac accagcctcc ccagcggttc gccatcaaa
 480
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 aaggcggtct cagactcctg caaagaacca gtggccaatt cgagggaatc ctccccgtta
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 660
 atcgacggga ccaaaaaacc atccctgaag caaccggata gtcccagaag catctcaagt
 720
 gagaacagca gcaaaaggat cccgtcctct cccgcggggt ccacaccagc aatccccaaa
 780
 gtccgcataa aaaccattaa gacatcttct ggggaaatca agagaacagt gaccagggta
 840

ttgccagaag tggatcttga ctctggaaag aaaccttccg agcagacagc gtcggtcatg
 900
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 960
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 1020
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 1080
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 1140
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 1260
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 1380
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<210> 4324

<211> S14

<212> PRT

<213> Homo sapiens

<400> 4324

Xaa Tyr Ser Lys Asp Gly Ala Lys Ser Leu Lys Gly Asp Val Pro Ala
 1 5 10 15
 Ser Glu Val Thr Leu Lys Asp Ser Thr Phe Ser Gln Phe Ser Pro Ile
 20 25 30
 Ser Ser Ala Glu Glu Phe Asp Asp Asp Glu Lys Ile Glu Val Asp Asp
 35 40 45
 Pro Pro Asp Lys Glu Asp Met Arg Ser Ser Phe Arg Ser Asn Val Leu
 50 55 60
 Thr Gly Ser Ala Pro Gln Gln Asp Tyr Asp Lys Leu Lys Ala Leu Gly
 65 70 75 80
 Gly Glu Asn Ser Ser Lys Thr Gly Leu Ser Thr Ser Gly Asn Val Glu
 85 90 95
 Lys Asn Lys Ala Val Lys Arg Glu Thr Glu Ala Ser Ser Ile Asn Leu
 100 105 110
 Ser Val Tyr Glu Pro Phe Lys Val Arg Lys Ala Glu Asp Lys Leu Lys
 115 120 125
 Glu Ser Ser Asp Lys Val Leu Glu Asn Arg Val Leu Asp Gly Lys Leu
 130 135 140
 Ser Ser Glu Lys Asn Asp Thr Ser Leu Pro Ser Val Ala Pro Ser Lys
 145 150 155 160
 Thr Lys Ser Ser Ser Lys Leu Ser Ser Cys Ile Ala Ala Ile Ala Ala
 165 170 175
 Leu Ser Ala Lys Lys Ala Ala Ser Asp Ser Cys Lys Glu Pro Val Ala

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      180              185              190
Asn Ser Arg Glu Ser Ser Pro Leu Pro Lys Glu Val Asn Asp Ser Pro
      195              200              205
Arg Ala Ala Asp Lys Ser Pro Glu Ser Gln Asn Leu Ile Asp Gly Thr
      210              215              220
Lys Lys Pro Ser Leu Lys Gln Pro Asp Ser Pro Arg Ser Ile Ser Ser
      225              230              235              240
Glu Asn Ser Ser Lys Gly Ser Pro Ser Ser Pro Ala Gly Ser Thr Pro
      245              250              255
Ala Ile Pro Lys Val Arg Ile Lys Thr Ile Lys Thr Ser Ser Gly Glu
      260              265              270
Ile Lys Arg Thr Val Thr Arg Val Leu Pro Glu Val Asp Leu Asp Ser
      275              280              285
Gly Lys Lys Pro Ser Glu Gln Thr Ala Ser Val Met Ala Ser Val Thr
      290              295              300
Ser Leu Leu Ser Ser Pro Ala Ser Ala Val Leu Ser Ser Pro Pro
      305              310              315              320
Arg Ala Pro Leu Gln Ser Ala Val Val Thr Asn Ala Val Ser Pro Ala
      325              330              335
Glu Leu Thr Pro Lys Gln Val Thr Ile Lys Pro Val Ala Thr Ala Phe
      340              345              350
Leu Pro Val Ser Ala Val Lys Thr Ala Gly Ser Gln Val Ile Asn Leu
      355              360              365
Lys Leu Ala Asn Asn Thr Thr Val Lys Ala Thr Val Ile Ser Ala Ala
      370              375              380
Ser Val Gln Ser Ala Ser Ser Ala Ile Ile Lys Ala Ala Asn Ala Ile
      385              390              395              400
Gln Gln Gln Thr Val Val Val Pro Ala Ser Ser Leu Ala Asn Ala Lys
      405              410              415
Leu Val Pro Lys Thr Val His Leu Ala Asn Leu Asn Leu Leu Pro Gln
      420              425              430
Gly Ala Gln Ala Thr Ser Glu Leu Arg Gln Val Leu Thr Lys Pro Gln
      435              440              445
Gln Gln Ile Lys Gln Ala Ile Ile Asn Ala Ala Ala Ser Gln Pro Pro
      450              455              460
Lys Lys Val Ser Arg Val Gln Val Val Ser Ser Leu Gln Ser Ser Val
      465              470              475              480
Val Glu Ala Phe Asn Lys Val Leu Ser Ser Val Asn Pro Val Pro Val
      485              490              495
Tyr Ile Pro Asn Leu Ser Pro Pro Ala Asn Ala Gly Ile Thr Leu Pro
      500              505              510
Thr Arg

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<210> 4325

<211> 1405

<212> DNA

<213> Homo sapiens

<400> 4325

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60
cttctgcagg gactgtttca aggccttcta cgtccacaag ttcatacgca tgcgtggcaa
120

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gaaccggctc atctttccag gcgagaaggt agcgtctggg tcctgggggt ctgactgagc
 180
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 240
 cgccagctcc tccttgccct ttgaggacag actcgatgtc ctatagtgcc acgagggtgg
 300
 gtgtctgctc gtgttgagg tgccgtgccc tgagtgtgtt tttttctccc ccagggtgctc
 360
 ttggcgtggt ctggggggcc ttcgtccagc tccatggtct ggccaggtct tgaggggcctg
 420
 agccaagatt ctgcaaaaag actgcgcttt gtggcaggag tcctctttgt tgacgagggg
 480
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 540
 ctgcaagcaa ctgggttccc atggcatgtg gtggccttag aggaggtgtt cagcctgcca
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 720
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 960
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 1020
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 1080
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 1200
 ttcccctcca ctgtcagcac tgtgtacagg tgtgtgtggg tgtgtgcggg ggggtgcggg
 1260
 gtgtgtgctg tgtgcgggtg tgtgcgggtg gtgagctcac cactcgtgct caggccaggg
 1320
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 1380
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 1405

<210> 4326

<211> 336

<212> PRT

<213> Homo sapiens

<400> 4326

Met Phe Phe Leu Pro Gln Val Leu Leu Ala Trp Ser Gly Gly Pro Ser

1

5

10

15

Ser Ser Ser Met Val Trp Gln Val Leu Glu Gly Leu Ser Gln Asp Ser

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      20      25      30
Ala Lys Arg Leu Arg Phe Val Ala Gly Val Ile Phe Val Asp Glu Gly
      35      40      45
Ala Ala Cys Gly Gln Ser Leu Glu Glu Arg Ser Lys Thr Leu Ala Glu
      50      55      60
Val Lys Pro Ile Leu Gln Ala Thr Gly Phe Pro Trp His Val Val Ala
      65      70      75      80
Leu Glu Glu Val Phe Ser Leu Pro Pro Ser Val Leu Trp Cys Ser Ala
      85      90      95
Gln Glu Leu Val Gly Ser Glu Gly Ala Tyr Lys Ala Val Asp Ser
      100      105      110
Phe Leu Gln Gln Gln Tyr Val Leu Gly Ala Gly Gly Gly Pro Gly Pro
      115      120      125
Thr Gln Gly Glu Glu Gln Pro Pro Gln Pro Pro Leu Asp Pro Gln Asn
      130      135      140
Leu Ala Arg Pro Pro Ala Pro Ala Gln Thr Glu Ala Leu Ser Gln Leu
      145      150      155      160
Phe Cys Ser Val Arg Thr Leu Thr Ala Lys Glu Glu Leu Leu Gln Thr
      165      170      175
Leu Arg Thr His Leu Ile Leu His Met Ala Arg Ala His Gly Tyr Ser
      180      185      190
Lys Val Met Thr Gly Asp Ser Cys Thr Arg Leu Ala Ile Lys Leu Met
      195      200      205
Thr Asn Leu Ala Leu Gly Arg Gly Ala Phe Leu Ala Trp Asp Thr Gly
      210      215      220
Phe Ser Asp Glu Arg His Gly Asp Val Val Val Val Arg Pro Met Arg
      225      230      235      240
Asp His Thr Leu Lys Glu Val Ala Phe Tyr Asn Arg Leu Phe Ser Val
      245      250      255
Pro Ser Val Phe Thr Pro Ala Val Asp Thr Lys Ala Pro Glu Lys Ala
      260      265      270
Ser Ile His Arg Leu Met Glu Ala Phe Ile Leu Arg Leu Gln Thr Gln
      275      280      285
Phe Pro Ser Thr Val Ser Thr Val Tyr Arg Cys Val Trp Val Cys Ala
      290      295      300
Gly Gly Ala Arg Val Cys Ala Val Cys Gly Cys Val Arg Val Val Ser
      305      310      315      320
Ser Pro Leu Val Leu Arg Pro Gly Leu Arg Val Glu Pro Gln Pro Val
      325      330      335

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<210> 4327

<211> 551

<212> DNA

<213> Homo sapiens

<400> 4327

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120
tgtgcaggtg gggaaattta gaccctgaaa aagggatgcc ctgagatcac catgagattg
180
aggggcaagc agggctcacc ctgactggct cacttccag gcaccccat gagccaggc
240

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accgcctgcc accctcactc tccaggaaga gccaccgcgt ggtggccggg atcgtgtggt
 300
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 360
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 420
 acctctggga gaggaggggtg actccgacag cccttgctcg ccaggatgga gcctggactc
 480
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 540
 ccgcatcatg a
 551

<210> 4328

<211> 107

<212> PRT

<213> Homo sapiens

<400> 4328

Met	Pro	Ser	Arg	Val	Gln	Ala	Pro	Ser	Trp	Gln	Ala	Arg	Ala	Val	Gly
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Val	Thr	Leu	Leu	Ser	Gln	Arg	Trp	Val	Cys	Pro	Ile	Val	Val	Ser	Arg
		20						25				30			
Ala	Thr	Ser	Ser	Pro	Trp	Leu	Cys	Gly	Leu	Ser	Val	Ser	His	Pro	Gln
		35				40					45				
His	Leu	Asp	Gly	Leu	Arg	Val	Arg	Ala	Lys	Val	Arg	Arg	Pro	Gly	His
	50				55					60					
His	Thr	Ile	Pro	Ala	Thr	Thr	Arg	Trp	Leu	Phe	Leu	Glu	Ser	Glu	Gly
65				70					75					80	
Gly	Arg	Arg	Cys	Leu	Gly	Ser	Trp	Gly	Cys	Leu	Gly	Ser	Glu	Pro	Val
			85					90					95		
Arg	Val	Ser	Pro	Ala	Cys	Pro	Ser	Ile	Ser	Trp					
			100					105							

<210> 4329

<211> 3192

<212> DNA

<213> Homo sapiens

<400> 4329

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 120
 tgtacctaaa actttggctc gaaagcgaat ctggaataaa aagtacccca ttgtatcga
 180
 gcttggctag caagatgact ttatgtctaa agctcagact gataaggaga cttcagaaga
 240
 gaagccgcca gctggaggaa gggaggaccc ttagaagcca cccgcgcctc aggaggaaca
 300
 agatctagcc agcgagatca gatactctat ctctttggga gaaatggcgg agaaaaagag
 360
 gaatgggttta ggagatttat tctggcatct aagctaaagt cggaatacaa gaagtcacgc
 420

gggtgtctctg gaggtaaacc agggcttttg cctgcacaca gcagacacaa cagtcctgcc
480
gggcacactga cccacagccg cagcagcagc aaaggcagtg tggaggagat catgtcacag
540
ccaaagcaga aggagctggc aggcagcgtg cggcagaaga tgcttctcga ctacagcgtg
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tacctgggca ggtgtgtctcc ccaggaaaagc cgaagccccc agaggagccc cctgcagagt
660
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720
gaacaggaag cctgggtgaa tgccttgctt ggaagaatat ttggggactt cttaggagag
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1320
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1620
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1680
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1860
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1920
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1980
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2040

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 aatgtgtctg gaggggtggg agagggaattc tgtgagcctt ttcatttcgg tgacagaaga
 2160
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 2280
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 2580
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 2640
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 2700
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 2760
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 2820
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 2880
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 2940
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 3060
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 3180
 aaaaaaaaaa aa
 3192

<210> 4330

<211> 371

<212> PRT

<213> Homo sapiens

<400> 4330

Met Ser Gln Pro Lys Gln Lys Glu Leu Ala Gly Ser Val Arg Gln Lys
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 Met Leu Leu Asp Tyr Ser Val Tyr Met Gly Arg Cys Val Pro Gln Glu
 20 25 30
 Ser Arg Ser Pro Gln Arg Ser Pro Leu Gln Ser Ala Glu Ser Ser Pro
 35 40 45
 Thr Ala Gly Lys Lys Leu Pro Glu Val Pro Pro Ser Glu Glu Glu Glu

[illegible]

<210> 4331

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 4331

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120
gatttaaatg agcctttgca cctcagtttc cttcagaatg ctgcaaaact atatgctaca
180

gtatatgtga ttccatttgc agaagaggac ttatcagcag atgcccctctt gaatattctt
 240
 tcagaagtaa agattcagga attcaagcct tccaataagg ttgttcaaac agatgaaact
 300
 gcaaggaaac cagaccatgt tcctattagc agtgaagatg agaggaaatgc aattttccaa
 360
 ctagaaaagg ctattttatc taatgaagcc accaaaagtg acccttcagat ggcagtgcct
 420
 tcatttgaaa aagatgatga tcataatgga cacatagatt tcatcacagc tgcatacaaat
 480
 cttcgtgcca aaatgtacag cattgaacca gctgaccgtt tcaaaaacaa gcgcatagct
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 660
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 720
 aatggaatat catttacaat ttgggatcga tggaccgtac atggaaaaga agatttcacc
 780
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 840
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 900
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 1020
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 1080
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 1140
 ttcattaagc cttaatttta agggaaacat cagtaagaaa ctgcaactgaa gaattataaa
 1200
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 1260
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 1320
 tggataaaaa gaaggaaaaa atatgtatga ccggt
 1355

<210> 4332

<211> 345

<212> PRT

<213> Homo sapiens

<400> 4332

Glu Lys Tyr Phe Asn His Lys Ala Leu Gln Leu Leu His Cys Phe Pro
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 Leu Asp Ile Arg Leu Lys Asp Gly Ser Leu Phe Trp Gln Ser Pro Lys
 20 25 30
 Arg Pro Pro Ser Pro Ile Lys Phe Asp Leu Asn Glu Pro Leu His Leu
 35 40 45
 Ser Phe Leu Gln Asn Ala Ala Lys Leu Tyr Ala Thr Val Tyr Cys Ile

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      50              55              60
Pro Phe Ala Glu Glu Asp Leu Ser Ala Asp Ala Leu Leu Asn Ile Leu
65              70              75              80
Ser Glu Val Lys Ile Gln Glu Phe Lys Pro Ser Asn Lys Val Val Gln
      85              90              95
Thr Asp Glu Thr Ala Arg Lys Pro Asp His Val Pro Ile Ser Ser Glu
      100              105              110
Asp Glu Arg Asn Ala Ile Phe Gln Leu Glu Lys Ala Ile Leu Ser Asn
      115              120              125
Glu Ala Thr Lys Ser Asp Leu Gln Met Ala Val Leu Ser Phe Glu Lys
      130              135              140
Asp Asp Asp His Asn Gly His Ile Asp Phe Ile Thr Ala Ala Ser Asn
      145              150              155              160
Leu Arg Ala Lys Met Tyr Ser Ile Glu Pro Ala Asp Arg Phe Lys Thr
      165              170              175
Lys Arg Ile Ala Gly Lys Ile Ile Pro Ala Ile Ala Thr Thr Thr Ala
      180              185              190
Thr Val Ser Gly Leu Val Ala Leu Glu Met Ile Lys Val Thr Gly Gly
      195              200              205
Tyr Pro Phe Glu Ala Tyr Lys Asn Cys Phe Leu Asn Leu Ala Ile Pro
      210              215              220
Ile Val Val Phe Thr Glu Thr Thr Glu Val Arg Lys Thr Lys Ile Arg
      225              230              235              240
Asn Gly Ile Ser Phe Thr Ile Trp Asp Arg Trp Thr Val His Gly Lys
      245              250              255
Glu Asp Phe Thr Leu Leu Asp Phe Ile Asn Ala Val Lys Glu Lys Tyr
      260              265              270
Gly Ile Glu Pro Thr Met Val val Gln Gly Val Lys Met Leu Tyr Val
      275              280              285
Pro Val Met Pro Gly His Ala Lys Arg Leu Lys Leu Thr Met His Lys
      290              295              300
Leu Val Lys Pro Thr Thr Glu Lys Lys Tyr Val Asp Leu Thr Val Ser
      305              310              315              320
Phe Ala Pro Asp Ile Asp Gly Asp Glu Asp Leu Pro Gly Pro Pro Val
      325              330              335
Arg Tyr Tyr Phe Ser His Asp Thr Asp
      340              345

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<210> 4333

<211> 1278

<212> DNA

<213> Homo sapiens

<400> 4333

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120
cggaagcccc ccgcgctctc ccgagtgtcc aggatgtttt ccgtggctca cccagccgcc
180
aaggtgcgcg agcccagcgc gctggacctg gtgtacacgg cgctgaagcg gggcctgacg
240
gcctacttgg aagtgcacca gcaggagcaa gagaaatccc aggggcagat aagggagtcc
300

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aagaggaatt cccgcttggg cttcctgtat gatctggaca agcaagtcaa gtccattgaa
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 420
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 480
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 540
 tacacggagg taggggatgg gggcccatga agcagaggca cagggtgtgg cagggtctagt
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 660
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 720
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 780
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 840
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 aacctgtgg ttgtgggcag tgtctcctgt gagaccaagg acctgtttgc gcgcctgccc
 960
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 1080
 acagtacca agcgtctctc cacctatagc cagagcccac cggacacacc ctcaactcgg
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<210> 4334

<211> 189

<212> PRT

<213> Homo sapiens

<400> 4334

Arg Pro Gln Arg Arg Leu Leu Ser Ala Arg Val Asn Arg Ser Gln Ser
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 20 25 30
 Val Phe Ser Pro Pro Gly Pro Pro Arg Lys Pro Pro Ala Leu Ser Arg
 35 40 45
 Val Ser Arg Met Phe Ser Val Ala His Pro Ala Ala Lys Val Pro Gln
 50 55 60
 Pro Glu Arg Leu Asp Leu Val Tyr Thr Ala Leu Lys Arg Gly Leu Thr
 65 70 75 80
 Ala Tyr Leu Glu Val His Gln Gln Glu Gln Glu Lys Leu Gln Gly Gln
 85 90 95
 Ile Arg Glu Ser Lys Arg Asn Ser Arg Leu Gly Phe Leu Tyr Asp Leu

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<210> 4336

<211> 325

<212> PRT

<213> Homo sapiens

<400> 4336

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Cys	Arg	Cys	Arg	Ala	Glu	Glu	Leu	Gly	Arg	Gly	Ile	Ala	Leu	Phe	Gln
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Met	Ser	Phe	Leu	Val	Ala	Ser	Gln	Thr	Val	Gln	Ser	Phe	Leu	Arg	Val
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<210> 4337

<211> 461

<212> DNA

<213> Homo sapiens

<400> 4337

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<210> 4338

<211> 118

<212> PRT

<213> Homo sapiens

<400> 4338

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		20					25					30			
Thr	Trp	Phe	Pro	Ser	Ser	Gly	Ala	His	Gly	Gly	Glu	Val	Glu	Gly	Gly
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Arg	Arg	Glu	Gly	Ala	Thr	Cys	Cys	Ser	Val	Glu	Lys	Gln	Gln	Ser	Pro
	50				55					60					
Leu	Gln	Pro	Ala	Gln	Leu	Ala	Phe	Leu	Thr	Leu	Ser	Leu	Pro	Gly	Leu
	65			70				75					80		
Cys	Gly	Arg	Glu	Gly	Gln	Ala	Arg	Trp	Pro	Ala	Arg	Asp	Val	Val	Phe
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<210> 4339

<211> 5269

<212> DNA

<213> Homo sapiens

<400> 4339

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<211> 1088

<212> PRT

<213> Homo sapiens

<400> 4340

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Gly	Gly	Asp	Glu	Thr	Ala	Glu	Arg	Thr	Glu	Ala	Pro	Gly	Thr	Pro	Glu
			20						25				30		
Gly	Pro	Glu	Pro	Glu	Arg	Pro	Ser	Pro	Gly	Asp	Gly	Asn	Pro	Arg	Glu
		35					40					45			
Asn	Ser	Pro	Phe	Leu	Asn	Asn	Val	Glu	Val	Glu	Gln	Glu	Ser	Phe	Phe
		50				55					60				
Glu	Gly	Lys	Asn	Met	Ala	Leu	Phe	Glu	Glu	Glu	Met	Asp	Ser	Asn	Pro
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Met	Val	Ser	Ser	Leu	Leu	Asn	Lys	Leu	Ala	Asn	Tyr	Thr	Asn	Leu	Ser
			85						90					95	
Gln	Gly	Val	Val	Glu	His	Glu	Glu	Asp	Glu	Glu	Ser	Arg	Arg	Arg	Glu
			100					105					110		
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		210				215					220				
Leu	Thr	Tyr	Ile	Ser	Pro	Gly	Ala	Ala	Ile	Phe	Gln	Ala	Glu	Ala	Ala
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Glu Gln Glu Arg Glu Ala Gln Leu Ile His Asp Arg Asn Thr Ala Ser
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<211> 693

<212> DNA

<213> Homo sapiens

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<210> 4342
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 <212> PRT
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<210> 4343
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<400> 4343

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<210> 4344
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<212> PRT

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 Ser Lys Tyr Glu Glu Asp Val Lys Ile His Asn His Thr His Ile Trp
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 Gly Ser Tyr Trp Lys Glu Gly Arg Trp Gly Tyr Lys Cys Cys His Ser
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 Phe Phe Lys Tyr Ser Tyr Cys Thr Gly Glu Ala Gly Lys Glu Ile Val
 450 455 460
 Asn Ser Glu Glu Cys Ile Ile Asn Glu Ile Thr Gly Glu Glu Ser Val
 465 470 475 480
 Lys Lys Pro Gln Thr Leu Met Glu Leu His Gln Glu Lys Leu Lys Glu
 485 490 495
 Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys His Arg Lys Ser Ser
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 Ser Asp Ser Asp Asp Glu Glu Lys Lys His Glu Lys Leu Lys Lys Ala
 515 520 525
 Leu Asn Ala Glu Glu Ala Arg Leu Leu His Val Lys Glu Thr Met Gln
 530 535 540
 Ile Asp Glu Arg Lys Arg Pro Tyr Asn Ser Met Tyr Glu Thr Arg Glu
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<210> 4355

<211> 1741

<212> DNA

<213> Homo sapiens

<400> 4355

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<210> 4356

<211> 509

<212> PRT

<213> Homo sapiens

<400> 4356

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Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu Ile Val			
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Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn Thr Val			
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Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro Gln Ala			
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Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys Asn Gly			
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Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe Val Asn			
	100	105	110
Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu Thr Ala			
	115	120	125
His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr Val Pro			
	130	135	140
Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala Ala Arg			
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Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser Ala Ala			
	165	170	175
Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys Ser Asn			
	180	185	190
Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser Val Met			
	195	200	205
Glu Val Asn Ser Gly Ile Tyr Arg Val Leu Ser Thr Asn Thr Asp Asp			
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Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr Leu Ala			
	225	230	235
Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn Ala Arg			
	245	250	255
Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His Ser Leu			
	260	265	270
Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr Glu Gly			
	275	280	285
Gln Asp Phe Asp Cys Asn Val Ser Arg Ala Arg Phe Glu Leu Leu Cys			
	290	295	300
Ser Pro Leu Phe Asn Lys Cys Ile Glu Ala Ile Arg Gly Leu Leu Asp			
	305	310	315
Gln Asn Gly Phe Thr Ala Asp Asp Ile Asn Lys Val Val Leu Cys Gly			
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Gly Ser Ser Arg Ile Pro Lys Leu Gln Gln Leu Ile Lys Asp Leu Phe			
	340	345	350
Pro Ala Val Glu Leu Leu Asn Ser Ile Pro Pro Asp Glu Val Ile Pro			
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Ile Gly Ala Ala Ile Glu Ala Gly Ile Leu Ile Gly Lys Glu Asn Leu			
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Leu Val Glu Asp Ser Leu Met Ile Glu Cys Ser Ala Arg Asp Ile Leu			
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Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val Leu Phe			
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Pro Ser Gly Thr Pro Leu Pro Ala Arg Arg Gln His Thr Leu Gln Ala			
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Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser Asp Gly			

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          485              490              495
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<210> 4357
 <211> 421
 <212> DNA
 <213> Homo sapiens

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<210> 4358
 <211> 115
 <212> PRT
 <213> Homo sapiens

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<400> 4358
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20     25     30
Gln Lys Pro Trp Pro Ser Pro Ala Val Phe Phe Arg Arg Asn Val Arg
35     40     45
Gly Leu Pro Pro Arg Phe Ser Ser Pro Thr Pro Leu Trp Arg Lys Val
50     55     60
Leu Ser Thr Ala Val Val Gly Ala Pro Leu Leu Leu Gly Ala Arg Tyr
65     70     75     80
Val Met Ala Glu Ala Arg Glu Lys Arg Arg Met Arg Leu Val Val Asp
85     90     95
Gly Met Gly Arg Phe Cys Arg Ser Leu Lys Val Gly Leu Gln Ile Ser
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115

<210> 4359
<211> 3661
<212> DNA
<213> Homo sapiens

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<211> 670

<212> PRT

<213> Homo sapiens

<400> 4360

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			20				25						30		
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		35					40				45				
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	50				55						60				
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65					70				75						80
Ser	Thr	Pro	Arg	Arg	Ser	Asp	Ser	Ala	Ile	Ser	Val	Arg	Ser	Leu	His
			85						90					95	
Ser	Glu	Ser	Ser	Met	Ser	Leu	Arg	Ser	Thr	Phe	Ser	Leu	Pro	Glu	Glu
			100				105						110		
Glu	Glu	Glu	Pro	Glu	Pro	Leu	Val	Phe	Ala	Glu	Gln	Pro	Ser	Val	Lys
		115					120				125				
Leu	Cys	Cys	Gln	Leu	Cys	Cys	Ser	Val	Phe	Lys	Asp	Pro	Val	Ile	Thr
	130				135						140				
Thr	Cys	Gly	His	Thr	Phe	Cys	Arg	Arg	Cys	Ala	Leu	Lys	Ser	Glu	Lys
145					150					155					160
Cys	Pro	Val	Asp	Asn	Val	Lys	Leu	Thr	Val	Val	Val	Asn	Asn	Ile	Ala
			165						170					175	
Val	Ala	Glu	Gln	Ile	Gly	Glu	Leu	Phe	Ile	His	Cys	Arg	His	Gly	Cys

Arg Val Ala			180			185			190		
			Gly	Ser	Gly	Lys	Pro	Ile	Phe	Glu	Val
Gly Cys Pro			195			200			205		
Ser Cys Asp			Tyr	Arg	Pro	Val	Arg	Cys	Pro	Asn	Asn
Pro Leu Leu			210			215			220		
Ile Lys Cys			Pro	His	Ser	Lys	Tyr	Gly	Cys	Thr	Phe
Asp Thr Tyr			225			230			235		
Glu Phe Leu			Gln	Gln	Thr	Asp	Asp	Arg	Phe	His	Glu
Leu Ala Gln			240			245			250		
Lys Leu Ser			Glu	Lys	Ile	Asp	Gln	Leu	Glu	Lys	Ser
Phe Asp Val			255			260			265		
Glu Phe Arg			Arg	Asp	Ala	Ser	Met	Leu	Asn	Asp	Glu
Asn Ala Arg			270			275			280		
Ile Phe Lys			Cys	Lys	Gly	Thr	Phe	Val	Gly	His	Asn
Cys Leu Cys			285			290			295		
Asp Lys Thr			Ile	Lys	Val	Trp	Asp	Thr	Cys	Thr	Thr
Lys Thr Leu			300			305			310		
Gly Cys Lys			Leu	Tyr	Ser	Gly	Ser	Ala	Asp	Gln	Leu
Asp Ile Gln			315			320			325		
Pro Val Cys			Thr	Leu	Val	Trp	Asp	Thr	Cys	Thr	Thr
Leu Lys Glu			330			335			340		
Ile Cys Lys			Leu	Tyr	Ser	Gly	Ser	Ala	Asp	Gln	Leu
Asp Thr Tyr			345			350			355		
Ser Val Cys			Thr	Leu	Val	Trp	Asp	Thr	Cys	Thr	Thr
Leu Lys Glu			360			365			370		
Ile Cys Lys			Leu	Tyr	Ser	Gly	Ser	Ala	Asp	Gln	Leu
Asp Thr Tyr			375			380			385		
Ser Val Cys			Thr	Leu	Val	Trp	Asp	Thr	Cys	Thr	Thr
Leu Lys Glu			390			395			400		
Ile Cys Lys			Leu	Tyr	Ser	Gly	Ser	Ala	Asp	Gln	Leu
Asp Thr Tyr			405			410			415		
Ser Val Cys			Thr	Leu	Val	Trp	Asp	Thr	Cys	Thr	Thr
Leu Lys Glu			420			425			430		
Ile Cys Lys			Leu	Tyr	Ser	Gly	Ser	Ala	Asp	Gln	Leu
Asp Thr Tyr											

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Leu Arg Val Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu
625                      630                      635                      640
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Phe Ser Gly Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys
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<210> 4361
 <211> 574
 <212> DNA
 <213> Homo sapiens

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<400> 4361
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574

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<210> 4362
 <211> 116
 <212> PRT
 <213> Homo sapiens

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<400> 4362
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20          25          30
Asp Met Gln Gln His Glu Cys Ala Met Ser Trp Arg Ala His Tyr Gly
35          40          45
Glu Val Tyr Ser Val Glu Phe Ser Tyr Asp Glu Asn Thr Val Tyr Ser
50          55          60
Ile Gly Glu Asp Gly Lys Val Gly Gly Ser Arg Ile Gln Ile Arg Glu
65          70          75          80
His Arg Asp Asp Met Trp Ala Gly Cys Arg Leu Trp Pro Tyr Leu Leu
85          90          95
Leu Ala Leu Gln Pro Gly Ala Ser Phe Cys Ser Phe Val Ile Cys Arg

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<210> 4363			
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<212> DNA			
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<211> 75
 <212> PRT
 <213> Homo sapiens

<400> 4364
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 Lys Val Ala Gln Ala Leu Phe Ser Val Leu Gly Lys Pro Ala Val Ser
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 Phe Arg Gly Gln Leu Val Gln Pro Ala Gly Ser Val Gln Ile Pro Asp
 35 40 45
 Asn His Ser Ser Thr Arg Ala Gln Arg Pro Gly Pro Gly Gly Arg Ser
 50 55 60
 Ser Ala Cys Val Pro Thr Ser Thr Ser Met Arg
 65 70 75

<210> 4365
 <211> 469
 <212> DNA
 <213> Homo sapiens

<400> 4365
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 180
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 240
 cgcgagggcg acaagctggg ggcgggtgctg gagaacgaat acaccggcgc caaggaagag
 300
 cgggtggtcg accaggtggg ggtggagaac ggtgtgcgtc cggatgagga aatctactac
 360
 gggctcaagg aaggttcgcg caacaaggcg cagatcgatg tcgaagccct gttcgcgac
 420
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 469

<210> 4366
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 4366
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 20 25 30
 Asp Lys Gly Ser Gln Val Glu Ile Val Thr Asp Asp Ile Lys Pro Gly
 35 40 45
 Val Ala Ile Gly Gly Thr Ser Phe Pro Thr Tyr Tyr Arg Ser Met Tyr
 50 55 60
 Pro Lys Glu Val Ile Met Thr Gly Asp Met Met Leu Glu Lys Val Tyr

65		70		75		80									
Arg	Glu	Gly	Asp	Lys	Leu	Val	Ala	Val	Leu	Glu	Asn	Glu	Tyr	Thr	Gly
			85						90					95	
Ala	Lys	Glu	Glu	Arg	Val	Val	Asp	Gln	Val	Val	Val	Glu	Asn	Gly	Val
		100					105					110			
Arg	Pro	Asp	Glu	Glu	Ile	Tyr	Tyr	Gly	Leu	Lys	Glu	Gly	Ser	Arg	Asn
		115				120					125				
Lys	Gly	Gln	Ile	Asp	Val	Glu	Ala	Leu	Phe	Ala	Ile	Lys	Pro	Gln	Pro
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<210> 4367

<211> 852

<212> DNA

<213> Homo sapiens

<400> 4367

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240
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300
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720
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<210> 4368

<211> 102

<212> PRT

<213> Homo sapiens

<400> 4368
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 20 25 30
 Phe Glu Glu Thr Leu Asn Ile Leu Ile Tyr Glu Thr Pro Arg Gly Pro
 35 40 45
 Asp Pro Ala Leu Leu Glu Ala Thr Gly Gly Ala Ala Gly Ala Gly Gly
 50 55 60
 Ala Gly Arg Gly Glu Asp Glu Glu Asn Arg Glu His Arg Val Arg Arg
 65 70 75 80
 Ile His Val Arg Arg His Ile Thr His Asp Glu Arg Pro His Gly Gln
 85 90 95
 Gln Ile Val Phe Lys Asp
 100

<210> 4369
 <211> 1264
 <212> DNA
 <213> Homo sapiens

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 240
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 420
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 480
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 780
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 960

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<210> 4370

<211> 322

<212> PRT

<213> Homo sapiens

<400> 4370

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 Trp Ala Phe Lys Met Asp Tyr Glu Thr Thr Glu Lys Glu Val Ala Glu
 35 40 45
 Pro Leu Leu Asp Leu Lys Glu Gly Ile Asp Gln Leu Glu Asn Asn Lys
 50 55 60
 Thr Leu Gly Phe Ile Leu Ser Thr Leu Leu Ala Ile Gly Asn Phe Leu
 65 70 75 80
 Asn Gly Thr Asn Ala Lys Ala Phe Glu Leu Ser Tyr Leu Glu Lys Val
 85 90 95
 Pro Glu Val Lys Asp Thr Val His Lys Gln Ser Leu Leu His His Val
 100 105 110
 Cys Thr Met Val Val Glu Asn Phe Pro Asp Ser Ser Asp Leu Tyr Ser
 115 120 125
 Glu Ile Gly Ala Ile Thr Arg Ser Ala Lys Val Asp Phe Asp Gln Leu
 130 135 140
 Gln Asp Asn Leu Cys Gln Met Glu Arg Arg Cys Lys Ala Ser Trp Asp
 145 150 155 160
 His Leu Lys Ala Ile Ala Lys His Glu Met Lys Pro Val Leu Lys Gln
 165 170 175
 Arg Met Ser Glu Phe Leu Lys Asp Cys Ala Glu Arg Ile Ile Leu
 180 185 190
 Lys Ile Val His Arg Arg Ile Ile Asn Arg Phe His Ser Phe Leu Leu
 195 200 205
 Phe Met Gly His Pro Pro Tyr Ala Ile Arg Glu Val Asn Ile Asn Lys
 210 215 220
 Phe Cys Arg Ile Ile Ser Glu Phe Ala Leu Glu Tyr Arg Thr Thr Arg
 225 230 235 240
 Glu Arg Val Leu Gln Gln Lys Gln Lys Arg Ala Asn His Arg Glu Arg
 245 250 255
 Asn Lys Thr Arg Gly Lys Met Ile Thr Asp Ser Gly Lys Phe Ser Gly
 260 265 270
 Ser Ser Pro Ala Pro Pro Ser Gln Pro Gln Gly Leu Ser Tyr Ala Glu

	275					280						285			
Asp	Ala	Ala	Glu	His	Glu	Asn	Met	Lys	Ala	Val	Leu	Lys	Thr	Ser	Ser
	290					295					300				
Pro	Ser	Arg	Ser	Pro	Leu	His	Ile	Pro	Ser	Pro	Ser	Cys	Gln	Leu	Cys
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Phe	Ser														

<210> 4371

<211> 907

<212> DNA

<213> Homo sapiens

<400> 4371

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240
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360
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480
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540
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660
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720
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780
tacggcggcg cccaccagac tctcgggctg agcgggaacc tcatgccag cagcttcggg
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atgatca
907

<210> 4372

<211> 302

<212> PRT

<213> Homo sapiens

<400> 4372

Thr Phe Lys Met Ala Glu Cys Gly Ala Ser Gly Ser Gly Ser Ser Gly

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Asn Leu Glu Asn Ala Lys Arg Phe Ala Ile Asp Ile Gly Gly Ser Leu
      35
Thr Lys Leu Ala Tyr Tyr Ser Thr Val Gln His Lys Val Ala Lys Val
      50
Arg Ser Phe Asp His Ser Gly Lys Asp Thr Glu Arg Glu His Glu Pro
      65
Pro Tyr Glu Ile Ser Val Gln Glu Glu Ile Thr Ala Arg Leu His Phe
      85
Ile Lys Phe Glu Asn Thr Tyr Ile Glu Ala Cys Leu Asp Phe Ile Lys
      100
Asp His Leu Val Asn Thr Glu Thr Lys Val Ile Gln Ala Thr Gly Gly
      115
Gly Ala Tyr Lys Phe Lys Asp Leu Ile Glu Glu Lys Leu Arg Leu Lys
      130
Val Asp Lys Glu Asp Val Met Thr Cys Leu Ile Lys Gly Cys Asn Phe
      145
Val Leu Lys Asn Ile Pro His Glu Ala Phe Val Tyr Gln Lys Asp Ser
      165
Asp Pro Glu Phe Arg Phe Gln Thr Asn His Pro His Ile Phe Pro Tyr
      180
Leu Leu Val Asn Ile Gly Ser Gly Val Ser Ile Val Lys Val Glu Thr
      195
Glu Asp Arg Phe Glu Trp Val Gly Gly Ser Ser Ile Gly Gly Gly Thr
      210
Phe Trp Gly Leu Gly Ala Leu Leu Thr Lys Thr Lys Lys Phe Asp Glu
      225
Leu Leu His Leu Ala Ser Arg Gly Gln His Ser Asn Val Asp Met Leu
      245
Val Arg Asp Val Tyr Gly Gly Ala His Gln Thr Leu Gly Leu Ser Gly
      260
Asn Leu Ile Ala Ser Ser Phe Gly Lys Ser Ala Thr Ala Asp Gln Glu
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Phe Ser Lys Glu Asp Met Ala Lys Ser Leu Leu His Met Ile
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<210> 4373

<211> 1017

<212> DNA

<213> Homo sapiens

<400> 4373

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180
gaaaaaagggg gggcgcaaaa atggctgggg caattataga aaacatgagc accaagaagc
240
tgtgcattgt tggtgggatt ctgctcgtgt tccaaatcat cgctttctgt gtggggaggc
300

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tgattgtccc agggcccaca acggcagtggt cctacatgtc ggtgaaatgt gtggatgccc
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 540
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 780
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<210> 4374

<211> 272

<212> PRT

<213> Homo sapiens

<400> 4374

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 Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
 35 40 45
 Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
 50 55 60
 Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
 65 70 75 80
 Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
 85 90 95
 Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
 100 105 110
 Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
 115 120 125
 Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
 130 135 140
 Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
 145 150 155 160
 Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
 165 170 175
 Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His

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 1860
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<210> 4376

<211> 399

<212> PRT

<213> Homo sapiens

<400> 4376

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 20 25 30
 Val Pro His Ser Ser Ser Thr Phe Arg Leu Thr Ala Ser Phe Gly Arg
 35 40 45
 Ala Gly Pro Gly Met Leu His Thr Thr Gln Leu Tyr Gln His Val Pro
 50 55 60
 Glu Thr Arg Trp Pro Ile Val Tyr Ser Pro Arg Tyr Asn Ile Thr Phe
 65 70 75 80
 Met Gly Leu Glu Lys Leu His Pro Phe Asp Ala Gly Lys Trp Gly Lys
 85 90 95
 Val Ile Asn Phe Leu Lys Glu Glu Lys Leu Leu Ser Asp Ser Met Leu
 100 105 110
 Val Glu Ala Arg Glu Ala Ser Glu Glu Asp Leu Leu Val Val His Thr
 115 120 125
 Arg Arg Tyr Leu Asn Glu Leu Lys Trp Ser Phe Ala Val Ala Thr Ile

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Thr Glu Ile Pro Pro Val Ile Phe Leu Pro Asn Phe Leu Val Gln Arg
145              150              155
Lys Val Leu Arg Pro Leu Arg Thr Gln Thr Gly Gly Thr Ile Met Ala
      165              170              175
Gly Lys Leu Ala Val Glu Arg Gly Trp Ala Ile Asn Val Gly Gly Gly
      180              185              190
Phe His His Cys Ser Ser Asp Arg Gly Gly Gly Phe Cys Ala Tyr Ala
      195              200              205
Asp Ile Thr Leu Ala Ile Lys Phe Leu Phe Glu Arg Val Glu Gly Ile
      210              215              220
Ser Arg Ala Thr Ile Ile Asp Leu Asp Ala His Gln Gly Asn Gly His
225              230              235
Glu Arg Asp Phe Met Asp Asp Lys Cys Val Thr Cys Met Asp Val Tyr
      245              250              255
Asn Arg His Ile Tyr Pro Gly Asp Arg Phe Ala Lys Gln Ala Ile Arg
      260              265              270
Arg Lys Val Glu Leu Glu Trp Gly Thr Glu Asp Asp Glu Tyr Leu Asp
      275              280              285
Lys Val Glu Arg Asn Ile Lys Lys Ser Leu Gln Glu His Leu Pro Asp
      290              295              300
Val Val Val Tyr Asn Ala Gly Thr Asp Ile Leu Glu Gly Asp Arg Leu
305              310              315
Gly Gly Leu Ser Ile Ser Pro Ala Gly Ile Val Lys Arg Asp Glu Leu
      325              330              335
Val Phe Arg Met Val Arg Gly Arg Arg Val Pro Ile Leu Met Val Thr
      340              345              350
Ser Gly Gly Tyr Gln Lys Arg Thr Ala Arg Ile Ile Ala Asp Ser Ile
      355              360              365
Leu Asn Leu Phe Gly Leu Gly Leu Ile Gly Pro Glu Ser Pro Ser Val
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Ser Ala Gln Asn Ser Asp Thr Pro Leu Leu Pro Pro Ala Val Pro
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<210> 4377

<211> 812

<212> DNA

<213> Homo sapiens

<400> 4377

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420

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<210> 4378

<211> 233

<212> PRT

<213> Homo sapiens

<400> 4378

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 35 40 45
 Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln Ala Gln Leu
 50 55 60
 Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys Ala Leu Asp Leu
 65 70 75 80
 Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu Ala Leu Pro
 85 90 95
 Ala Asp Gly Arg Val Val Thr Cys Glu Val Asp Ala Gln Pro Pro Glu
 100 105 110
 Leu Gly Arg Pro Leu Trp Arg Gln Ala Glu Ala Glu His Lys Ile Arg
 115 120 125
 Leu Arg Leu Lys Pro Ala Leu Glu Thr Leu Asp Glu Leu Leu Ala Ala
 130 135 140
 Gly Glu Ala Gly Thr Phe Asp Val Ala Val Val Asp Ala Asp Lys Glu
 145 150 155 160
 Asn Cys Ser Ala Tyr Tyr Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly
 165 170 175
 Gly Ile Leu Ala Val Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln
 180 185 190
 Pro Pro Lys Gly Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu
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 Asp Gly Leu Thr Leu Ala Phe Lys Ile
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<210> 4379

<211> 2347

<212> DNA

<213> Homo sapiens

<400> 4379

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720
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<210> 4380

<211> 652

<212> PRT

<213> Homo sapiens

<400> 4380

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				20				25					30		
Arg	Gly	Ala	Leu	Arg	Thr	Leu	Ser	Leu	Leu	Ala	Ala	Gln	Gly	Leu	Trp
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Ala	Gln	Thr	Ser	Val	Leu	His	Arg	Glu	Asp	Leu	Glu	Arg	Leu	Gly	Val
			50			55					60				
Gln	Glu	Ser	Asp	Leu	Arg	Leu	Phe	Leu	Asp	Gly	Asp	Ile	Leu	Arg	Gln
65					70				75				80		
Asp	Arg	Val	Ser	Lys	Gly	Cys	Tyr	Ser	Phe	Ile	His	Leu	Ser	Phe	Gln
				85					90				95		
Gln	Phe	Leu	Thr	Ala	Leu	Phe	Tyr	Thr	Leu	Glu	Lys	Glu	Glu	Glu	Glu
				100				105					110		
Asp	Arg	Asp	Gly	His	Thr	Trp	Asp	Ile	Gly	Asp	Val	Gln	Lys	Leu	Leu
			115				120					125			
Ser	Gly	Val	Glu	Arg	Leu	Arg	Asn	Pro	Asp	Leu	Ile	Gln	Ala	Gly	Tyr

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 Tyr Ser Phe Gly Leu Ala Asn Glu Lys Arg Ala Lys Glu Leu Glu Ala
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 Thr Phe Gly Cys Arg Met Ser Pro Asp Ile Lys Gln Glu Leu Leu Arg
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 Cys Asp Ile Ser Cys Lys Gly Gly His Ser Thr Val Thr Asp Leu Gln
 180
 Glu Leu Leu Gly Cys Leu Tyr Glu Ser Gln Glu Glu Glu Leu Val Lys
 195
 Glu Val Met Ala Gln Phe Lys Glu Ile Ser Leu His Leu Asn Ala Val
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 Asp Val Val Pro Ser Ser Phe Cys Val Lys His Cys Arg Asn Leu Gln
 225
 Lys Met Ser Leu Gln Val Ile Lys Glu Asn Leu Pro Glu Asn Val Thr
 245
 Ala Ser Glu Ser Asp Ala Glu Val Glu Arg Ser Gln Asp Asp Gln His
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 Met Leu Pro Phe Trp Thr Asp Leu Cys Ser Ile Phe Gly Ser Asn Lys
 275
 Asp Leu Met Gly Leu Ala Ile Asn Asp Ser Phe Leu Ser Ala Ser Leu
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 Val Arg Ile Leu Cys Glu Gln Ile Ala Ser Asp Thr Cys His Leu Gln
 305
 Arg Val Val Phe Lys Asn Ile Ser Pro Ala Asp Ala His Arg Asn Leu
 325
 Xaa Pro Xaa Ala Leu Arg Gly His Lys Thr Val Thr Tyr Leu Thr Leu
 340
 Gln Gly Asn Asp Gln Asp Asp Met Phe Pro Ala Leu Cys Glu Val Leu
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 Arg His Pro Glu Cys Asn Leu Arg Tyr Leu Gly Leu Val Ser Cys Ser
 370
 Ala Thr Thr Gln Gln Trp Ala Asp Leu Ser Leu Ala Leu Glu Val Asn
 385
 Gln Ser Leu Thr Cys Val Asn Leu Ser Asp Asn Glu Leu Leu Asp Glu
 405
 Gly Ala Lys Leu Leu Tyr Thr Thr Leu Arg His Pro Lys Cys Phe Leu
 420
 Gln Arg Leu Ser Leu Glu Asn Cys His Leu Thr Glu Ala Asn Cys Lys
 435
 Asp Leu Ala Ala Val Leu Val Val Ser Arg Glu Leu Thr His Leu Cys
 450
 Leu Ala Lys Asn Pro Ile Gly Asn Thr Gly Val Lys Phe Leu Cys Glu
 465
 Gly Leu Arg Tyr Pro Glu Cys Lys Leu Gln Thr Leu Val Leu Trp Asn
 485
 Cys Asp Ile Thr Ser Asp Gly Cys Cys Asp Leu Thr Lys Leu Leu Gln
 500
 Glu Lys Ser Ser Leu Leu Cys Leu Asp Leu Gly Leu Asn His Ile Gly
 515
 Val Lys Gly Met Lys Phe Leu Cys Glu Ala Leu Arg Lys Pro Leu Cys
 530
 Asn Leu Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro Pro Phe Ser
 545
 Cys Glu Asp Val Cys Ser Ala Leu Ser Cys Asn Gln Ser Leu Val Thr
 555
 560

565										570					575				
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580										585					590				
Phe	Glu	Thr	Leu	Thr	Cys	Ser	Ser	Gly	Thr	Leu	Arg	Thr	Leu	Arg	Leu				
595										600					605				
Lys	Ile	Asp	Asp	Phe	Asn	Asp	Gly	Leu	Asn	Lys	Leu	Leu	Glu	Glu	Ile				
610										615					620				
Glu	Glu	Lys	Asn	Pro	Gln	Leu	Ile	Ile	Asp	Thr	Glu	Lys	His	His	Pro				
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<210> 4381

<211> 1638

<212> DNA

<213> Homo sapiens

<400> 4381

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120	cagtacaagg	gcaccatgcg	cgaggcagcg	cgtgccatgc	acctctctaa
180	aggcagcggg	agcagatgga	ggtgctgaag	cagcgcatcg	ccgaggagac
240	tcgcaggttg	acaagaggtt	ctcggcgcat	tacgacgcgc	tggaggccga
300	agcgcggttg	gcctggtgac	cctgaacgac	atgaaggccc	ggcaggagcg
360	gagcgcgagc	ggcagctggc	caagcgccag	cacctggagg	agcagcggct
420	cggcagcggg	agcaggagca	gcggcgcgag	cgcaagcgta	agatctcctg
480	gcactagacg	acctcgatga	ccaggccgag	gcggccgagg	ccaggcgcgc
540	ggcaagaacc	ccgacgttga	caccagcttc	ctgccagacc	gcgaccgcga
600	aaccgcgtcc	gagaggagct	gcgccaagag	tgggaggcgc	agcgcgagaa
660	gagggatagg	aggtcacctt	cagctactgg	gacggctcgg	gccaccggcg
720	gtgcgcaagg	gcaacacggt	gcagcagttc	ctgaagaagg	cgctgcaggg
780	gacttctctg	agctgcgctc	cgccggcggt	gagcagctca	tgttcatcaa
840	atcctgcccg	actaccacac	cttctacgac	ttcatcatcg	ccaggggcag
900	gggcccgtct	tcagcttcga	tgtgcacgat	gacgtgcgcc	tgctcgcaga
960	gagaagggac	agtcgcacgc	gggcaagggt	gtgctgcgca	gctggtacga
1020	cacatcttcc	ccgcgacggc	ctgggaggcc	tatgaccccc	agaagaagtg
1080					ggacaagtac

accatccgct aacaccgcc tgccagagcg gaaaccgggg gtggggggag acactcattt
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 1638

<210> 4382

<211> 325

<212> PRT

<213> Homo sapiens

<400> 4382

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 20 25 30
 Gln Arg Ile Ala Glu Glu Thr Ile Leu Lys Ser Gln Val Asp Lys Arg
 35 40 45
 Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Ala
 50 55 60
 Val Gly Leu Val Thr Leu Asn Asp Met Lys Ala Arg Gln Glu Ala Leu
 65 70 75 80
 Val Arg Glu Arg Glu Arg Gln Leu Ala Lys Arg Gln His Leu Glu Glu
 85 90 95
 Gln Arg Leu Gln Gln Glu Arg Gln Arg Glu Gln Glu Gln Arg Arg Glu
 100 105 110
 Arg Lys Arg Lys Ile Ser Cys Leu Ser Phe Ala Leu Asp Asp Leu Asp
 115 120 125
 Asp Gln Ala Asp Ala Ala Glu Ala Arg Arg Ala Gly Asn Leu Gly Lys
 130 135 140
 Asn Pro Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Asp Arg Glu Glu
 145 150 155 160
 Glu Glu Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Gln
 165 170 175
 Arg Glu Lys Val Lys Asp Glu Glu Met Glu Val Thr Phe Ser Tyr Trp
 180 185 190
 Asp Gly Ser Gly His Arg Arg Thr Val Arg Val Arg Lys Gly Asn Thr
 195 200 205
 Val Gln Gln Phe Leu Lys Lys Ala Leu Gln Gly Leu Arg Lys Asp Phe

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      210              215              220
Leu Glu Leu Arg Ser Ala Gly Val Glu Gln Leu Met Phe Ile Lys Glu
225              230              235
Asp Leu Ile Leu Pro His Tyr His Thr Phe Tyr Asp Phe Ile Ile Ala
      245              250              255
Arg Ala Arg Gly Lys Ser Gly Pro Leu Phe Ser Phe Asp Val His Asp
      260              265              270
Asp Val Arg Leu Leu Ser Asp Ala Thr Met Glu Lys Asp Glu Ser His
      275              280              285
Ala Gly Lys Val Val Leu Arg Ser Trp Tyr Glu Lys Asn Lys His Ile
      290              295              300
Phe Pro Ala Ser Arg Trp Glu Ala Tyr Asp Pro Glu Lys Lys Trp Asp
305              310              315              320
Lys Tyr Thr Ile Arg
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<210> 4383
 <211> 419
 <212> DNA
 <213> Homo sapiens

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<400> 4383
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120
aaggagtccc agtatatcaa gtatctctgc tgtgatgaca caagaaccct taaccagtgg
180
gtcatgggaa tacggatagc caagtatggg aagactctct atgataacta ccagcgggct
240
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300
ccagctcagc catttacagg acctaaaaca ggcaccaccc agcccaatgg acagattccc
360
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419

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<210> 4384
 <211> 139
 <212> PRT
 <213> Homo sapiens

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<400> 4384
Arg Asp Leu Ala Cys Phe Ile Gln Phe Glu Asn Val Asn Ile Tyr Tyr
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Gly Thr Gln His Lys Met Lys Tyr Lys Ala Pro Thr Asp Tyr Cys Phe
      20      25      30
Val Leu Lys His Pro Gln Ile Gln Lys Glu Ser Gln Tyr Ile Lys Tyr
      35      40      45
Leu Cys Cys Asp Asp Thr Arg Thr Leu Asn Gln Trp Val Met Gly Ile
      50      55      60
Arg Ile Ala Lys Tyr Gly Lys Thr Leu Tyr Asp Asn Tyr Gln Arg Ala
      65      70      75      80
Val Ala Lys Ala Gly Leu Ala Ser Arg Trp Thr Asn Leu Gly Thr Val

```

	85		90		95										
Asn	Ala	Ala	Ala	Pro	Ala	Gln	Pro	Phe	Thr	Gly	Pro	Lys	Thr	Gly	Thr
	100							105					110		
Thr	Gln	Pro	Asn	Gly	Gln	Ile	Pro	Gln	Ala	Thr	His	Phe	Phe	Ser	Ala
	115						120					125			
Val	Leu	Gln	Glu	Ala	Gln	Arg	His	Ala	Glu	Asn					
	130					135									

<210> 4385

<211> 754

<212> DNA

<213> Homo sapiens

<400> 4385

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120
ggctctggtc agagtcggag tcagagtccc aggaggggag tggagggtc aggcactggt
180
gcccccttggt gcctcttagg ctcgaggcct tgggacaggc ccccgagcac aaagtgaggc
240
tgtctatgga gttctgcagc acgtgcacag cagaccatat atcactcagt tcttcttgga
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420
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660
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<210> 4386

<211> 85

<212> PRT

<213> Homo sapiens

<400> 4386

Gly	Cys	Leu	Trp	Ser	Ser	Ala	Ala	Arg	Ala	Gln	Gln	Thr	Ile	Tyr	His
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Ser	Val	Pro	Ser	Gly	Gly	His	Pro	Ser	Ser	Ser	His	Trp	Leu	Pro	Ala
		20					25						30		
Val	Ser	Leu	Gln	Ser	Pro	Asp	Arg	Arg	Leu	Ser	His	Asp	Pro	Ala	Ala
	35						40					45			
Ser	Ser	Trp	Ser	Gly	Phe	Cys	Gly	Ile	Ser	Pro	Ala	Phe	Ser	Ala	Phe

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          50          55          60
Ser Glu Cys Ser Pro Ser Ser Leu Arg Ser His Pro Pro Ala Leu Leu
65          70          75          80
Gln Ala Ala Glu Ser
          85

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<210> 4387
<211> 341
<212> DNA
<213> Homo sapiens

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<400> 4387
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60
ggggcccccc aaaagggggg ggggggaagg gggttttccc accccaaaaa accccccccc
120
ccccccgggn ggggggaag gggggggggg tttttccccc ctcccccccc ccctaaaaaa
180
aaaaccggga aaattttttt tcccccccc ccaaaaaaaa aaaaaaaacc ggggggcccc
240
cctttttttg gggggggggg tttttttttt tttttttttt tttttttttt ttttttttac
300
aaaacagaga atgtttattg tgccagaggg tggagtgtgc n
341

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<210> 4388
<211> 113
<212> PRT
<213> Homo sapiens

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<400> 4388
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Lys Lys Lys Gly Gly Pro Pro Gln Lys Gly Gly Gly Arg Gly Phe
20          25          30
Ser His Pro Lys Lys Pro Pro Pro Pro Gly Xaa Gly Gly Arg Gly
35          40          45
Gly Gly Phe Phe Pro Pro Pro Pro Pro Pro Lys Lys Lys Thr Arg Lys
50          55          60
Ile Phe Phe Pro Pro Pro Pro Lys Lys Lys Lys Lys Pro Gly Gly Pro
65          70          75          80
Pro Phe Phe Gly Gly Gly Phe Phe Phe Phe Phe Phe Phe Phe
85          90          95
Phe Phe Phe Tyr Lys Thr Glu Asn Val Tyr Cys Ala Arg Gly Trp Ser
100          105          110
Val

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<210> 4389
<211> 1895
<212> DNA
<213> Homo sapiens

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<400> 4389

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120
ccagcgggtg acggcgattc tgcccgtag aaggcattgc gtggagctct cgcagcctcc
180
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240
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360
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660
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720
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1620

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1895

<210> 4390

<211> 335

<212> PRT

<213> Homo sapiens

<400> 4390

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		20					25						30		
Ser	Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ala	Leu	Arg	Ala	Ser	Val	Glu
		35					40					45			
Arg	Arg	Leu	Ser	Arg	His	Asp	Val	Val	Ile	Leu	Asp	Ser	Leu	Asn	Tyr
		50				55					60				
Ile	Lys	Gly	Phe	Arg	Tyr	Glu	Leu	Tyr	Cys	Leu	Ala	Arg	Ala	Ala	Arg
65				70					75					80	
Thr	Pro	Leu	Cys	Leu	Val	Tyr	Cys	Val	Arg	Pro	Gly	Gly	Pro	Ile	Ala
			85						90					95	
Gly	Pro	Gln	Val	Ala	Gly	Ala	Asn	Glu	Asn	Pro	Gly	Arg	Asn	Val	Ser
			100					105					110		
Val	Ser	Trp	Arg	Pro	Arg	Ala	Glu	Glu	Asp	Gly	Arg	Ala	Gln	Ala	Ala
		115					120					125			
Gly	Ser	Ser	Val	Leu	Arg	Glu	Leu	His	Thr	Ala	Asp	Ser	Val	Val	Asn
		130				135					140				
Gly	Ser	Ala	Gln	Ala	Asp	Val	Pro	Lys	Glu	Leu	Glu	Arg	Glu	Glu	Ser
145				150						155					160
Gly	Ala	Ala	Glu	Ser	Pro	Ala	Leu	Val	Thr	Pro	Asp	Ser	Glu	Lys	Ser
			165						170					175	
Ala	Lys	His	Gly	Ser	Gly	Ala	Phe	Tyr	Ser	Pro	Glu	Leu	Leu	Glu	Ala
		180						185						190	
Leu	Thr	Leu	Arg	Phe	Glu	Ala	Pro	Asp	Ser	Arg	Asn	Arg	Trp	Asp	Arg
		195					200					205			
Pro	Leu	Phe	Thr	Leu	Val	Gly	Ile	Glu	Glu	Pro	Leu	Pro	Pro	Ala	Gly
		210				215						220			
Ile	Arg	Ser	Ala	Leu	Phe	Glu	Asn	Arg	Ala	Pro	Pro	Pro	His	Gln	Ser
225				230						235					240
Thr	Gln	Ser	Gln	Pro	Leu	Ala	Ser	Gly	Ser	Phe	Leu	His	Gln	Leu	Asp
			245						250					255	
Gln	Val	Thr	Ser	Gln	Val	Leu	Ala	Gly	Leu	Met	Glu	Ala	Gln	Lys	Ser
		260						265					270		
Ala	Val	Pro	Gly	Asp	Leu	Leu	Thr	Leu	Pro	Gly	Thr	Thr	Glu	His	Leu
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Arg	Phe	Thr	Arg	Pro	Leu	Thr	Met	Ala	Glu	Leu	Ser	Arg	Leu	Arg	Arg

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Gln Phe Ile Ser Tyr Thr Lys Met His Pro Asn Asn Glu Asn Leu Pro				
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<210> 4391

<211> 988

<212> DNA

<213> Homo sapiens

<400> 4391

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<210> 4392

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<212> PRT

<213> Homo sapiens

<400> 4392

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<210> 4394
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 4394

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Asp Pro Glu Arg Ser Ser Pro Ala Leu Gly Val Ala Gly Arg Ser Arg
          35           40           45
Glu Lys Leu Gln Arg Val Leu Glu Lys Ala Ala Leu Lys Leu Gly Arg
          50           55           60
Pro Thr Leu Ser Ser Glu Val Gly Ile Ile Cys Asp Ile Ala Asn
65           70           75           80
Pro Ala Ser Leu Asp Glu Met Ala Lys Gln Ala Thr Val Val Leu Asn
          85           90           95
Cys Val Gly Pro Tyr Arg Phe Tyr Gly Glu Pro Val Ile Lys Ala Cys
          100          105          110
Ile Glu Asn Gly Ala Ser Cys Ile Asp Ile Ser Gly Glu Pro Gln Phe
          115          120          125
Leu Glu Leu Met Gln Leu Lys Tyr His Glu Lys Ala Ala Asp Lys Gly
          130          135          140
Val Tyr Ile Ile Gly Ser Ser Gly Phe Asp Ser Ile Pro Ala Asp Leu
145          150          155          160
Gly Val Ile Tyr Thr Arg Asn Lys Met Asn Gly Thr Leu Thr Ala Val
          165          170          175
Glu Ser Phe Leu Thr Ile His Ser Gly Pro Glu Gly Leu Ser Ile His
          180          185          190
Asp Gly Thr Trp Lys Ser Ala Ile Tyr Gly Phe Gly Asp Gln Ser Asn
          195          200          205
Leu Arg Lys Leu Arg Asn Val Ser Asn Leu Lys Pro Val Pro Leu Ile
          210          215          220
Gly Pro Lys Leu Lys Arg Arg Trp Pro Ile Ser Tyr Cys Arg Glu Leu
225          230          235          240
Lys Gly Tyr Ser Ile Pro Phe Met Gly Ser Asp Val Ser Val Val Arg
          245          250          255
Arg Thr Gln Arg Tyr Leu Tyr Glu Asn Leu Glu Glu Ser Pro Val Gln
          260          265          270
Tyr Ala Ala Tyr Val Thr Val Gly Ile Thr Ser Val Ile Lys Leu
          275          280          285
Met Phe Ala Gly Leu Phe Phe Leu Phe Phe Val Arg Phe Gly Ile Gly
          290          295          300
Arg Gln Leu Leu Ile Lys Phe Pro Trp Phe Phe Ser Phe Gly Tyr Phe
305          310          315          320
Ser Lys Gln Gly Pro Thr Gln Lys Gln Ile Asp Ala Ala Ser Phe Thr
          325          330          335
Leu Thr Phe Phe Gly Gln Gly Tyr Ser Gln Gly Thr Gly Thr Asp Lys
          340          345          350
Asn Lys Pro Asn Ile Lys Ile Cys Thr Gln Val Lys Gly Pro Glu Ala
          355          360          365
Gly Tyr Val Ala Thr Pro Ile Ala Met Val Gln Ala Ala Met Thr Leu

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370	375	380
Leu Ser Asp Ala Ser His Leu Pro Lys Ala Gly Gly Val Phe Thr Pro		
385	390	395
Gly Ala Ala Phe Ser Lys Thr Lys Leu Ile Asp Arg Leu Asn Lys His		400
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<210> 4395

<211> 1893

<212> DNA

<213> Homo sapiens

<400> 4395

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<210> 4396

<211> 463

<212> PRT

<213> Homo sapiens

<400> 4396

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		20						25					30		
Ser	Gly	Asp	Leu	Pro	Gln	Ala	Ala	Ser	His	Leu	Gln	Glu	Leu	Leu	Ala
		35					40					45			
Ser	Thr	Glu	Ser	Ile	Arg	Leu	Glu	Val	Gly	Val	Thr	Gly	Glu	Ser	Gly
	50					55				60					
Ala	Gly	Lys	Ser	Ser	Leu	Ile	Asn	Ala	Leu	Arg	Gly	Leu	Glu	Ala	Glu
65					70					75				80	
Asp	Pro	Gly	Ala	Ala	Leu	Thr	Gly	Val	Met	Glu	Thr	Thr	Met	Gln	Pro
			85					90						95	
Ser	Pro	Tyr	Pro	His	Pro	Gln	Phe	Pro	Asp	Val	Thr	Leu	Trp	Asp	Leu
			100					105					110		
Pro	Gly	Ala	Gly	Ser	Pro	Gly	Cys	Pro	Ala	Asp	Lys	Tyr	Leu	Lys	Gln
		115					120					125			
Val	Asp	Phe	Ser	Arg	Tyr	Asp	Phe	Phe	Leu	Leu	Val	Ser	Pro	Arg	Arg
	130					135					140				
Cys	Gly	Ala	Val	Glu	Thr	Arg	Leu	Ala	Ala	Glu	Ile	Leu	Cys	Gln	Gly
145					150					155				160	
Lys	Lys	Phe	Tyr	Phe	Val	Arg	Thr	Lys	Val	Asp	Glu	Asp	Leu	Ala	Ala
			165					170						175	
Thr	Arg	Thr	Gln	Arg	Pro	Ser	Gly	Phe	Arg	Glu	Ala	Ala	Val	Leu	Gln


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      180              185              190
Glu Ile Arg Asp His Cys Ala Glu Arg Leu Arg Glu Ala Gly Val Ala
      195              200              205
Asp Pro Arg Ile Phe Leu Val Ser Asn Leu Ser Pro Ala Arg Tyr Asp
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Phe Pro Thr Leu Val Ser Thr Trp Glu His Asp Leu Pro Ser His Arg
      225              230              235              240
Arg His Ala Gly Leu Leu Ser Leu Pro Asp Ile Ser Leu Glu Ala Leu
      245              250              255
Gln Lys Lys Lys Ala Met Leu Gln Glu Gln Val Leu Lys Thr Ala Leu
      260              265              270
Val Leu Gly Val Ile Gln Ala Leu Pro Val Pro Gly Leu Ala Ala Ala
      275              280              285
Tyr Asp Asp Ala Leu Leu Ile His Ser Leu Arg Gly Tyr His Arg Ser
      290              295              300
Phe Gly Leu Asp Asp Asp Ser Leu Ala Lys Leu Ala Glu Gln Val Gly
      305              310              315              320
Lys Gln Ala Gly Asp Leu Arg Ser Val Ile Arg Ser Pro Leu Ala Asn
      325              330              335
Glu Val Ser Pro Glu Thr Val Leu Arg Leu Tyr Ser Gln Ser Ser Asp
      340              345              350
Gly Ala Met Arg Val Ala Arg Ala Phe Glu Arg Gly Ile Pro Val Phe
      355              360              365
Gly Thr Leu Val Ala Gly Gly Ile Ser Phe Gly Ala Val Tyr Thr Met
      370              375              380
Leu Gln Gly Cys Leu Asn Glu Met Ala Glu Asp Ala Gln Arg Val Arg
      385              390              395              400
Ile Lys Ala Leu Glu Asp Asp Glu Pro Gln Pro Glu Val Ser Leu Glu
      405              410              415
Val Ala Ser Asp Asn Gly Val Glu Lys Gly Gly Ser Gly Glu Gly Gly
      420              425              430
Gly Glu Glu Ala Pro Leu Ser Thr Cys Arg Lys Leu Gly Leu Leu Leu
      435              440              445
Lys Tyr Ile Leu Asp Ser Trp Lys Lys His Asp Ser Glu Glu Lys
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<210> 4397

<211> 2543

<212> DNA

<213> Homo sapiens

<400> 4397

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360

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<210> 4398

<211> 354

<212> PRT

<213> Homo sapiens

<400> 4398

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			20					25				30			
Arg	Asp	Pro	Asp	Lys	Tyr	Cys	Pro	Ser	Tyr	Asn	Lys	Ser	Pro	Gln	Ser
		35				40					45				
Asn	Ser	Pro	Val	Leu	Leu	Ser	Arg	Leu	His	Phe	Glu	Lys	Asp	Ala	Asp
		50				55					60				
Ser	Ser	Glu	Arg	Ile	Ile	Ala	Pro	Met	Arg	Trp	Gly	Leu	Val	Pro	Ser
				70						75				80	
Trp	Phe	Lys	Glu	Ser	Asp	Pro	Ser	Lys	Leu	Gln	Phe	Asn	Thr	Thr	Asn
			85					90					95		
Cys	Arg	Ser	Asp	Thr	Val	Met	Glu	Lys	Arg	Ser	Phe	Lys	Val	Pro	Leu
			100					105					110		
Gly	Lys	Gly	Arg	Arg	Cys	Val	Val	Leu	Ala	Asp	Gly	Phe	Tyr	Glu	Trp
		115				120						125			
Gln	Arg	Cys	Gln	Gly	Thr	Asn	Gln	Arg	Gln	Pro	Tyr	Phe	Ile	Tyr	Phe
		130				135					140				
Pro	Gln	Ile	Lys	Thr	Glu	Lys	Ser	Gly	Ser	Ile	Gly	Ala	Ala	Asp	Ser
			150							155				160	
Pro	Glu	Asn	Trp	Glu	Lys	Val	Trp	Asp	Asn	Trp	Arg	Leu	Leu	Thr	Met
			165					170						175	
Ala	Gly	Ile	Phe	Asp	Cys	Trp	Glu	Pro	Pro	Glu	Gly	Gly	Asp	Val	Leu
			180					185					190		
Tyr	Ser	Tyr	Thr	Ile	Ile	Thr	Val	Asp	Ser	Cys	Lys	Gly	Leu	Ser	Asp
			195				200					205			
Ile	His	His	Arg	Met	Pro	Ala	Ile	Leu	Asp	Gly	Glu	Glu	Ala	Val	Ser

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225                230                235                240
Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
      245                250                255
Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
      260                265                270
Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Arg Met Leu
      275                280                285
Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
      290                295                300
Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
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Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr Ala Gly Leu Leu Glu Gln
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Trp Leu Lys Arg Glu Lys Glu Glu Glu Pro Val Ala Lys Arg Pro Tyr
      340                345                350
Ser Gln

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<210> 4399
 <211> 723
 <212> DNA
 <213> Homo sapiens

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 gagcggcacc acagtagtcc aaagagagag ctcccgcggc ggaatcgggga catggtggag
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 420
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 480
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 723

<210> 4400

<211> 241
 <212> PRT
 <213> Homo sapiens

<400> 4400
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 35 40 45
 Ala Leu Asp Glu Gln Leu Val Gln Val Lys Glu Ala Glu Arg His His
 50 55 60
 Ser Ser Pro Lys Arg Glu Leu Pro Pro Gly Ile Gly Asp Met Val Glu
 65 70 75 80
 Leu Met Gly Val Gln Asp Gln His Met Asp Glu Arg Asp Val Arg Arg
 85 90 95
 Phe Gln Leu Lys Ile Ala Glu Leu Asn Ser Val Ile Arg Lys Leu Glu
 100 105 110
 Asp Arg Asn Thr Leu Leu Ala Asp Glu Arg Asn Glu Leu Leu Lys Arg
 115 120 125
 Ser Arg Glu Thr Glu Val Gln Leu Lys Pro Leu Val Glu Lys Asn Lys
 130 135 140
 Arg Met Asn Lys Lys Asn Glu Asp Leu Leu Gln Ser Ile Gln Arg Met
 145 150 155 160
 Glu Glu Lys Ile Lys Asn Leu Thr Arg Glu Asn Val Glu Met Lys Glu
 165 170 175
 Lys Leu Ser Ala Gln Ala Ser Leu Lys Arg His Thr Ser Leu Asn Asp
 180 185 190
 Leu Ser Leu Thr Arg Asp Glu Gln Glu Ile Glu Phe Leu Arg Leu Gln
 195 200 205
 Val Leu Glu Gln Gln His Val Ile Asp Asp Leu Ser Leu Glu Arg Glu
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 225 230 235 240
 Lys

<210> 4401
 <211> 1131
 <212> DNA
 <213> Homo sapiens

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 300

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 420
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 480
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 720
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 780
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 840
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<210> 4402

<211> 252

<212> PRT

<213> Homo sapiens

<400> 4402

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Thr	Ala	Arg	Lys	Ser	Ile	Thr	Val	Ile	Cys	Asp	Phe	Tyr	Ser	Leu	Ile
		35					40					45			
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		50				55				60					
Gln	Tyr	Gly	Arg	Trp	Ala	Val	Val	Ser	Gly	Ala	Thr	Asp	Gly	Ile	Gly
65				70					75					80	
Lys	Ala	Tyr	Ala	Glu	Glu	Leu	Ala	Ser	Arg	Gly	Leu	Asn	Ile	Ile	Leu
			85					90					95		
Ile	Ser	Arg	Asn	Glu	Glu	Lys	Leu	Gln	Val	Val	Ala	Lys	Asp	Ile	Ala
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Val	Gly	Ile	Leu	Val	Asn	Asn	Val	Gly	Val	Phe	Tyr	Pro	Tyr	Pro	Gln

145		150		155		160									
Tyr	Phe	Thr	Gln	Leu	Ser	Glu	Asp	Lys	Leu	Trp	Asp	Ile	Ile	Asn	Val
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Asn	Ile	Ala	Ala	Ala	Ser	Leu	Met	Val	His	Val	Val	Leu	Pro	Gly	Met
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Val	Glu	Arg	Lys	Lys	Gly	Ala	Ile	Val	Thr	Ile	Ser	Ser	Gly	Leu	Leu
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Leu	Gln	Pro	Thr	Pro	Gln	Leu	Ala	Ala	Phe	Ser	Ala	Ser	Lys	Ala	Tyr
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Leu	Asp	His	Phe	Ser	Arg	Ala	Leu	Gln	Tyr	Glu	Tyr	Ala	Ser	Lys	Gly
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Ile	Phe	Val	Gln	Ser	Leu	Xaa	Pro	Phe	Tyr	Val	Ala				
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<210> 4403

<211> 4237

<212> DNA

<213> Homo sapiens

<400> 4403

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<210> 4404

<211> 779

<212> PRT

<213> Homo sapiens

<400> 4404

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 Asn Asn His Gly Asn Phe Gln Gly Asp Ser Asn Phe Asn Arg Met Trp
 50 55 60
 Gln Pro Glu Trp Gly Met His Gln Gln Pro Pro His Pro Pro Pro Asp
 65 70 75 80
 Gln Pro Trp Met Pro Pro Thr Pro Gly Pro Met Asp Ile Val Pro Pro
 85 90 95
 Ser Glu Asp Ser Asn Ser Gln Asp Ser Gly Glu Phe Ala Pro Asp Asn
 100 105 110
 Arg His Ile Phe Asn Gln Asn Asn His Asn Phe Gly Gly Pro Pro Asp
 115 120 125
 Asn Phe Ala Val Gly Pro Val Asn Gln Phe Asp Tyr Gln His Gly Ala
 130 135 140
 Ala Phe Gly Pro Pro Gln Gly Gly Phe His Pro Pro Tyr Trp Gln Pro
 145 150 155 160
 Gly Pro Pro Gly Pro Pro Ala Pro Pro Gln Asn Arg Arg Glu Arg Pro
 165 170 175
 Ser Ser Phe Arg Asp Arg Gln Arg Ser Pro Ile Ala Leu Pro Val Lys
 180 185 190
 Gln Glu Pro Pro Gln Ile Asp Ala Val Lys Arg Arg Thr Leu Pro Ala
 195 200 205
 Trp Ile Arg Glu Gly Leu Glu Lys Met Glu Arg Glu Lys Gln Lys Lys
 210 215 220
 Leu Glu Lys Glu Arg Met Glu Gln Gln Arg Ser Gln Leu Ser Lys Lys
 225 230 235 240
 Lys Lys Lys Ala Thr Glu Asp Ala Glu Gly Gly Asp Gly Pro Arg Leu
 245 250 255
 Pro Gln Arg Ser Lys Phe Asp Ser Asp Glu Glu Glu Asp Thr Glu
 260 265 270
 Asn Val Glu Ala Ala Ser Ser Gly Lys Val Thr Arg Ser Pro Ser Pro
 275 280 285
 Val Pro Gln Glu Glu His Ser Asp Pro Glu Met Thr Glu Glu Glu Lys
 290 295 300
 Glu Tyr Gln Met Met Leu Leu Thr Lys Met Leu Leu Thr Glu Ile Leu
 305 310 315 320
 Leu Asp Val Thr Asp Glu Glu Ile Tyr Tyr Val Ala Lys Asp Ala His
 325 330 335
 Arg Lys Ala Thr Lys Ala Pro Ala Lys Gln Leu Ala Gln Ser Ser Ala
 340 345 350
 Leu Ala Ser Leu Thr Gly Leu Gly Gly Leu Gly Gly Tyr Gly Ser Gly
 355 360 365
 Asp Ser Glu Asp Glu Arg Ser Asp Arg Gly Ser Glu Ser Ser Asp Thr

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385              390              395              400
Trp Arg Lys Glu Lys Glu Gln Gln Leu Leu His Asp Lys Gln Met Glu
      405              410              415
Glu Glu Lys Gln Gln Thr Glu Arg Val Thr Lys Glu Met Asn Glu Phe
      420              425              430
Ile His Lys Glu Gln Asn Ser Leu Ser Leu Leu Glu Ala Arg Glu Ala
      435              440              445
Asp Gly Asp Val Val Asn Glu Lys Lys Arg Thr Pro Asn Glu Thr Thr
      450              455              460
Ser Val Leu Glu Pro Lys Lys Glu His Lys Glu Lys Glu Lys Gln Gly
465              470              475              480
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      485              490              495
Arg Thr Ser Ser Thr Ser Ser Thr Val Ser Ser Ser Ser Tyr Ser Ser
      500              505              510
Ser Ser Gly Ser Ser Arg Thr Ser Ser Arg Ser Ser Ser Pro Lys Arg
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Lys Lys Arg His Ser Arg Ser Arg Ser Pro Thr Ile Lys Ala Arg Arg
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Glu Lys Asp Phe Lys Phe Ser Ser Gln Asp Asp Arg Leu Lys Arg Lys
      675              680              685
Arg Glu Ser Glu Arg Thr Phe Ser Arg Ser Gly Ser Ile Ser Val Lys
      690              695              700
Ile Ile Arg His Asp Ser Arg Gln Asp Ser Lys Lys Ser Thr Thr Lys
705              710              715              720
Asp Ser Lys Lys His Ser Gly Ser Asp Ser Ser Gly Arg Ser Ser Ser
      725              730              735
Glu Ser Pro Gly Ser Ser Lys Glu Lys Lys Ala Lys Lys Pro Lys His
      740              745              750
Ser Arg Ser Arg Ser Val Glu Lys Ser Gln Arg Ser Gly Lys Lys Ala
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Ser Arg Lys His Lys Ser Lys Ser Arg Ser Arg
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<211> 918

<212> DNA

<213> Homo sapiens

<400> 4405

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<210> 4406

<211> 138

<212> PRT

<213> Homo sapiens

<400> 4406

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 35 40 45
 Gly Asn Lys Ser Asp Leu Ser Gln Ala Arg Glu Val Pro Thr Glu Glu
 50 55 60
 Ala Arg Met Phe Ala Glu Asn Asn Gly Leu Leu Phe Leu Glu Thr Ser
 65 70 75 80
 Ala Leu Asp Ser Thr Asn Val Glu Leu Ala Phe Glu Thr Val Leu Lys

85 90 95

Glu Ile Phe Ala Lys Val Ser Lys Gln Arg Gln Asn Ser Ile Arg Thr
100 105 110
Asn Ala Ile Thr Leu Gly Ser Ala Gln Ala Gly Gln Glu Pro Gly Pro
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Gly Glu Lys Arg Ala Cys Cys Ile Ser Leu
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<211> 974
<212> DNA
<213> Homo sapiens
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900 aaaaagtttt cccacaaaaa tatttatgtg ttatcatcta tatctggata agttttaaatt
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<210> 4408
<211> 158
<212> PRT
<213> Homo sapiens
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<400> 4408

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Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile
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His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys Ala Ala Leu Ser
 20           25           30
Ala Tyr Asp Met Val Leu Val Glu Asp Glu Glu Val Asn Arg Met His
 35           40           45
Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Lys Tyr Phe Ser
 50           55           60
Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Ile Phe Gln Glu
 65           70           75           80
Lys Val Thr Lys Val His Leu Ser Ile Cys Phe Pro Glu Tyr Thr Gly
 85           90           95
Pro Asn Thr Phe Glu Asp Ala Gly Asn Tyr Ile Lys Asn Gln Phe Leu
100           105           110
Asp Leu Asn Leu Lys Lys Glu Asp Lys Glu Ile Tyr Ser His Met Thr
115           120           125
Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp Ala Val Thr
130           135           140
Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu Phe
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<210> 4409

<211> 4217

<212> DNA

<213> Homo sapiens

<400> 4409

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gaaaggtttc agtacaagta ccagctacgc tcccacatga gcattcatat tgggcacaaa
780

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cagttcatgt gccagtgggt tggcaaggat ttcaacatga agcagtactt cgacgaacac
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2400

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 4200
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 4217

<210> 4410
 <211> 405
 <212> PRT
 <213> Homo sapiens

<400> 4410
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 Gln Gly Pro Arg Gly Ser Arg Ser Ser Arg Ala Asp Pro Pro Pro His
 20 25 30
 Ser His Met Ala Thr Arg Ser Arg Glu Asn Ala Arg Arg Gly Thr
 35 40 45
 Pro Glu Pro Glu Glu Ala Gly Arg Arg Gly Gly Lys Arg Pro Lys Pro
 50 55 60
 Pro Pro Gly Val Ala Ser Ala Ser Ala Arg Gly Pro Pro Ala Thr Asp
 65 70 75 80
 Gly Leu Gly Ala Lys Val Lys Leu Glu Glu Lys Gln His His Pro Cys
 85 90 95
 Gln Lys Cys Pro Arg Val Phe Asn Asn Arg Trp Tyr Leu Glu Lys His
 100 105 110
 Met Asn Val Thr His Ser Arg Met Gln Ile Cys Asp Gln Cys Gly Lys
 115 120 125
 Arg Phe Leu Leu Glu Ser Glu Leu Leu Leu His Arg Gln Thr Asp Cys
 130 135 140
 Glu Arg Asn Ile Gln Cys Val Thr Cys Gly Lys Ala Phe Lys Lys Leu
 145 150 155 160
 Trp Ser Leu His Glu His Asn Lys Ile Val His Gly Tyr Ala Glu Lys
 165 170 175
 Lys Phe Ser Cys Glu Ile Cys Glu Lys Lys Phe Tyr Thr Met Ala His
 180 185 190
 Val Arg Lys His Met Val Ala His Thr Lys Asp Met Pro Phe Thr Cys
 195 200 205
 Glu Thr Cys Gly Lys Ser Phe Lys Arg Ser Met Ser Leu Lys Val His
 210 215 220
 Ser Leu Gln His Ser Gly Glu Lys Pro Phe Arg Cys Glu Asn Cys Asp
 225 230 235 240
 Glu Arg Phe Gln Tyr Lys Tyr Gln Leu Arg Ser His Met Ser Ile His
 245 250 255
 Ile Gly His Lys Gln Phe Met Cys Gln Trp Cys Gly Lys Asp Phe Asn
 260 265 270
 Met Lys Gln Tyr Phe Asp Glu His Met Lys Thr His Thr Gly Glu Lys
 275 280 285
 Pro Phe Ile Cys Glu Ile Cys Gly Lys Ser Phe Thr Ser Arg Pro Asn
 290 295 300
 Met Lys Arg His Arg Thr His Thr Gly Glu Lys Pro Tyr Pro Cys

```

305          310          315          320
Asp Val Cys Gly Gln Arg Phe Arg Phe Ser Asn Met Leu Lys Ala His
          325          330          335
Lys Glu Lys Cys Phe Arg Val Ser His Thr Leu Ala Gly Asp Gly Val
          340          345          350
Pro Ala Ala Pro Gly Leu Pro Pro Thr Gln Pro Gln Ala His Ala Leu
          355          360          365
Pro Leu Leu Pro Gly Leu Pro Gln Thr Leu Pro Pro Pro His Leu
          370          375          380
Pro Pro Pro Pro Pro Leu Phe Pro Thr Thr Ala Ser Pro Gly Gly Arg
385          390          395          400
Met Asn Ala Asn Asn
          405

```

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<210> 4411
<211> 484
<212> DNA
<213> Homo sapiens

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<400> 4411
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120
caaaagagga gtttaggggtg gctatgggtgc aggggcagct gtatgcttca cctcaaatgt
180
tactgtcttc tctctccatc aaggaggaag ggcccaggct ggggttagga gggctagggg
240
cccaggctgt gtgtccctt tttctctct ggtgcctgc ccccccacgc tgtcatctcc
300
ctcagtgcca gtgggggttc atcactgggt cttcaggctc cttgcccatg gctggtgggtg
360
ttcaggtgg gcccaaccag gcggcccctg cctctaggca gcgcgtaggt ttccttgggc
420
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480
atcc
484

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<210> 4412
<211> 113
<212> PRT
<213> Homo sapiens

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<400> 4412
Met Val Gln Gly Gln Leu Tyr Ala Ser Pro Gln Met Leu Leu Ser Ser
1          5          10          15
Leu Ser Ile Lys Glu Glu Gly Pro Arg Leu Gly Leu Gly Gly Leu Gly
20          25          30
Ala Gln Ala Val Cys Pro Leu Phe Ser Ser Trp Cys Pro Ala Pro Pro
35          40          45
Arg Cys His Leu Pro Gln Trp Gln Trp Gly Phe Ile Thr Gly Ser Ser
50          55          60
Gly Pro Leu Pro Met Ala Gly Gly Val Pro Gly Gly Pro Asn Gln Ala

```

```

65              70              75              80
Ala Pro Ala Ser Arg Gln Arg Val Gly Phe Leu Gly Gln Pro Gln Ser
              85              90              95
Cys Gln Arg Gln His Val Ser Leu His Arg Ser His Gln Ala Pro Leu
              100              105              110
Asp

```

<210> 4413

<211> 1097

<212> DNA

<213> Homo sapiens

<400> 4413

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atggcgctgc tttttgcacg ttctttgcgc ttgtgcgcgt ggggagccaa acgattggga
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gttgccctcca cagagcgcca gagaggcgctc agtttcaaac tggaagaaaa aaccgcccac
120
agcagcctgg cactcttcag agatgatacg ggtgtcaaat atggcttggt gggattggag
180
cccaccaagg tgccttgaat gtggagcgct tccgggagtt ggcaggtgct ggcagacaca
240
gcggtcacca gtggcagaca ctactgggaa gtgacagtga agcgctccca gcagttccgg
300
ataggagtgg cagatgtgga catgtcccg gatagctgca ttggtgttga tgatcgttcc
360
tgggtgttca cctatgccca gcgcaagtgg tacaccatgt tggccaacga gaaagcccca
420
gttgagggta ttgggcagcc agagaagggtg gggctgttgc ttgagtagta ggcccagaag
480
ctgagcctgg tggatgtgag ccaggtctct gtggttcaca cgctacagac agatttccgg
540
gggtccagtg tgccctgctt tgctctctgg gatggggagc tgctgaccca ttcagggtct
600
gaggtgcccc agggcctcta gtatgtccat tactggagtc cctaatacag cctttggcca
660
gcctcctttt gaaagtgtcc gaagcctttt tactttgcct caagcaacct ctagctccca
720
caattcagtg ttgggtcttc tgtgcaatat catgatcatc ttcctcatcc cctaccttgt
780
gaaagctagg catacagcca aacctcctt tccccaccc accaactact gccaatttcc
840
taggctacca tgggtgtatc ttccttgacc tgcttccttc agtcctctg cctccctttg
900
cccaggcctt tctcagactg tattccatcc tggggtctta tcattcagct ttgtttgaat
960
ttattaatca ccatgatacc tctccctccc tttgtccaca tgtaacttgt tcttggggct
1020
ctaccagatg gctgaagagt aaatccttcc tacctctggc tgaaaaaaaa aaaaaaaaaa
1080
aaaaaaaaaa aaaaaaa
1097

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<210> 4414

<211> 65
 <212> PRT
 <213> Homo sapiens

<400> 4414
 Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
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 Lys Arg Leu Gly Val Ala Ser Thr Glu Arg Gln Arg Gly Val Ser Phe
 20 25 30
 Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
 35 40 45
 Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
 50 55 60
 Pro
 65

<210> 4415
 <211> 775
 <212> DNA
 <213> Homo sapiens

<400> 4415
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 60
 tccagcagaa agagacaaaag atctttgttc aaaatattct gaaaaaggta aactaactgc
 120
 attattgaat acacaaaagg aatgttaccg ttacttggtc atagtcaaaag gtgaagttaa
 180
 aaaaaaaggg aagttaaata actgaagtaa tggtttgccc aaatagcaaa cgtaggatac
 240
 aggcgtgggc aaagagcagc tactgaagct catgaggagg atgctggata tagggtaggt
 300
 aacttgacaa atgcctctgc ttctttggaa ccttcttcct agatcacccc cacaaattcc
 360
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 420
 atatttgcca acagaatgag atagttaa aaataatcaa tttctgtgtg agacaagaca
 480
 tgtctgaatc catttctcct ggggtaggag gaggtaatga acattaacgt tctgcattcc
 540
 aatctcctaa aatggaattt aaccagatag atatcgcttg agattttaa gcaggagata
 600
 ccataagtaa tgatactcca ggctgtaaa gcatttttca ttgtcccaca ttgcagctaa
 660
 atgagtataa actcgacagt gttctgattt cacaacatat gcatttatga caactgctaa
 720
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 775

<210> 4416
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 4416

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Met Lys Asn Ala Leu Gln Ala Trp Ser Ile Ile Thr Tyr Gly Ile Ser
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Cys Phe Lys Ile Ser Ser Asp Ile Tyr Leu Val Lys Phe His Phe Arg
 20           25           30
Arg Leu Arg Cys Arg Thr Leu Met Phe Ile Thr Ser Ser Tyr Pro Lys
 35           40           45
Arg Asn Gly Phe Arg His Val Leu Ser Gln Gln Glu Ile Asp Phe Phe
 50           55           60
Leu Asn Tyr Leu Ile Leu Leu Pro Asn Ile Thr Glu Val Met Arg Ser
 65           70           75           80
Leu Val Thr Phe Gly Cys Cys Ala Leu Lys Glu Pro Gly Leu Glu Phe
 85           90           95
Val Gly Val Ile
          100

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<210> 4417

<211> 980

<212> DNA

<213> Homo sapiens

<400> 4417

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nnacgcgtga gggaaaagca gaggcagttg gaggtagcgc aagttgaaaa ccagctgtcta
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aaaatgaagg tggaatcgtc ccaagaagcc aatgctgagg tgatgcgaga gatgaccaag
120
aagctgtaca gccagtatga ggagaagctg caggaagaac agaggaaagca cagtgtctgag
180
aaggaggctc ttttggaaga aaccaatagt tttctgaaag cgattgaaga agccaataaa
240
aagatgcaag cagcagagat cagcctagag gagaagacc agaggatcgg ggagctggac
300
aggctgattg agcgcatgga aaaggaacgt catcaactgc aacttcaact cctagaacat
360
gaaacagaaa tgtctgggga gttaactgat tctgacaagg aaaggatca gcagttggag
420
gagggcatcag ccagcctccg tgagcggatc agacacctag atgacatggg gcattgccag
480
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600
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660
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720
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780
acgtgactt aggcactcag aggcatacac tttttacaga tggacaaaag ctctggaacc
840
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900
ggaatgggaa tcgctgaggc tctgatccac ttctaagaca ggaaggaag tgaaggcaga
960

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gtgagcaggt aagagagggg
980

<210> 4418
<211> 263
<212> PRT
<213> Homo sapiens

<400> 4418
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Asn Gln Leu Leu Lys Met Lys Val Glu Ser Ser Gln Glu Ala Asn Ala
20 25 30
Glu Val Met Arg Glu Met Thr Lys Lys Leu Tyr Ser Gln Tyr Glu Glu
35 40 45
Lys Leu Gln Glu Glu Gln Arg Lys His Ser Ala Glu Lys Glu Ala Leu
50 55 60
Leu Glu Glu Thr Asn Ser Phe Leu Lys Ala Ile Glu Glu Ala Asn Lys
65 70 75 80
Lys Met Gln Ala Ala Glu Ile Ser Leu Glu Glu Lys Asp Gln Arg Ile
85 90 95
Gly Glu Leu Asp Arg Leu Ile Glu Arg Met Glu Lys Glu Arg His Gln
100 105 110
Leu Gln Leu Gln Leu Leu Glu His Glu Thr Glu Met Ser Gly Glu Leu
115 120 125
Thr Asp Ser Asp Lys Glu Arg Tyr Gln Gln Leu Glu Glu Ala Ser Ala
130 135 140
Ser Leu Arg Glu Arg Ile Arg His Leu Asp Asp Met Val His Cys Gln
145 150 155 160
Gln Lys Lys Val Lys Gln Met Val Glu Glu Ile Glu Ser Leu Lys Lys
165 170 175
Lys Val Gln Gln Lys Gln Leu Leu Ile Leu Gln Leu Leu Glu Lys Ile
180 185 190
Ser Phe Leu Glu Gly Glu Asn Asn Glu Leu Gln Ser Arg Leu Asp Tyr
195 200 205
Leu Thr Glu Thr Gln Ala Lys Thr Glu Val Glu Thr Arg Glu Ile Gly
210 215 220
Val Gly Cys Asp Leu Leu Pro Ser Pro Thr Gly Arg Thr Arg Glu Ile
225 230 235 240
Val Met Pro Ser Arg Asn Tyr Thr Pro Tyr Thr Arg Val Leu Glu Leu
245 250 255
Ser Ser Lys Lys Thr Leu Thr
260

<210> 4419
<211> 369
<212> DNA
<213> Homo sapiens

<400> 4419
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cagggtcttg ctctgntcac ccaggctgga gtgcagtgg ggcgatcttg ctcactgcaa
120

cctccgcctc cccagctcaa gcaactctcc tgccccagcc acccaagttn aaattacagg
 180
 cccgtgccac cacaccggc caatttctgt atttttagta gagacggggg ttcacatat
 240
 tggccaggac ggtctcaaac tcctggcccc atgtgatect cccaccttgg cctcccaagg
 300
 tgctgggtatt acaggcgtga gccaccactg cgccctggcca gattttgtct tttttgagc
 360
 agtctcagn
 369

<210> 4420

<211> 91

<212> PRT

<213> Homo sapiens

<400> 4420

Xaa	Ile	Pro	Cys	Ile	Glu	Ser	Ala	Arg	Ile	His	Thr	Ile	Tyr	Tyr	Val
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Phe	Ile	Leu	Arg	Gln	Gly	Leu	Ala	Leu	Xaa	Thr	Gln	Ala	Gly	Val	Gln
		20						25					30		
Trp	Cys	Asp	Leu	Gly	Ser	Leu	Gln	Pro	Pro	Pro	Pro	Gln	Leu	Lys	Gln
		35					40					45			
Leu	Ser	Cys	Pro	Ser	His	Pro	Ser	Xaa	Asn	Tyr	Arg	Pro	Val	Pro	Pro
	50				55						60				
His	Pro	Ala	Asn	Phe	Cys	Ile	Phe	Ser	Arg	Asp	Gly	Val	Ser	Pro	Tyr
	65				70				75					80	
Trp	Pro	Gly	Arg	Ser	Gln	Thr	Pro	Gly	Pro	Met					
			85						90						

<210> 4421

<211> 1356

<212> DNA

<213> Homo sapiens

<400> 4421

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 120
 ctgggggtgtg ctagagagag gaaagctgga ggaggagagc tgagctggtg gttaccccat
 180
 gccaggagggg ccaaggcaag aagcctgcag cccagagat actgaccctg tccctgcgcc
 240
 tccaggggcac aactgaacta acggaatggc ttaatcagat agctcgagaa ctgccactac
 300
 cactccctcc ctgcccactc ctcccaaagt ccacctgttc ccgcaagagt cccacctcac
 360
 aagcaaccac cagaggctga tacaatggc cgctgtatgt ttgctaaagt gacagtgaca
 420
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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 4426

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Thr Lys Arg Lys Ala	Ile Ala Ala Glu Asp	Pro Ser Leu Asp Phe Arg	
	50	55	60
Asn Asn Pro Thr Lys	Glu Asp Leu Gly Lys	Leu Gln Pro Leu Val Ala	
	65	70	75
Ser Tyr Leu Cys Ser	Asp Val Thr Ser Val	Pro Ser Lys Glu Ser Leu	
	85	90	95
Lys Leu Gln Gly Val	Phe Ser Lys Gln Thr	Val Leu Lys Ser His Pro	
	100	105	110
Leu Leu Ser Gln Ser	Tyr Glu Leu Arg Ala	Glu Leu Leu Gly Arg Gln	
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	130	135	140
Gly Gln Thr Ala Leu	Pro Gln Ala Pro Val	Asn Gly Leu Ala Lys Lys	
	145	150	155
Leu Thr Lys Ser Ser	Thr His Ser Asp His	Asp Asn Ser Thr Ser Leu	
	165	170	175
Asn Gly Gly Lys Arg	Ala Leu Thr Ser Ser	Ala Leu His Gly Gly Glu	
	180	185	190
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Ala Leu Gln Gly Ser	Ser Arg Leu Ser Pro	Gly Thr Asp Ser Ser Ser	
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Asn Leu Gly Gly Val	Lys Leu Glu Gly Lys	Lys Ser Pro Leu Ser Ser	
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Ile Leu Phe Ser Ala	Leu Asp Ser Asp Thr	Arg Ile Thr Ala Leu Leu	
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Leu Gly Gly Phe Leu	Glu Lys Thr Leu Ser	Lys Leu Pro Asn Leu Glu	
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Ser Leu Arg Pro Arg	Ser Gln Leu Met Leu	Thr Arg Lys Ala Glu Ala	
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Ala Leu Arg Lys Ala	Ala Ser Glu Thr Thr	Ser Glu Gly Leu Ser	
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Asn Phe Leu Lys Ser	Asn Ser Ile Ser Glu	Glu Leu Glu Arg Phe Thr	
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Ala Ser Gly Ile Ala	Asn Leu Arg Cys Ser	Glu Gln Ala Phe Asp Ser	
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	405	410	415
Glu Leu Thr Arg Ala	Asp Pro Glu Gln Arg	His Val Pro Leu Arg Arg	
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<210> 4427

<211> 4474

〔212〕 DNA

<213> Homo sapiens

<400> 4427

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<211> 763

<212> PRT

<213> Homo sapiens

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 Ser Lys Glu Leu His Ser Glu Phe Ser Glu Val Met Asn Glu Ile Trp
 65 70 75 80
 Ala Ser Asp Gln Ile Arg Ser Ala Val Leu Ile Ser Ser Lys Pro Gly
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 Lys Leu Glu Lys Ser Thr Lys Pro Ile Val Ala Ala Ile Asn Gly Ser
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 Ser Pro Lys Arg Asp Lys Gly Leu Val Glu Lys Leu Thr Ala Tyr Ala
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 325 330 335
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 Ala Gly Leu Met Gly Ala Gly Ile Ala Gln Val Ser Val Asp Lys Gly
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 Leu Asp Tyr Gln Gly Phe Glu Lys Ala Asp Met Val Ile Glu Ala Val
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 Thr Thr Glu Lys Thr Ser Lys Asp Thr Ser Ala Ser Ala Val Ala Val
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<211> 981

<212> DNA

<213> Homo sapiens

<400> 4429

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<213> Homo sapiens

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<211> 447

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 4435

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783

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<210> 4436

<211> 261
 <212> PRT
 <213> Homo sapiens

<400> 4436
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 Asp Glu Glu Asp Met Phe Met Val Val Asp Leu Leu Leu Gly Gly Asp
 35 40 45
 Leu Arg Tyr His Leu Gln Gln Asn Val His Phe Thr Glu Gly Thr Val
 50 55 60
 Lys Leu Tyr Ile Cys Glu Leu Ala Leu Ala Leu Glu Tyr Leu Gln Arg
 65 70 75 80
 Tyr His Ile Ile His Arg Asp Ile Lys Pro Asp Asn Ile Leu Leu Asp
 85 90 95
 Glu His Gly His Val His Ile Thr Asp Phe Asn Ile Ala Thr Val Val
 100 105 110
 Lys Gly Ala Glu Arg Ala Ser Ser Met Ala Gly Thr Lys Pro Tyr Met
 115 120 125
 Ala Pro Glu Val Phe Gln Val Tyr Met Asp Arg Gly Pro Gly Tyr Ser
 130 135 140
 Tyr Pro Val Asp Trp Trp Ser Leu Gly Ile Thr Ala Tyr Glu Leu Leu
 145 150 155 160
 Arg Gly Trp Arg Pro Tyr Glu Ile His Ser Val Thr Pro Ile Asp Glu
 165 170 175
 Ile Leu Asn Met Phe Lys Val Glu Arg Val His Tyr Ser Ser Thr Trp
 180 185 190
 Cys Lys Gly Met Val Ala Leu Leu Arg Lys Leu Leu Thr Lys Asp Pro
 195 200 205
 Glu Ser Arg Val Ser Ser Leu His Asp Ile Gln Ser Val Pro Tyr Leu
 210 215 220
 Ala Asp Met Asn Trp Asp Ala Val Phe Lys Lys Ala Leu Met Pro Gly
 225 230 235 240
 Phe Val Pro Asn Lys Gly Arg Leu Asn Cys Asp Pro Thr Phe Glu Leu
 245 250 255
 Glu Glu Met Ile Leu
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<210> 4437
 <211> 620
 <212> DNA
 <213> Homo sapiens

<400> 4437
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<210> 4438

<211> 206

<212> PRT

<213> Homo sapiens

<400> 4438

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Lys	Arg	Asp	Val	Val	Lys	Thr	Ile	Arg	Glu	Val	Gln	Pro	Asp	Val	Val
			20					25					30		
Val	Val	Glu	Leu	Cys	Gln	Tyr	Arg	Val	Ser	Met	Leu	Lys	Met	Asp	Glu
		35					40					45			
Ser	Thr	Leu	Leu	Arg	Glu	Ala	Gln	Glu	Leu	Ser	Leu	Glu	Lys	Leu	Gln
		50				55					60				
Gln	Ala	Val	Arg	Gln	Asn	Gly	Leu	Met	Ser	Gly	Leu	Met	Gln	Met	Leu
65					70					75				80	
Leu	Leu	Lys	Val	Ser	Ala	His	Ile	Thr	Glu	Gln	Leu	Gly	Met	Ala	Pro
			85						90					95	
Gly	Gly	Glu	Phe	Arg	Glu	Ala	Phe	Lys	Glu	Ala	Ser	Lys	Val	Pro	Phe
			100					105					110		
Cys	Lys	Phe	His	Leu	Gly	Asp	Arg	Pro	Ile	Pro	Val	Thr	Phe	Lys	Arg
		115				120						125			
Ala	Ile	Ala	Ala	Leu	Ser	Phe	Trp	Gln	Lys	Val	Arg	Leu	Ala	Trp	Gly
		130				135				140					
Leu	Cys	Phe	Leu	Ser	Asp	Pro	Ile	Ser	Lys	Asp	Asp	Val	Glu	Arg	Cys
145					150					155				160	
Lys	Gln	Lys	Asp	Leu	Leu	Glu	Gln	Met	Met	Ala	Glu	Met	Ile	Gly	Glu
			165						170					175	
Phe	Pro	Asp	Leu	His	Arg	Thr	Ile	Val	Ser	Glu	Arg	Asp	Val	Tyr	Leu
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Thr	Tyr	Met	Leu	Arg	Gln	Ala	Ala	Arg	Arg	Leu	Glu	Leu	Pro		
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<210> 4439

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 4439

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120
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180
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240
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300
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360
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420
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480
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720
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780
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900
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1620

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 1740
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 1980
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 2121

<210> 4440

<211> 82

<212> PRT

<213> Homo sapiens

<400> 4440

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Leu	Arg	Phe	Ala	Phe	Ile	Asp	Val	Gly	Ile	Phe	Arg	Asn	Ser	Ala	Pro
			20					25				30			
Arg	Leu	Ser	Met	Ile	Gly	Ala	Asp	Ser	Ser	Glu	Glu	Lys	Phe	Leu	Arg
		35				40						45			
Arg	Ile	Gly	Arg	Phe	Gly	Tyr	Gly	Tyr	Gly	Pro	Tyr	Gln	Pro	Val	Pro
	50				55					60					
Glu	Gln	Pro	Leu	Tyr	Pro	Gln	Pro	Tyr	Gln	Pro	Gln	Tyr	Gln	Gln	Tyr
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Thr	Phe														

<210> 4441

<211> 2055

<212> DNA

<213> Homo sapiens

<400> 4441

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<210> 4442

<211> 517

<212> PRT

<213> Homo sapiens

<400> 4442

Met	Gly	Arg	Lys	Ser	Lys	Lys	Trp	Gly	Lys	Lys	Val	Ser	Arg	Tyr	Glu	1	5	10	15
Gly	Lys	Val	Arg	Leu	Lys	Lys	Val	Pro	Ala	Lys	Lys	Leu	Val	Pro	Ala	20	25	30	35
Trp	Lys	Glu	Lys	Val	Leu	Trp	Ala	Leu	Leu	Ala	Val	Leu	Leu	Ala	Ser	40	45	50	55
Trp	Arg	Leu	Trp	Ala	Ile	Lys	Asp	Phe	Gln	Glu	Cys	Thr	Trp	Gln	Val	60	65	70	75
Val	Leu	Asn	Glu	Phe	Lys	Arg	Val	Gly	Glu	Ser	Gly	Val	Ser	Asp	Ser	80	85	90	95
Phe	Phe	Glu	Gln	Glu	Pro	Val	Asp	Thr	Val	Ser	Ser	Leu	Phe	His	Met	100	105	110	115
Leu	Val	Asp	Ser	Pro	Ile	Asp	Pro	Ser	Glu	Lys	Tyr	Leu	Gly	Phe	Pro	120	125	130	135
Tyr	Tyr	Leu	Lys	Ile	Asn	Tyr	Ser	Cys	Glu	Glu	Lys	Pro	Ser	Glu	Asp	140	145	150	155
Thr	Phe	Gln	Ser	Pro	Val	Asn	Phe	Tyr	Arg	Trp	Lys	Ile	Glu	Gln	Leu	160	165	170	175
Gln	Ile	Gln	Met	Glu	Ala	Ala	Pro	Phe	Arg	Ser	Lys	Gly	Gly	Pro	Gly	180	185	190	195
Gly	Gly	Gly	Arg	Asp	Arg	Asn	Leu	Ala	Gly	Met	Asn	Ile	Asn	Gly	Phe	200	205	210	215
Leu	Lys	Arg	Asp	Arg	Asp	Asn	Asn	Ile	Gln	Phe	Thr	Val	Gly	Glu	Glu	220	225	230	235
Leu	Phe	Asn	Leu	Met	Pro	Gln	Tyr	Phe	Val	Gly	Val	Ser	Ser	Arg	Pro	240	245	250	255
Ser	Leu	Val	Glu	Val	Asn	Gly	Val	Gly	Gln	Met	Leu	Ser	Ile	Asp	Ser	260	265	270	275
Cys	Trp	Val	Gly	Ser	Phe	Tyr	Cys	Pro	His	Ser	Gly	Phe	Thr	Ala	Thr	280	285	290	295
Ile	Tyr	Asp	Thr	Ile	Ala	Thr	Glu	Ser	Thr	Leu	Phe	Ile	Arg	Gln	Asn	300	305	310	315
Gln	Leu	Val	Tyr	Tyr	Phe	Thr	Gly	Thr	Tyr	Thr	Thr	Leu	Tyr	Glu	Arg	320	325	330	335
Asn	Arg	Gly	Ser	Gly	Glu	Cys	Ala	Val	Ala	Gly	Pro	Thr	Pro	Gly	Glu	340	345	350	355

325 330 335
 Gly Thr Leu Val Asn Pro Ser Thr Glu Gly Ser Trp Ile Arg Val Leu
 340 345 350
 Ala Ser Glu Cys Ile Lys Lys Leu Cys Pro Val Tyr Phe His Ser Asn
 355 360 365
 Gly Ser Glu Tyr Ile Met Ala Leu Thr Thr Gly Lys His Glu Gly Tyr
 370 375 380
 Val His Phe Gly Thr Ile Arg Val Thr Thr Cys Ser Ile Ile Trp Ser
 385 390 395 400
 Glu Tyr Ile Ala Gly Glu Tyr Thr Leu Leu Leu Val Glu Ser Gly
 405 410 415
 Tyr Gly Asn Ala Ser Lys Arg Phe Gln Val Val Ser Tyr Asn Thr Ala
 420 425 430
 Ser Asp Asp Leu Glu Leu Leu Tyr His Ile Pro Glu Phe Ile Pro Glu
 435 440 445
 Ala Arg Gly Leu Glu Phe Leu Met Ile Leu Gly Thr Glu Ser Tyr Thr
 450 455 460
 Ser Thr Ala Met Ala Pro Lys Gly Ile Phe Cys Asn Pro Tyr Asn Asn
 465 470 475 480
 Leu Ile Phe Ile Trp Gly Asn Phe Leu Leu Gln Arg Ser Gly Thr Ser
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 Trp Arg Ala Ala Thr Gly Ser Thr Ser Cys Ser Leu Pro Arg Ala Gly
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 Arg Cys Thr Ser Ala
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<210> 4443

<211> 692

<212> DNA

<213> Homo sapiens

<400> 4443

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 360
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692

<210> 4444

<211> 108

<212> PRT

<213> Homo sapiens

<400> 4444

Met	Ser	Val	Cys	Leu	Leu	Val	Gly	Leu	Thr	Asn	Ser	Ser	Thr	Trp	Ser
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Leu	Met	Pro	Asn	Gln	Val	Gln	Thr	Thr	Leu	Leu	Phe	Cys	Val	Thr	Leu
			20					25					30		
Cys	Glu	Ala	Ser	Cys	Lys	Leu	Asp	Ser	Leu	Pro	Ser	Ala	Pro	Ser	Pro
			35				40					45			
Lys	Ala	Gly	Leu	Gln	Glu	Val	Arg	Pro	Ala	Leu	Gln	Ala	Thr	Pro	Val
			50				55				60				
Leu	Gly	Leu	Leu	Leu	Ser	Ser	Ser	Phe	Leu	Arg	Val	Thr	Glu	Pro	Gly
							70				75			80	
Arg	Glu	Val	Gly	Cys	Gly	Leu	Pro	Cys	Pro	Tyr	Ser	His	Leu	Leu	Gln
				85					90					95	
Leu	Pro	Pro	Cys	Trp	Thr	His	Gln	Gln	Gln	Ser	Lys				
			100						105						

<210> 4445

<211> 901

<212> DNA

<213> Homo sapiens

<400> 4445

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300
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420
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720

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 900
 a
 901

<210> 4446

<211> 140

<212> PRT

<213> Homo sapiens

<400> 4446

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Lys	Met	Asp	Leu	Pro	Pro	Gly	Asp	Pro	Gly	Val	Leu	Pro	Leu	Ser	Cys
			20					25					30		
Pro	Gln	Glu	Cys	Pro	Asp	Pro	His	Ser	Tyr	Pro	Gly	Pro	Arg	Ser	Pro
			35				40						45		
Thr	Pro	Gly	Leu	Pro	Ser	Ser	Ala	Val	Asn	Asp	Asp	Leu	Leu	Leu	Leu
			50				55					60			
Pro	Ser	Ser	Leu	Pro	Ser	Val	Thr	Lys	Gly	Leu	Pro	Arg	Cys	Gln	Leu
65					70					75				80	
Trp	Asn	Glu	Gly	Cys	Pro	Trp	Glu	Val	Met	Ile	Leu	Arg	Tyr	Thr	Gly
				85					90					95	
Ala	Gln	Gln	Ile	Ala	Ser	Ser	Tyr	Pro	Gln	Thr	Val	Phe	Ala	Cys	Met
			100					105					110		
Gln	Pro	Leu	Ala	Leu	Pro	Leu	Cys	Gly	Arg	Lys	Pro	Ala	Gln	Gly	His
			115				120						125		
Thr	Ala	Gly	Gln	Gln	Gln	His	Ser	Trp	Ser	Gln	Ile				
			130				135				140				

<210> 4447

<211> 951

<212> DNA

<213> Homo sapiens

<400> 4447

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<210> 4448

<211> 263

<212> PRT

<213> Homo sapiens

<400> 4448

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Ser	Ser	Pro	Gly	Ser	Gln	Ala	Pro	Asp	Thr	Ala	Leu	Arg	Ala	Met	Ala
			20					25					30		
Asp	Arg	Gly	Pro	Trp	Arg	Val	Gly	Val	Val	Gly	Tyr	Gly	Arg	Leu	Gly
	35					40					45				
Gln	Ser	Leu	Val	Ser	Arg	Leu	Leu	Ala	Gln	Gly	Ser	Glu	Leu	Gly	Leu
	50				55					60					
Glu	Leu	Val	Phe	Val	Trp	Asn	Arg	Asp	Pro	Gly	Arg	Met	Ala	Gly	Ser
65					70				75					80	
Val	Pro	Pro	Ala	Leu	Gln	Leu	Glu	Asp	Leu	Thr	Thr	Leu	Glu	Glu	Arg
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His	Pro	Asp	Leu	Val	Val	Glu	Val	Ala	His	Pro	Lys	Ile	Ile	His	Glu
			100					105					110		
Ser	Gly	Val	Gln	Ile	Leu	Arg	His	Ala	Asn	Leu	Leu	Ser	Leu	Arg	Val
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Thr	Met	Ala	Thr	His	Pro	Asp	Gly	Phe	Arg	Leu	Glu	Gly	Pro	Leu	Ala
	130				135					140					
Ala	Ala	His	Ser	Pro	Gly	Pro	Cys	Thr	Val	Leu	Tyr	Glu	Gly	Pro	Val
145				150						155				160	
Arg	Gly	Leu	Cys	Pro	Phe	Ala	Pro	Arg	Asn	Ser	Asn	Thr	Met	Ala	Ala
			165					170					175		
Ala	Ala	Leu	Ala	Ala	Pro	Ser	Leu	Gly	Phe	Asp	Gly	Val	Ile	Gly	Val
	180						185					190			
Leu	Val	Ala	Asp	Thr	Ser	Leu	Thr	Asp	Met	His	Val	Val	Asp	Val	Glu
	195					200				205					
Leu	Ser	Gly	Pro	Arg	Gly	Pro	Thr	Gly	Arg	Ser	Phe	Ala	Val	His	Thr
210				215							220				
Arg	Arg	Glu	Asn	Pro	Ala	Glu	Pro	Gly	Ala	Val	Thr	Gly	Ser	Ala	Thr

225	230	235	240
Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser			
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<210> 4449

<211> 1365

<212> DNA

<213> Homo sapiens

<400> 4449

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1260

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 1365

<210> 4450
 <211> 194
 <212> PRT
 <213> Homo sapiens

<400> 4450
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 Gly Pro Gln Asn Arg Tyr Ala Leu Ile Cys Gln Gln Cys Phe Ser His
 35 40 45
 Asn Gly Met Ala Leu Lys Glu Glu Phe Glu Tyr Ile Ala Phe Arg Cys
 50 55 60
 Ala Tyr Cys Phe Phe Leu Asn Pro Ala Arg Lys Thr Arg Pro Gln Ala
 65 70 75 80
 Pro Arg Leu Pro Glu Phe Ser Phe Glu Lys Arg Gln Val Val Glu Gly
 85 90 95
 Ser Ser Ser Val Gly Pro Leu Pro Ser Gly Ser Val Leu Ser Ser Asp
 100 105 110
 Asn Gln Phe Asn Glu Glu Ser Leu Glu His Asp Val Leu Asp Asp Asn
 115 120 125
 Thr Glu Gln Thr Asp Asp Lys Ile Pro Ala Thr Glu Gln Thr Asn Gln
 130 135 140
 Val Ile Glu Lys Ala Ser Asp Ser Glu Glu Pro Glu Glu Lys Gln Glu
 145 150 155 160
 Thr Glu Asn Glu Glu Ala Ser Val Ile Glu Thr Asn Ser Thr Val Pro
 165 170 175
 Gly Ala Asp Ser Ile Pro Asp Pro Glu Leu Ser Gly Glu Ser Leu Thr
 180 185 190
 Ala Glu

<210> 4451
 <211> 1637
 <212> DNA
 <213> Homo sapiens

<400> 4451
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<210> 4452

<211> 328

<212> PRT

<213> Homo sapiens

<400> 4452

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Lys Tyr Asn Phe Tyr Leu Pro Phe Phe Gly Pro Ile Met Thr
      35           40           45
Phe Asp Arg Phe His Ala Gln Val Ser Gln Val Glu Pro Val Arg Arg
      50           55           60
Glu Gly Glu Leu Trp His Ile Arg Ala Gln Ala Gly Leu Ser Val Val
      65           70           75           80
Ala Ile Met Ala Val Asp Ile Phe Phe His Phe Phe Tyr Ile Leu Thr
      85           90           95
Ile Pro Ser Asp Leu Lys Phe Ala Asn Arg Leu Pro Asp Ser Ala Leu
      100          105          110
Ala Gly Leu Ala Tyr Ser Asn Leu Val Tyr Asp Trp Val Lys Ala Ala
      115          120          125
Val Leu Phe Gly Val Val Asn Thr Val Ala Cys Leu Asp His Leu Asp
      130          135          140
Pro Pro Gln Pro Pro Lys Cys Ile Thr Ala Leu Tyr Val Phe Ala Glu
      145          150          155          160
Thr His Phe Asp Arg Gly Ile Asn Asp Trp Leu Cys Lys Tyr Val Tyr
      165          170          175
Asn His Ile Gly Gly Glu His Ser Ala Val Ile Pro Glu Leu Ala Ala
      180          185          190
Thr Val Ala Thr Phe Ala Ile Thr Thr Leu Trp Leu Gly Pro Cys Asp
      195          200          205
Ile Val Tyr Leu Trp Ser Phe Leu Asn Cys Phe Gly Leu Asn Phe Glu
      210          215          220
Leu Trp Met Gln Lys Leu Ala Glu Trp Gly Pro Leu Ala Arg Ile Glu
      225          230          235          240
Ala Ser Leu Ser Val Gln Met Ser Arg Arg Val Arg Ala Leu Phe Gly
      245          250          255
Ala Met Asn Phe Trp Ala Ile Ile Met Tyr Asn Leu Val Ser Leu Asn
      260          265          270
Ser Leu Lys Phe Thr Glu Leu Val Ala Arg Arg Leu Leu Thr Gly
      275          280          285
Phe Pro Gln Thr Thr Leu Ser Ile Leu Phe Val Thr Tyr Cys Gly Val
      290          295          300
Gln Leu Val Lys Glu Arg Glu Thr Leu Ala Leu Glu Glu Glu Gln
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Lys Gln Asp Lys Glu Lys Pro Glu
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<210> 4453

<211> 685

<212> DNA

<213> Homo sapiens

<400> 4453

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180

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<210> 4454

<211> 207

<212> PRT

<213> Homo sapiens

<400> 4454

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 35 40 45
 Gly Pro Leu Ser Leu Gly Ser Ser Ile Gln Pro Leu Ser Gln Gln Arg
 50 55 60
 Gln Asp Cys Gly Pro Leu Cys Phe Leu Asn Arg Ala Gln Gly Ser Gln
 65 70 75 80
 Gly Met Pro Ser Leu Gln His Ser Thr Leu Trp Ser Gln Trp Ser Arg
 85 90 95
 Arg Ser Ser Leu Lys Tyr Tyr Tyr Arg Gly Glu Arg Pro Ile Leu Ala
 100 105 110
 Met Leu Leu Tyr Leu Pro Arg Pro Lys Thr Val Leu Cys Ser Phe Ser
 115 120 125
 Cys Ser Glu Ile Arg Ser Gln Asn Ser Arg Arg His Ser Phe Gly Lys
 130 135 140
 Lys Gly His Ala Phe Val Leu Tyr Leu Ile Leu Val Ser Glu Ala Leu
 145 150 155 160
 Ile Pro Val Asp Cys Gly Leu Arg Trp Ser Pro Pro Gln Asp Pro Gln
 165 170 175
 Leu Gln Arg Gln Arg Arg Met Lys Glu Glu Gln Pro Pro Gln Asp Leu
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 Leu His Trp Glu Pro His Pro Thr Phe Ser Val Pro Phe Thr Arg
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<210> 4455

<211> 882

<212> DNA

<213> Homo sapiens

<400> 4455

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<210> 4456

<211> 261

<212> PRT

<213> Homo sapiens

<400> 4456

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		20						25					30		
Ile	Tyr	Glu	Leu	Thr	Val	Leu	Lys	Asp	Arg	Phe	Thr	Gly	Met	His	Lys
		35						40				45			
Gly	Cys	Ala	Phe	Leu	Thr	Tyr	Cys	Glu	Arg	Glu	Ser	Ala	Leu	Lys	Ala
	50					55					60				
Gln	Ser	Ala	Leu	His	Glu	Gln	Lys	Thr	Leu	Pro	Gly	Met	Asn	Arg	Pro
	65				70				75					80	
Ile	Gln	Val	Lys	Pro	Ala	Asp	Ser	Glu	Ser	Arg	Gly	Asp	Ser	Ser	Cys
			85					90					95		
Leu	Arg	Gln	Pro	Pro	Ser	His	Arg	Lys	Leu	Phe	Val	Gly	Met	Leu	Asn

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Asn  Ile  Glu  Glu  Cys  Thr  Ile  Leu  Arg  Gly  Pro  Asp  Gly  Asn  Ser  Lys
          130          135          140
Gly  Cys  Ala  Phe  Val  Lys  Tyr  Ser  Ser  His  Ala  Glu  Ala  Gln  Ala  Ala
145          150          155          160
Ile  Asn  Ala  Leu  His  Gly  Ser  Gln  Thr  Met  Pro  Gly  Ala  Ser  Ser  Ser
          165          170          175
Leu  Val  Val  Lys  Phe  Ala  Asp  Thr  Asp  Lys  Glu  Arg  Thr  Met  Arg  Arg
          180          185          190
Met  Gln  Gln  Met  Ala  Gly  Gln  Met  Gly  Met  Phe  Asn  Pro  Met  Ala  Ile
          195          200          205
Pro  Phe  Gly  Ala  Tyr  Gly  Ala  Tyr  Ala  Gln  Ala  Leu  Met  Gln  Gln  Gln
210          215          220
Ala  Ala  Leu  Met  Ala  Ser  Val  Ala  Gln  Gly  Gly  Tyr  Leu  Asn  Pro  Met
225          230          235          240
Ala  Ala  Phe  Ala  Ala  Gln  Met  Gln  Gln  Met  Ala  Ala  Leu  Asn  Met
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<210> 4457

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 4457

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780

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<210> 4458

<211> 405

<212> PRT

<213> Homo sapiens

<400> 4458

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 Lys Gly Gly Tyr Leu Met Leu Ser Phe Ile Asp Phe Cys Pro Phe Ser
 35 40 45
 Val Met Arg Leu Arg Ser Leu Pro Ser Pro Gln Arg Tyr Thr Arg Gln
 50 55 60
 Glu Arg Tyr Arg Ala Arg Pro Pro Arg Val Leu Glu Arg Ser Gly Phe
 65 70 75 80
 His Asn Glu Asn Ser Leu Ala Ile Tyr Gln Gly Leu Val Tyr Tyr Leu
 85 90 95
 Leu Trp Leu His Ser Val Tyr Asp Lys Asp Tyr Tyr Phe Phe Leu Ala
 100 105 110
 Ser Asn Trp Arg Ser Ala Gly Gly Val Ser Ile Glu Met Asp Ser Tyr
 115 120 125
 Glu Lys Ile Tyr Asn Leu Glu Ser Ala Tyr Glu Leu Pro Glu Arg Ile
 130 135 140
 Phe Leu Asp Lys Gly Thr Glu Tyr Ser Phe Ala Ile Phe Leu Ser Ala
 145 150 155 160
 Gln Gly His Ser Phe Arg Thr Gln Ser Glu Leu Gly Leu Arg Gly Thr
 165 170 175
 Arg Val Glu Pro Glu Gly Arg Gly Glu Gly Tyr Gln Asn Leu Gly Ala

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      180              185              190
Trp Gly Ala Gly Thr Pro Ser Glu Gly Arg Gly Leu Ser Val Asp Val
      195              200              205
Gly Val Val Leu Ala Asp Pro Gly Cys Ile Glu Ala Ser Val Lys Gln
      210              215              220
Glu Val Leu Ile Asn Arg Asn Ser Val Leu Phe Ser Ile Thr Leu Lys
      225              230              235              240
Asp Lys Lys Leu Cys Tyr Asp Gln Gly Ile Ser Gly His His Leu Met
      245              250              255
Glu Thr Ser Met Thr Val Asn Val Arg Ser Lys Pro Gly Gly Glu Gly
      260              265              270
Lys Arg Leu Ala Phe Asp Ile Thr Tyr Thr Leu Glu Tyr Ser Arg Leu
      275              280              285
Lys Asn Lys His Tyr Phe Asp Cys Val Asn Val Asn Pro Glu Met Pro
      290              295              300
Cys Phe Leu Phe Arg Asp Ser Val Tyr Val Leu Leu Val Val Gly Gly
      305              310              315              320
Gly Pro Thr Leu Asp Ser Leu Lys Asp Tyr Ser Glu Asp Glu Ile Tyr
      325              330              335
Arg Phe Asn Ser Pro Leu Asp Lys Thr Asn Ser Leu Ile Trp Thr Thr
      340              345              350
Arg Thr Thr Arg Thr Thr Lys Asp Ser Ala Phe His Ile Met Ser His
      355              360              365
Glu Ser Pro Gly Ile Glu Trp Leu Cys Leu Glu Asn Ala Pro Cys Tyr
      370              375              380
Asp Asn Val Pro Gln Gly Ile Phe Ala Pro Glu Phe Phe Phe Lys Val
      385              390              395              400
Leu Val Ser Asn Arg
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<210> 4459

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 4459

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540

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 1020
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<210> 4460

<211> 121

<212> PRT

<213> Homo sapiens

<400> 4460

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Ala	Pro	Pro	Ser	Arg	Ala	Ala	Arg	Arg	Ala	Arg	Ala	Leu	Ser	Pro	Ser
			20					25				30			
Gly	Lys	Glu	Arg	Ala	Ala	Pro	Ser	Gln	Gly	Ser	Pro	Arg	Cys	Cys	Pro
		35				40					45				
Leu	Ser	Pro	Gly	Ser	Ala	Arg	Gly	Ala	Arg	Gly	Glu	Asn	Gln	Pro	Arg
	50				55						60				
Ser	Arg	Gly	Arg	Ala	Ala	Asn	Gly	Arg	Ala	Pro	Pro	Gly	Pro	Leu	Thr
65				70				75						80	
Arg	Arg	Leu	Ala	Gly	Arg	Ala	Arg	Thr	Pro	Arg	Pro	Lys	Trp	Leu	Phe
			85				90						95		
Gln	Gly	Ala	Ser	Gln	Ala	Gly	Glu	Leu	Gly	Lys	Gln	Arg	Arg	Met	Pro
			100				105					110			
Gly	Leu	Val	Lys	Arg	Val	Arg	Asp	Val							
		115					120								

<210> 4461

<211> 488

<212> DNA

<213> Homo sapiens

<400> 4461

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 120

tacctggcag acttcccca ggaactgtcc atcaaatata tggccagatc gttccgtggg
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 240
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 360
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 488

<210> 4462

<211> 96

<212> PRT

<213> Homo sapiens

<400> 4462

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Asn	Pro	Tyr	Asn	Asn	Leu	Ile	Phe	Ile	Trp	Gly	Asn	Phe	Leu	Leu	Gln
			20					25					30		
Ser	Ser	Asn	Lys	Glu	Asn	Phe	Ile	Tyr	Leu	Ala	Asp	Phe	Pro	Lys	Glu
		35				40					45				
Leu	Ser	Ile	Lys	Tyr	Met	Ala	Arg	Ser	Phe	Arg	Gly	Ala	Val	Ala	Ile
50					55				60						
Val	Thr	Glu	Thr	Glu	Glu	Val	Gly	Cys	Pro	Ala	Leu	Leu	Pro	Ile	Pro
65				70					75					80	
Ser	Leu	Pro	Thr	Pro	Lys	Pro	Gln	Gly	Pro	Leu	Phe	Pro	Pro	Ser	Gln
			85					90						95	

<210> 4463

<211> 2662

<212> DNA

<213> Homo sapiens

<400> 4463

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 180
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 240
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 420

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480
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540
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 2160
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 2520
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 2640
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 2662

<210> 4464

<211> 519

<212> PRT

<213> Homo sapiens

<400> 4464

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		20						25				30			
Val	Arg	Asp	Val	Ala	Lys	Met	Leu	Pro	Thr	Leu	Gly	Gly	Glu	Glu	Gly
		35					40					45			
Val	Ser	Arg	Ile	Tyr	Ala	Asp	Pro	Thr	Lys	Arg	Leu	Glu	Leu	Tyr	Phe
	50					55				60					
Arg	Pro	Lys	Asp	Pro	Tyr	Cys	His	Pro	Val	Cys	Ala	Asn	Arg	Phe	Ser
65					70				75				80		
Thr	Ser	Ser	Leu	Leu	Leu	Arg	Ile	Arg	Lys	Arg	Thr	Arg	Arg	Gln	Lys
			85					90					95		
Gly	Val	Leu	Gly	Thr	Glu	Ala	His	Ser	Glu	Val	Thr	Phe	Asp	Met	Glu
		100						105				110			
Ile	Leu	Gly	Ile	Ile	Ser	Thr	Ile	Tyr	Lys	Phe	Gln	Gly	Met	Ser	Asp
		115				120					125				
Phe	Gln	Tyr	Leu	Ala	Val	His	Thr	Glu	Ala	Gly	Gly	Lys	His	Thr	Ser
	130				135					140					
Met	Tyr	Asp	Lys	Val	Leu	Met	Leu	Arg	Pro	Glu	Lys	Glu	Ala	Phe	Phe
145					150					155				160	
His	Gln	Glu	Leu	Pro	Leu	Tyr	Ile	Pro	Pro	Pro	Ile	Phe	Ser	Arg	Leu
			165					170					175		
Asp	Ala	Pro	Val	Asp	Tyr	Phe	Tyr	Arg	Pro	Glu	Thr	Gln	His	Arg	Glu
			180					185					190		
Gly	Tyr	Asn	Asn	Pro	Pro	Ile	Ser	Gly	Glu	Asn	Leu	Ile	Gly	Leu	Ser

[illegible]

<210> 4465

<211> 1291

<212> DNA

<213> Homo sapiens

<400> 4465

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180

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 360
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 420
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 480
 catgaaagca agatgttgct caaatgcca ggtgtgtctg accaagctgt ggccgaggcc
 540
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 660
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 720
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 780
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 840
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 1020
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 1140
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 1200
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 1260
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 1291

<210> 4466

<211> 93

<212> PRT

<213> Homo sapiens

<400> 4466

Gly Leu Glu Arg Gln Val Arg Ala Glu Ile Glu His Lys Lys Glu Glu
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 20 25 30
 Asp Thr Ile Gly Gln Met Arg Arg Xaa Ala Val Gly Leu Val Asp Ala
 35 40 45
 Val Lys Ala Thr Asp Gln Tyr Cys Ala Arg Leu Arg Gln Ala Gly Ser
 50 55 60
 Ala Ala Pro Arg Pro Pro Arg Ala Gln Gln Pro Gln Gln Pro Ser Gln

<213> Homo sapiens

<400> 4468

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Lys Glu His Leu Ser Gln Leu Glu Ser Pro Val Val Phe Cys His Asn
 20          25          30
Asp Leu Leu Cys Lys Asn Ile Ile Tyr Asp Ser Ile Lys Gly His Val
 35          40          45
Arg Phe Ile Asp Tyr Glu Tyr Ala Gly Tyr Asn Tyr Gln Ala Phe Asp
 50          55          60
Ile Gly Asn His Phe Asn Glu Phe Ala Gly Val Asn Glu Val Asp Tyr
 65          70          75
Cys Leu Tyr Pro Ala Arg Glu Thr Gln Leu Gln Trp Leu His Tyr Tyr
 85          90          95
Leu Gln Ala Gln Lys Gly Met Ala Val Thr Pro Arg Glu Val Gln Arg
100          105          110
Leu Tyr Val Gln Val Asn Lys Phe Ala Leu Ala Ser His Phe Phe Trp
115          120          125
Ala Leu Trp Ala Leu Ile Gln Asn Gln Tyr Ser Thr Ile Asp Phe Asp
130          135          140
Phe Leu Arg Tyr Ala Val Ile Arg Phe Asn Gln Tyr Phe Lys Val Lys
145          150          155
Pro Gln Ala Ser Ala Leu Glu Met Pro Lys
165          170

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<210> 4469

<211> 409

<212> DNA

<213> Homo sapiens

<400> 4469

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tcacaatttc aggaaaatgg ctaccctgtg aggagagaaa gccacccaat gatgctgata
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<210> 4470

<211> 55

<212> PRT

<213> Homo sapiens

<400> 4470

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Ile Tyr Asp Ala Gln His Ala Asn Leu Ala Gly Thr Leu Ser Gly His

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Ala Ser Trp	Val Leu Asn Val Ala Phe Cys Pro Asp Asp Thr His Phe		
	20	25	30
Val Ser Arg Ser Gln Cys Trp Ser Gly Leu Gly Trp Pro Arg Gln Leu			
	35	40	45
Glu Ser Arg Arg Trp Thr Thr			
50	55		

<210> 4471

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 4471

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 780
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 1020
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 1140
 aagacatccg ggtactacat ttccatccct tccctatctt gacaccaa atgtggtgag
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acagccctcc cccaaccca ggccagtcag gcacaatccc cccaccccc aaacgtcctg
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 1620
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<210> 4472

<211> 160

<212> PRT

<213> Homo sapiens

<400> 4472

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 20 25 30
 Phe Gly Glu Gly Leu Leu Glu Ala Glu Leu Ala Ala Leu Cys Pro Thr
 35 40 45
 Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val
 50 55 60
 Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val
 65 70 75 80
 Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His
 85 90 95
 Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe
 100 105 110
 Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp
 115 120 125
 Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile
 130 135 140
 Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Ala Ala Ala Lys
 145 150 155 160

<210> 4473

<211> 1255

<212> DNA

<213> Homo sapiens

<400> 4473

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 180
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 420
 aaacagatga agtctataga tgcaggaccg gtggatgcct ggactttggc attctctccg
 480
 gactcccagc atctggcaac aggaactcac atggggaaag tgaacatttt ttggtgtgaa
 540
 agtggaaaaa aagaatactc ttgggacct agaggaaaat tcactcttag tattgcatac
 600
 agtctctgat gaaaatacct gccagcggga gccatagatg gaatcatcaa tatttttgat
 660
 attgcaactg gaaaacttct gcataccctg gaaggccatg ccattgcccac tcgctccttg
 720
 accttttccc cggactccca gctccttgct actgcttcag atgatggcta catcaagatc
 780
 tatgatgtac aacatgcaa ttggctggc acgctgagcg gccatgcctc ctgggtgctg
 840
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 900
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 960
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 1020
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 1080
 gagaatgtac ggattgatca tgacattcct taccttctta ggctgtgtta aaagaatat
 1140
 agcatttatt gtagcaaaga cttaaatttt gtagatacaa tatgaatctt ttcattgttt
 1200
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 1255

<210> 4474

<211> 305

<212> PRT

<213> Homo sapiens

<400> 4474

Met	Thr	Asn	Gln	Tyr	Gly	Ile	Leu	Phe	Lys	Gln	Glu	Gln	Ala	His	Asp
1					5				10					15	
Asp	Ala	Ile	Trp	Ser	Val	Ala	Trp	Gly	Thr	Asn	Lys	Lys	Glu	Asn	Ser
				20				25					30		
Glu	Thr	Val	Val	Thr	Gly	Ser	Leu	Asp	Asp	Leu	Val	Lys	Val	Trp	Lys


```

          35          40          45
Trp Arg Asp Glu Arg Leu Asp Leu Gln Trp Ser Leu Glu Gly His Gln
  50          55          60
Leu Gly Val Val Ser Val Asp Ile Ser His Thr Leu Pro Ile Ala Ala
  65          70          75          80
Ser Ser Ser Leu Asp Ala His Ile Arg Leu Trp Asp Leu Glu Asn Gly
          85          90          95
Lys Gln Met Lys Ser Ile Asp Ala Gly Pro Val Asp Ala Trp Thr Leu
          100          105          110
Ala Phe Ser Pro Asp Ser Gln His Leu Ala Thr Gly Thr His Met Gly
          115          120          125
Lys Val Asn Ile Phe Gly Val Glu Ser Gly Lys Lys Glu Tyr Ser Leu
          130          135          140
Asp Thr Arg Gly Lys Phe Ile Leu Ser Ile Ala Tyr Ser Pro Asp Gly
          145          150          155          160
Lys Tyr Leu Ala Ser Gly Ala Ile Asp Gly Ile Ile Asn Ile Phe Asp
          165          170          175
Ile Ala Thr Gly Lys Leu Leu His Thr Leu Glu Gly His Ala Met Pro
          180          185          190
Ile Arg Ser Leu Thr Phe Ser Pro Asp Ser Gln Leu Leu Val Thr Ala
          195          200          205
Ser Asp Asp Gly Tyr Ile Lys Ile Tyr Asp Val Gln His Ala Asn Leu
          210          215          220
Ala Gly Thr Leu Ser Gly His Ala Ser Trp Val Leu Asn Val Ala Phe
          225          230          235          240
Cys Pro Asp Asp Thr His Phe Val Ser Ser Ser Ser Asp Lys Ser Val
          245          250          255
Lys Val Trp Asp Val Gly Thr Arg Thr Cys Val His Thr Phe Phe Asp
          260          265          270
His Gln Asp Gln Val Trp Gly Val Lys Tyr Asn Gly Asn Gly Ser Lys
          275          280          285
Ile Val Ser Val Gly Asp Asp Gln Glu Ile His Ile Tyr Asp Cys Pro
          290          295          300
Ile
305

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<210> 4475

<211> 475

<212> DNA

<213> Homo sapiens

<400> 4475

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acgcgtgaac ccgtgagctt gggaggggat atcgccaag cgaggctctt ctgatccgcg
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120
tggtctgtcg tgaagctgga gagccgtgca aggcgacaga gcctctctgtg tggcccgctc
180
tggcgctctg gggcaagggc tgacttgagc tgcttcgtct gctcatctgc tgtctgccag
240
ctgccctcag acctcctcct ggggtgcagcc cggtcccaact tgagaggggag tgggtcttca
300
cttagggggg taggcacatc cctgtttgct cettgccecg acagcctcgt caatgcccg
360

```

ccacttctga gggctggagg gacaggaact tcctttcttc cccctttctg tctcctcgcg
 420
 tgggtacaaa agcacgtctg tagtccatgt gtgtgaagag aggacgcatt ctaga
 475

<210> 4476
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 4476
 Met Cys Leu Pro Pro Lys Val Lys Thr Thr Ser Leu Ser Ser Gly Asn
 1 5 10 15
 Gly Leu His Pro Gly Gly Gly Leu Arg Ala Ala Gly Arg Gln Gln Met
 20 25 30
 Ser Arg Arg Ser Ser Ser Ser Gln Pro Leu Pro Gln Ser Ala Arg Thr
 35 40 45
 Gly His Thr Glu Gly Ser Val Ala Leu His Gly Ser Pro Ala Ser Arg
 50 55 60
 Gln Thr Ser Gln Arg Trp Thr Val Cys Gln Gly Trp Asp Trp Asn Ser
 65 70 75 80
 Arg Arg Ser Leu Asp Thr Ser Gly Ile Arg Glu Thr Ser Leu Gly Arg
 85 90 95
 Tyr Pro Leu Pro Ser Ser Arg Val His Ala
 100 105

<210> 4477
 <211> 1153
 <212> DNA
 <213> Homo sapiens

<400> 4477
 ctcttggcct ggcctcctgc agtgccacgc tccgtgtatt tgacaagctg agttggacac
 60
 tccatgtggt agagtgtcag tttgtcaaat accccaagtg cggcacatgc ttaccagctc
 120
 taggccaggg cagatgggat atgacgaatg gactgccagc tggatacaag gatgtccacc
 180
 aagcaccaag ttctcacaag ttattttatg tgactttgca ggaactgagg cattatatct
 240
 gaggacacca ggggaaaagt gtggcatctc agggaaaatac agccctgggc tgtgtctaca
 300
 cacaccatga gagtgtctgat gggggcgcaa tagtcttgaa aatgtataaa gtgtccagga
 360
 atggaagtgc tctttgatcc attattatct tcttctctca tattcccttc ccagagtctc
 420
 ctatctagga catcagcatt ctacacaaag cctaattggc tatctgagta agcaggggctt
 480
 agaaattcac tttcttgata ctcaagtcttg ccttctaaac actccttgat cttgcctacc
 540
 tctccctctt tccacatgct ttttctgta ggaacacttt ctccatttat tctgtcctat
 600
 ccaattcttc cctatatctc ctggaccagc taaagtcag tgtttccaga gacttttgaa
 660

```

agtcaactta cactttttcc ttcttcattc acaaagctct tcttccctgg gccctggat
720
gtatgccttt ctctcctact gtctaatagc acctcgtaaa ttgtcaatga acttttctaa
780
gggggtattct tgaattccca actagattgt gagcttctgg aagacaaggc tatgtctttg
840
attgtttgtct cccctaccac agcccagtag tttagttaca gaaaataata aatatttact
900
gattgattga ctttcctctt gtccactagc tttagggttg ggggccaaat tctaccctgg
960
attttgaaaa attcaaaactg tgaacaccac aatgttatag agcatatgag gtagtagcca
1020
gcatgaagga tgttttcttc ctgagaaaca gtgtcaaggg ctggaggaag agggcaaaat
1080
agcagactca gagggccaaat aaattttggt attacttggt cacacaaggt tatacaggtg
1140
ttttcttgta gga
1153

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<210> 4478
<211> 118
<212> PRT
<213> Homo sapiens

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<400> 4478
Met Trp Lys Arg Gly Glu Val Gly Lys Ile Lys Glu Cys Leu Glu Gly
1 5 10 15
Lys Thr Glu Tyr Gln Glu Ser Glu Phe Leu Ser Pro Ala Tyr Ser Asp
20 25 30
Lys Pro Leu Gly Leu Cys Glu Asn Ala Asp Val Leu Asp Arg Arg Leu
35 40 45
Trp Glu Gly Asn Met Lys Glu Glu Asn Asn Asn Glu Ser Lys Ser Thr
50 55 60
Ser Ile Pro Gly His Phe Ile His Phe Gln Asp Tyr Cys Ala Pro Ile
65 70 75 80
Ser Thr Leu Met Val Cys Val Asp Thr Ala Gln Gly Cys Ile Ser Leu
85 90 95
Arg Cys His Thr Phe Pro Leu Val Ser Ser Asp Ile Met Pro Gln Phe
100 105 110
Leu Gln Ser His Ile Lys
115

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<210> 4479
<211> 2158
<212> DNA
<213> Homo sapiens

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<400> 4479
nngcggcggc ctgcggcggg ttcggtgggc ccaatcccg ggcggtgcgg ctgtttcggg
60
cgcgggcccc gcttttccgc accctgctcc ggctcgact acggcgagcc tgagcgcgcc
120
ggcgccccac gcgcagcaca gggagagatg agcagcacca gcagtaagag ggctccgacc
180

```

acggcaacccc agaggtctgaa gcaggactac cttcgcatta agaaagacccc ggtgccttac
240
atctgtgtccg agcccccctc ttcgaatatt ctcgagtggc actatgtcgt ccgaggccca
300
gagatgaccc cttatgaagg tggtctattac catggaaaac taattttttcc cagagaattt
360
cctttcaaac ctcccagtat ctatatgac actcccaacg ggaggtttaa gtgcaacacc
420
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480
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540
atagagacgt cggacttcac gaaaagacaa ctggcagtg cagagttagc atttaatttg
600
aaagataaag tcttttgta attatttct gaagtctgg aggagattaa acaaaaacag
660
aaagcacaag acgaactcag tagcagaccc cagactctcc ccttgccaga cgtggttcca
720
gacggggaga cgcacctcgt ccagaacggg attcagctgc tcaacgggca tgcgccgggg
780
gccgtcccaa acctcgcagg gctccagcag gccaaccggc accacggact cctgggtggc
840
gccctgggca actgtttgt gatagtggg ttgtagcct ttgcttacac ggtcaagtac
900
gtgctgagga gcatcgcgca ggagtggag ccaggcgccg agaccacaag cgcactgag
960
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1080
gtgactgggc tttggaggag actggagcct cagccctgtc ctggccacgg gccgctgggg
1140
ctggtgtggg tgggccttgt gtgctggatt tgtagcttat cttccgtgtt gtctttggac
1200
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1260
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1380
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1440
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1560
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1680
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1740
tggtggaagg cggaggaccg gagtccctgc agaagggccc gtgcaactcg gggcctccct
1800

cacatcccgt gccccctgcg ctggccttca cagtaggtaa tggctccggc cgggtgtttc
 1860
 gctgtccacg gaacatggca gaggggcacc ccggcccgga aagacgccag agccagcagg
 1920
 ggctgtttcg ggccgcgtgg ctccccgggt ctccgcccgtc tcccctcttc tgcgtctgtt
 1980
 ccgtgacttc gcctgggtgg gatgtaccgc aggtgcatcg cgctcaggtg gggcacggcc
 2040
 gccggcaaga aaccaccctt gtccggaggc gggcgtgaga caagcccagc ccgcacgcgc
 2100
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 2158

<210> 4480

<211> 308

<212> PRT

<213> Homo sapiens

<400> 4480

Xaa Arg Arg Pro Ala Ala Gly Ser Val Gly Pro Ile Pro Gly Arg Cys
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 Gly Cys Phe Gly Arg Gly Pro Arg Phe Ser Ala Pro Cys Ser Gly Leu
 20 25 30
 Asp Tyr Gly Glu Pro Glu Arg Gly Gly Pro Arg Ala Ala Gln Gly
 35 40 45
 Glu Met Ser Ser Thr Ser Ser Lys Arg Ala Pro Thr Thr Ala Thr Gln
 50 55 60
 Arg Leu Lys Gln Asp Tyr Leu Arg Ile Lys Lys Asp Pro Val Pro Tyr
 65 70 75 80
 Ile Cys Ala Glu Pro Leu Pro Ser Asn Ile Leu Glu Trp His Tyr Val
 85 90 95
 Val Arg Gly Pro Glu Met Thr Pro Tyr Glu Gly Tyr Tyr His Gly
 100 105 110
 Lys Leu Ile Phe Pro Arg Glu Phe Pro Phe Lys Pro Pro Ser Ile Tyr
 115 120 125
 Met Ile Thr Pro Asn Gly Arg Phe Lys Cys Asn Thr Arg Leu Cys Leu
 130 135 140
 Ser Ile Thr Asp Phe His Pro Asp Thr Trp Asn Pro Ala Trp Ser Val
 145 150 155 160
 Ser Thr Ile Leu Thr Gly Leu Leu Ser Phe Met Val Glu Lys Gly Pro
 165 170 175
 Thr Leu Gly Ser Ile Glu Thr Ser Asp Phe Thr Lys Arg Gln Leu Ala
 180 185 190
 Val Gln Ser Leu Ala Phe Asn Leu Lys Asp Lys Val Phe Cys Glu Leu
 195 200 205
 Phe Pro Glu Val Val Glu Glu Ile Lys Gln Lys Gln Lys Ala Gln Asp
 210 215 220
 Glu Leu Ser Ser Arg Pro Gln Thr Leu Pro Leu Pro Asp Val Val Pro
 225 230 235 240
 Asp Gly Glu Thr His Leu Val Gln Asn Gly Ile Gln Leu Leu Asn Gly
 245 250 255
 His Ala Pro Gly Ala Val Pro Asn Leu Ala Gly Leu Gln Gln Ala Asn
 260 265 270
 Arg His His Gly Leu Leu Gly Gly Ala Leu Ala Asn Leu Phe Val Ile

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                275                280                285
Val Gly Phe Ala Ala Phe Ala Tyr Thr Val Lys Tyr Val Leu Arg Ser
   290                295                300
Ile Ala Gln Glu
305

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<210> 4481
<211> 320
<212> DNA
<213> Homo sapiens

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<400> 4481
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60
gggtggggcc tcggaacctc ctgctgtgca gccagaaaac aggactcggc ctgtccaccc
120
acgtggggag gggaccccg gctggggcttc gtaggggctt caaggacccc tgacttctgg
180
ggtgtgcctg acagcagggg agggcccaga gctggccttg gccatgtcca gtccttaatt
240
gacctttgtc ccttccttcc cctgcctctc tgtgcgtcgc tggactcggc acggggagttc
300
tcacgaatgg gcacccaatt
320

```

```

<210> 4482
<211> 101
<212> PRT
<213> Homo sapiens

```

```

<400> 4482
Met Gly Cys Ala Trp Arg Leu Gly Gly Cys Ile Trp Thr Ala Ser Gly
 1          5          10          15
Trp Gly Leu Gly Thr Ser Cys Cys Ala Ala Arg Lys Gln Asp Ser Ala
 20          25          30
Cys Pro Pro Thr Trp Gly Gly Asp Pro Gly Leu Gly Phe Val Gly Ala
 35          40          45
Ser Arg Thr Pro Asp Phe Trp Gly Val Pro Asp Ser Arg Gly Gly Pro
 50          55          60
Arg Ala Gly Leu Gly His Val Gln Ser Leu Ile Asp Leu Cys Pro Phe
 65          70          75          80
Leu Pro Leu Pro Leu Cys Ala Ser Leu Asp Ser Pro Arg Glu Phe Ser
 85          90          95
Arg Met Gly Thr Gln
100

```

```

<210> 4483
<211> 1852
<212> DNA
<213> Homo sapiens

```

```

<400> 4483
nnggttgccg cgtgccggga gctgagttat agctgtgact tctgccctgc caggccgcac
60

```

acaagctggc tgacccgggt tgtaaaaatg gaatttcaag cagtagtgat ggcagtaggt
120
ggaggatctc ggatgacaga cctaacttcc agcattccca aacctctgct tccagttggg
180
aacaacacct taatttggtta cccattgaac ctgcttgagc gtgttggtt tgaagaagtc
240
attgtgggtta caaccaggga tgttcaaaag gctctatgtg cagaattcaa gatgaaaatg
300
aagccagata ttgtgtgtat tcctgatgac gctgacatgg gaactgcaga ttctttgcgc
360
tacatatatc caaaacttaa gacagatgtg ctgggtgcta gctgtgatct gataacagac
420
gttgcccttac atgaggttgt ggacctgttt agagcttatg atgcatcact tgctatgttg
480
atgagaaaag gccaatagat catagaacct gttcccgtc aaaaggggaa aaaaaagca
540
gtggagcagc gtgacttcac tggagtggac agcacaggaa agaggctgct cttcatggct
600
aatgaagcag acttggatga agagctggtc attaagggat ccacctaca gaagcatcct
660
agaatacgtt tccacacggg tcttgtggat gccacctct actgtttgaa aaaatacatc
720
gtggatttcc taatggaaaa tgggtcaata acttctatcc ggagtgaact gattccatat
780
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840
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960
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1020
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1080
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1260
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1320
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1380
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1440
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1500
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1560
tggagacttg tggagcagtc caaagctcca tgtcaggtgg gctccaggtg tacacagtg
1620
atgttcattg gtcatgtggg aaagatcatc tggagcaagt gtgtgggaca ggacagatc
1680

agtggcctaa ctcttgtgtg ccaagatgta tcggtggggc agcagctgtc caatgtaaag
 1740
 ctccataggaa ggctactttc tgactggctg acccaaccca gtccatgaaag tatccctcac
 1800
 ctaaaaggac ctgggagtac ttcaagccct taccctaacc agcctttcta ga
 1852

<210> 4484

<211> 452

<212> PRT

<213> Homo sapiens

<400> 4484

Met	Glu	Phe	Gln	Ala	Val	Val	Met	Ala	Val	Gly	Gly	Gly	Ser	Arg	Met	15
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Thr	Asp	Leu	Thr	Ser	Ser	Ile	Pro	Lys	Pro	Leu	Leu	Pro	Val	Gly	Asn	30
			20					25								
Lys	Pro	Leu	Ile	Trp	Tyr	Pro	Leu	Asn	Leu	Leu	Glu	Arg	Val	Gly	Phe	45
			35					40								
Glu	Glu	Val	Ile	Val	Val	Thr	Thr	Arg	Asp	Val	Gln	Lys	Ala	Leu	Cys	60
			50			55				60						
Ala	Glu	Phe	Lys	Met	Lys	Met	Lys	Pro	Asp	Ile	Val	Cys	Ile	Pro	Asp	80
65				70					75							
Asp	Ala	Asp	Met	Gly	Thr	Ala	Asp	Ser	Leu	Arg	Tyr	Ile	Tyr	Pro	Lys	95
			85						90							
Leu	Lys	Thr	Asp	Val	Leu	Val	Leu	Ser	Cys	Asp	Leu	Ile	Thr	Asp	Val	110
			100					105								
Ala	Leu	His	Glu	Val	Val	Asp	Leu	Phe	Arg	Ala	Tyr	Asp	Ala	Ser	Leu	125
			115					120								
Ala	Met	Leu	Met	Arg	Lys	Gly	Gln	Asp	Ser	Ile	Glu	Pro	Val	Pro	Gly	140
			130					135								
Gln	Lys	Gly	Lys	Lys	Lys	Ala	Val	Glu	Gln	Arg	Asp	Phe	Ile	Gly	Val	160
			145			150				155						
Asp	Ser	Thr	Gly	Lys	Arg	Leu	Leu	Phe	Met	Ala	Asn	Glu	Ala	Asp	Leu	175
			165						170							
Asp	Glu	Glu	Leu	Val	Ile	Lys	Gly	Ser	Ile	Leu	Gln	Lys	His	Pro	Arg	190
			180					185								
Ile	Arg	Phe	His	Thr	Gly	Leu	Val	Asp	Ala	His	Leu	Tyr	Cys	Leu	Lys	205
			195					200								
Lys	Tyr	Ile	Val	Asp	Phe	Leu	Met	Glu	Asn	Gly	Ser	Ile	Thr	Ser	Ile	220
			210					215								
Arg	Ser	Glu	Leu	Ile	Pro	Tyr	Leu	Val	Arg	Lys	Gln	Phe	Ser	Ser	Ala	240
			225			230				235						
Ser	Ser	Gln	Gln	Gly	Gln	Glu	Glu	Lys	Glu	Glu	Asp	Leu	Lys	Lys	Lys	255
			245						250							
Glu	Leu	Lys	Ser	Leu	Asp	Ile	Tyr	Ser	Phe	Ile	Lys	Glu	Ala	Asn	Thr	270
			260					265								
Leu	Asn	Leu	Ala	Pro	Tyr	Asp	Ala	Cys	Trp	Asn	Ala	Cys	Arg	Gly	Asp	285
			275					280								
Arg	Trp	Glu	Asp	Leu	Ser	Arg	Ser	Gln	Val	Arg	Cys	Tyr	Val	His	Ile	300
			290			295										
Met	Lys	Glu	Gly	Leu	Cys	Ser	Arg	Val	Ser	Thr	Leu	Gly	Leu	Tyr	Met	320
			305			310				315						
Glu	Ala	Asn	Arg	Gln	Val	Pro	Lys	Leu	Leu	Ser	Ala	Leu	Cys	Pro	Glu	


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          325          330          335
Glu Pro Pro Val His Ser Ser Ala Gln Ile Val Ser Lys His Leu Val
          340          345          350
Gly Val Asp Ser Leu Ile Gly Pro Glu Thr Gln Ile Gly Glu Lys Ser
          355          360          365
Ser Ile Lys Arg Ser Val Ile Gly Ser Ser Cys Leu Ile Lys Asp Arg
          370          375          380
Val Thr Ile Thr Asn Cys Leu Leu Met Asn Ser Val Thr Val Glu Glu
          385          390          395          400
Gly Ser Asn Ile Gln Gly Ser Val Ile Cys Asn Asn Ala Val Ile Glu
          405          410          415
Lys Gly Ala Asp Ile Lys Asp Cys Leu Ile Gly Ser Gly Gln Arg Ile
          420          425          430
Glu Ala Lys Ala Lys Arg Val Asn Glu Val Ile Val Gly Asn Asp Gln
          435          440          445
Leu Met Glu Ile
          450

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<210> 4485

<211> 513

<212> DNA

<213> Homo sapiens

<400> 4485

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ggatccacgt cagcccgaca tcgctgcttt atagccatgt tcacgtgtca tatgcgtctc
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agggtaccca aaatcacagg gccaaactcac ggggctccta ccactctagc cagtcatggg
120
gtcaggaata cccaccctc atccaaaatg tgtactcccc caaccttttg tgttcagacc
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360
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<210> 4486

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<212> PRT

<213> Homo sapiens

<400> 4486

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Leu Leu Ala Cys Gly Asp Val Glu Gly Lys Phe Asp Ile Leu Phe Asn
35          40          45
Arg Val Gln Ala Ile Gln Lys Lys Ser Gly Asn Phe Asp Leu Leu Leu
50          55          60
Cys Val Gly Asn Phe Phe Gly Ser Thr Gln Asp Ala Glu Trp Glu Glu
65          70          75          80
Tyr Lys Thr Gly Ile Lys Lys Ala Pro Ile Gln Thr Tyr Val Leu Gly
85          90          95
Ala Asn Asn Gln Glu Thr Val Lys Tyr Phe Gln Asp Ala Asp Gly Cys
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<210> 4489

<211> 2390

<212> DNA

<213> Homo sapiens

<400> 4489

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 Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu Leu
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Arg Ala Val	Thr Val Tyr	Asp Lys Pro	Ala Ser Phe	Lys Glu Thr	
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<210> 4491

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<212> DNA

<213> Homo sapiens

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<211> 674

<212> PRT

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<400> 4492

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 Glu Thr Gln Glu Thr Glu Lys Lys Leu Leu Phe Ile Ser Glu Pro Ile

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 Lys Cys Ser Met Leu Ser Thr Ala Glu Asp Asp Ile Arg Gln Asn Phe
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 465 470 475 480
 His Tyr Lys Cys Asn Ile Gln Ala Ser Val His Val Ser Asp Phe Ser
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<210> 4493

<211> 1829

<212> DNA

<213> Homo sapiens

<400> 4493

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<210> 4494

<211> 111

<212> PRT

<213> Homo sapiens

<400> 4494

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Leu Val His Leu Ala Leu Arg Phe Lys Cys Asn Gln Asn Cys Pro Gln
 50           55           60
Gly Pro Ala Ile Lys Ala Leu Ser Leu Ser Thr Phe Trp Tyr Leu Val
 65           70           75           80
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<210> 4495

<211> 3623

<212> DNA

<213> Homo sapiens

<400> 4495

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960

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<210> 4496

<211> 560

<212> PRT

<213> Homo sapiens

<400> 4496

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Leu	Asp	Pro	Asp	Trp	Thr	Pro	Asp	Gln	Tyr	Asp	Tyr	Ser	Tyr	Glu	Asp
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Tyr	Asn	Gln	Glu	Glu	Asn	Thr	Ser	Ser	Thr	Leu	Thr	His	Ala	Glu	Asn
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 225 230 235 240
 Gly Glu His Asn Phe Cys Arg Asn Pro Asp Ala Asp Glu Lys Pro Trp
 245 250 255
 Cys Phe Ile Lys Val Thr Asn Asp Lys Val Lys Trp Glu Tyr Cys Asp
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 Arg His Leu Lys Val Val Leu Gly Asp Gln Asp Leu Lys Lys Glu Glu
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 Tyr Asn Glu Arg Asp Glu Ile Pro His Asn Asp Ile Ala Leu Leu Lys
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<210> 4497

<211> 840

<212> DNA

<213> Homo sapiens

<400> 4497

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<210> 4498

<211> 280

<212> PRT

<213> Homo sapiens

<400> 4498

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Pro Lys Ala Ser Thr Thr Ser Asp Gly Asp Glu Ser Pro Pro Ser Ser
35          40          45
Pro Gly Asn Pro Val Gln Gly Gln Cys Gly Glu Glu Glu Asp Ser Leu

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Gly	Arg	Gly	Leu	Ala	Leu	Gln	Lys	Met	Gly	Gln	Glu	Glu	Glu	Ser	Pro
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<210> 4499

<211> 562

<212> DNA

<213> Homo sapiens

<400> 4499

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<210> 4500

<211> 91

<212> PRT

<213> Homo sapiens

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Glu	Lys	Ile	Met	Ser	Val	Leu	Ser	Glu	Arg	Gly	Leu	Phe	Arg	Gly	Leu
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<211> 1866

<212> DNA

<213> Homo sapiens

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<210> 4502

<211> 267

<212> PRT

<213> Homo sapiens

<400> 4502

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Gly Ala Cys Phe Glu Val Ile Leu Ile Ser Asp Ala Asn Thr Phe Gly
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Arg Pro Phe His Thr His Ser Cys Ala Arg Cys Pro Ala Asn Met Cys
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Lys His Lys Val Leu Ser Asp Tyr Leu Arg Glu Arg Ala His Asp Gly
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Val His Phe Glu Arg Leu Phe Tyr Val Gly Asp Gly Ala Asn Asp Phe
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Cys Pro Met Gly Leu Leu Ala Gly Gly Asp Val Ala Phe Pro Arg Arg
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<210> 4503

<211> 1983

<212> DNA

<213> Homo sapiens

<400> 4503

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 1983

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<211> 250

<212> PRT

<213> Homo sapiens

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      50      55      60
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      65      70      75      80
Thr Thr Val Ile Gln Asn Val Asn Lys Ala Gln Val Lys Ile Arg Ala
      85      90      95
Lys Lys Asp Asn Val Ala Gly Val Thr Leu Pro Val Phe Glu His Tyr
      100      105      110
His Glu Gly Thr Asp Ser Tyr Glu Leu Thr Gly Leu Ala Arg Gly Gly
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Ala Ile Lys Ile Thr Asn Arg Arg Val Asn Ala Ile Glu His Gly Glu
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Tyr Val Ile Ile Pro Arg Ile Glu Arg Thr Leu Ala Tyr Ile Ile Thr
      180      185      190
Glu Leu Asp Glu Arg Glu Arg Glu Glu Phe Tyr Arg Leu Lys Lys Ile
      195      200      205
Gln Glu Lys Lys Lys Ile Leu Lys Glu Lys Ser Glu Lys Asp Leu Glu
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<210> 4505

<211> 379

<212> DNA

<213> Homo sapiens

<400> 4505

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<210> 4506

<211> 121

<212> PRT

<213> Homo sapiens

<400> 4506

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Arg Arg Gln Trp Trp Leu Trp Leu Ser Ser Leu Ser Asn Gln Ile His
 35             40             45
Pro Thr Pro Ser Ala Gln Gly Gln Ala Ala Leu Arg Gln Thr Cys Pro
 50             55             60
His Leu Arg Glu Ser Gly Pro Leu Ser Val Arg His Val Ala Leu Leu
 65             70             75             80
Ala Leu Glu Thr Ala Ser His Pro Ser Gly Pro His Thr Asn Gln Ala
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<210> 4507

<211> 3664

<212> DNA

<213> Homo sapiens

<400> 4507

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<211> 172

<212> PRT

<213> Homo sapiens

<400> 4508

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Ser	Glu	Val	Val	Val	Lys	Asp	Arg	Glu	Thr	Gln	Arg	Ser	Arg	Gly
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Phe	Gly	Phe	Val	Thr	Phe	Glu	Asn	Ile	Asp	Asp	Ala	Lys	Asp	Ala
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Met	Ala	Met	Asn	Gly	Lys	Ser	Val	Asp	Gly	Arg	Gln	Ile	Arg	Val
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<212> DNA

<213> Homo sapiens

<400> 4509

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Pro Tyr Thr Val Pro Arg Asp Val Arg Ile Met Val His Pro His Val					
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Pro Val Ser Leu Pro Thr Gln Thr Ala Pro Lys Gln Pro Leu Phe Val					
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Pro Thr Thr Ser Gly Pro Ser Thr Pro Pro Gly Leu Val Leu Pro His					
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 <212> DNA
 <213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 4512

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65				70				75						80	
Ala	Asn	Lys	Val	Lys	Arg	Lys	Asp	Thr	Leu	Ala	Met	Lys	Leu	Asn	His
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Lys	Glu	Glu	Trp	Asn	Glu	Ile	Arg	His	Gln	Ile	Gly	Asn	Thr	Leu	Ile
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Glu	Leu	Leu	Ala	Arg	Lys	Ile	Leu	Arg	Phe	Asn	Glu	Tyr	Val	Glu	Val
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Thr	Asp	Ala	Gln	Asp	Tyr	Asp	Arg	Arg	Ala	Asp	Lys	Pro	Trp	Thr	Lys

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<212> DNA

<213> Homo sapiens

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<211> 901

<212> PRT

<213> Homo sapiens

<400> 4516

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Ala Arg Asp Pro Ala Ser Leu Thr Arg Gly Leu Cys Gln Ala Leu Val
 85           90           95
Pro Pro Gly Val Ala Ala Leu Leu Ala Phe Pro Glu Ala Arg Pro Glu
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Leu Leu Gln Leu His Phe Leu Ala Ala Thr Glu Thr Pro Val Leu
 115          120          125
Ser Leu Leu Arg Arg Glu Ala Arg Ala Pro Leu Gly Ala Pro Asn Pro
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Phe His Leu Gln Leu His Trp Ala Ser Pro Leu Glu Thr Leu Leu Asp
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Val Leu Val Ala Val Leu Gln Ala His Ala Trp Glu Asp Val Gly Leu
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Ala Leu Cys Arg Thr Gln Asp Pro Gly Gly Leu Val Ala Leu Trp Thr
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Ser Arg Ala Gly Arg Pro Pro Gln Leu Val Leu Asp Leu Ser Arg Arg
 195          200          205
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Pro Val Gly Gly Glu Ala Pro Val Pro Ala Ala Val Leu Leu Gly Cys
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His Trp Leu Leu Gly Thr Pro Leu Pro Pro Lys Ala Leu Pro Thr Ala
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Gly Leu Pro Pro Gly Leu Leu Ala Leu Gly Glu Val Ala Arg Pro Pro
 275          280          285
Leu Glu Ala Ala Ile His Asp Ile Val Gln Leu Val Ala Arg Ala Leu

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Pro	Val	Trp	Val	Thr	Gly	Ser	Ser	Gln	Val	His	Met	Ser	Arg	His	Phe		
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Lys	Val	Trp	Ser	Leu	Arg	Arg	Asp	Pro	Arg	Gly	Ala	Pro	Ala	Trp	Ala		
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Thr	Val	Gly	Ser	Trp	Arg	Tyr	Gly	Gln	Leu	Asp	Leu	Glu	Pro	Gly	Gly		
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Leu	Arg	Val	Val	Thr	Leu	Leu	Glu	His	Pro	Phe	Val	Phe	Ala	Arg	Asp		
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Pro	Asp	Glu	Asp	Gly	Gln	Cys	Pro	Ala	Gly	Gln	Leu	Cys	Leu	Asp	Pro		
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Gly	Thr	Asn	Asp	Ser	Ala	Thr	Leu	Asp	Ala	Leu	Phe	Ala	Ala	Leu	Ala		
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Ile	Asp	Leu	Leu	Glu	Arg	Leu	Ala	Glu	Asp	Thr	Pro	Phe	Asp	Phe	Glu		
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Leu	Tyr	Leu	Val	Gly	Asp	Gly	Lys	Tyr	Gly	Ala	Leu	Arg	Asp	Gly	Arg		
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Trp	Thr	Gly	Leu	Val	Gly	Asp	Leu	Leu	Ala	Gly	Arg	Ala	His	Met	Ala		
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Val	Thr	Ser	Phe	Ser	Ile	Asn	Ser	Ala	Arg	Ser	Gln	Val	Val	Asp	Phe		
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Thr	Ser	Pro	Phe	Phe	Ser	Thr	Ser	Leu	Gly	Ile	Met	Val	Arg	Ala	Arg		
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Ala	Ile	Leu	Phe	Arg	Thr	Val	Ser	Ser	Lys	Thr	Pro	Lys	Cys	Pro			
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Leu	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Val	Met	Val	Gly	Asp	Lys		
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Thr	Phe	Glu	Glu	Leu	Ser	Gly	Ile	His	Asp	Pro	Lys	Leu	His	His	Pro		
		675					680					685					
Ala	Gln	Gly	Phe	Arg	Phe	Gly	Thr	Val	Trp	Glu	Ser	Ser	Ala	Glu	Ala		
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Tyr	Ile	Lys	Lys	Ser	Phe	Pro	Asp	Met	His	Ala	His	Met	Arg	Arg	His		
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Ser	Ala	Pro	Thr	Thr	Pro	Arg	Gly	Val	Ala	Met	Leu	Thr	Ser	Asp	Pro		


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Pro Lys Leu Asn Ala Phe Ile Met Asp Lys Ser Leu Leu Asp Tyr Glu
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Val Ser Ile Asp Ala Asp Cys Lys Leu Thr Val Gly Lys Pro Phe
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Ala Ile Glu Gly Tyr Gly Ile Gly Leu Pro Gln Asn Ser Pro Leu Thr
              770              775              780
Ser Asn Leu Ser Glu Phe Ile Ser Arg Tyr Lys Ser Ser Gly Phe Ile
              785              790              795
Asp Leu Leu His Asp Lys Trp Tyr Lys Met Val Pro Cys Gly Lys Arg
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Val Phe Ala Val Thr Glu Thr Leu Gln Met Ser Ile Tyr His Phe Ala
              820              825              830
Gly Leu Phe Val Leu Leu Cys Leu Gly Leu Gly Ser Ala Leu Leu Ser
              835              840              845
Ser Leu Gly Glu His Ala Phe Phe Arg Leu Ala Leu Pro Arg Ile Arg
              850              855              860
Lys Gly Ser Arg Leu Gln Tyr Trp Leu His Thr Ser Gln Lys Ile His
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Glu Ala Glu Pro Arg
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<210> 4517

<211> 2275

<212> DNA

<213> Homo sapiens

<400> 4517

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720

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<210> 4518

<211> 650
 <212> PRT
 <213> Homo sapiens

<400> 4518

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Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly Gly Lys
 35           40           45
Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu Gly Pro Ser
 50           55           60
Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp Pro Glu Val Val
 65           70           75           80
Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu Phe Ser Arg Arg Lys
 85           90           95
Gly Lys Gly Gln Ala Gln Val Pro Ser Phe Arg Pro Tyr Leu Leu Thr
 100          105          110
Leu Phe Thr His Gln Ser Ser Trp Pro Thr Leu His Gln Cys Ile Arg
 115          120          125
Val Leu Leu Gly Lys Ser Arg Glu Gln Arg Phe Asp Pro Ser Ala Ser
 130          135          140
Leu Asp Phe Leu Trp Ala Cys Ile His Val Pro Arg Ile Trp Gln Gly
 145          150          155          160
Arg Asp Gln Arg Thr Pro Gln Lys Arg Arg Glu Glu Leu Val Leu Arg
 165          170          175
Val Gln Gly Pro Glu Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu
 180          185          190
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 195          200          205
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 210          215          220
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 245          250          255
Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu Leu
 260          265          270
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 275          280          285
Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp Ser Arg Ala
 290          295          300
Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys Arg Lys Leu Ala
 305          310          315          320
Val Ala His Pro Leu Leu Leu Arg His Leu Pro Met Ile Ala Ala
 325          330          335
Leu Leu His Gly Arg Thr His Leu Asn Phe Gln Glu Phe Arg Gln Gln
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          405          410          415
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          420          425          430
Asp Pro Leu His Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu
          435          440          445
Lys Ser Leu Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr
          450          455          460
Asp Arg Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser
465          470          475          480
Leu Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
          485          490          495
Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu Gly
          500          505          510
Glu Ser Gly Pro Ala Ser Pro Thr Pro Asp Leu Leu Glu Val Leu Ser
          515          520          525
Asp Ile Asp Glu Met Ser Arg Arg Arg Pro Glu Ile Leu Ser Phe Phe
530          535          540
Ser Thr Asn Leu Gln Arg Leu Met Ser Ser Ala Glu Glu Cys Cys Arg
545          550          555          560
Asn Leu Ala Phe Ser Leu Ala Leu Arg Ser Met Gln Asn Ser Pro Ser
          565          570          575
Ile Ala Ala Ala Phe Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln
          580          585          590
Asp Phe Glu Val Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala
          595          600          605
Leu Leu Cys Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu
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<210> 4519

<211> 2326

<212> DNA

<213> Homo sapiens

<400> 4519

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120
acagacaact atccggctta cggccagggg agcccctgca gctgcacaga accagtttct
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300
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420

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<210> 4520

<211> 617

<212> PRT

<213> Homo sapiens

<400> 4520

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		20						25					30		
Thr	Asn	Cys	Lys	Gln	Ala	Glu	Arg	Pro	Asn	Asn	Gln	Gln	Asn	Cys	Phe
		35					40					45			
Lys	Val	Cys	Asp	Trp	His	Lys	Glu	Leu	Tyr	Asp	Trp	Arg	Leu	Gly	Pro
	50					55				60					
Trp	Asn	Gln	Cys	Gln	Pro	Val	Ile	Ser	Lys	Ser	Leu	Glu	Lys	Pro	Leu
65				70					75					80	
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			85					90						95	
Ile	Gln	Lys	Asp	Lys	Asp	Ile	Pro	Ala	Glu	Asp	Ile	Ile	Cys	Glu	Tyr
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Phe	Glu	Pro	Lys	Pro	Leu	Leu	Glu	Gln	Ala	Cys	Leu	Ile	Pro	Cys	Gln
	115						120					125			
Gln	Asp	Cys	Ile	Val	Ser	Glu	Phe	Ser	Ala	Trp	Ser	Glu	Cys	Ser	Lys
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Thr	Cys	Gly	Ser	Gly	Leu	Gln	His	Arg	Thr	Arg	His	Val	Val	Ala	Pro
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Pro	Gln	Phe	Gly	Gly	Ser	Gly	Cys	Pro	Asn	Leu	Thr	Glu	Phe	Gln	Val
			165					170						175	
Cys	Gln	Ser	Ser	Pro	Cys	Glu	Ala	Glu	Glu	Leu	Arg	Tyr	Ser	Leu	His
		180						185					190		
Val	Gly	Pro	Trp	Ser	Thr	Cys	Ser	Met	Pro	His	Ser	Arg	Gln	Val	Arg
	195					200						205			
Gln	Ala	Arg	Arg	Arg	Gly	Lys	Asn	Lys	Glu	Arg	Glu	Lys	Asp	Arg	Ser
	210					215					220				
Lys	Gly	Val	Lys	Asp	Pro	Glu	Ala	Arg	Glu	Leu	Ile	Lys	Lys	Lys	Arg
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	260					265						270			
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	275					280						285			
Gln	Ser	Cys	Val	Ile	Thr	Lys	Glu	Cys	Gln	Val	Ser	Glu	Trp	Ser	Glu

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Lys Glu Cys Pro Glu Phe Glu Glu Lys Glu Pro Cys Leu Ser Gln Gly
              340              345              350
Asp Gly Val Val Pro Cys Ala Thr Tyr Gly Trp Arg Thr Thr Glu Trp
              355              360              365
Thr Glu Cys Arg Val Asp Pro Leu Leu Ser Gln Gln Asp Lys Arg Arg
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Gly Asn Gln Thr Ala Leu Cys Gly Gly Gly Ile Gln Thr Arg Glu Val
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Tyr Cys Val Gln Ala Asn Glu Asn Leu Leu Ser Gln Leu Ser Thr His
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Lys Asn Lys Glu Ala Ser Lys Pro Met Asp Leu Lys Leu Cys Thr Gly
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Pro Ile Pro Asn Thr Thr Gln Leu Cys His Ile Pro Cys Pro Thr Glu
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Cys Glu Val Ser Pro Trp Ser Ala Trp Gly Pro Cys Thr Tyr Glu Asn
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Cys Asn Asp Pro Gln Gly Lys Lys Gly Phe Lys Leu Arg Lys Arg Arg
465              470              475              480
Ile Thr Asn Glu Pro Thr Gly Gly Ser Gly Leu Thr Gly Asn Cys Pro
              485              490              495
His Leu Leu Glu Ala Ile Pro Cys Glu Glu Pro Ala Cys Tyr Asp Trp
              500              505              510
Lys Ala Val Arg Leu Gly Asp Cys Glu Pro Asp Asn Gly Lys Glu Cys
              515              520              525
Gly Pro Gly Thr Gln Val Gln Glu Val Val Cys Ile Asn Ser Asp Gly
              530              535              540
Glu Glu Val Asp Arg Gln Leu Cys Arg Asp Ala Ile Phe Pro Ile Pro
545              550              555              560
Val Ala Cys Asp Ala Pro Cys Pro Lys Asp Cys Val Leu Ser Thr Trp
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Ser Thr Trp Ser Ser Cys Ser His Thr Cys Ser Gly Lys Thr Thr Glu
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Gly Glu Ser Pro Ala Ser Asp Ala Ile
610              615

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<210> 4521

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 4521

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120

ttataccaat ataaacaatt actcaggaaa aaaagaaaat aaaaacttgc aaggggctaaa

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 840
 aaccttgcac actaaaaaaa ggaacacaaa aataaaccaa aagaaccga aaacctgaa
 900
 cttgcaggag aattttccaa agccgtaatt ataatgagag tgtttttaag tctataagaa
 960
 attaatatat caaacaata aagattaata agaatttgga atttgtatga aatggcaaa
 1020
 gaaaagccag gcgtggtggc ttacgcctgt aatgccagca ctttgggagg c
 1071

<210> 4522

<211> 189

<212> PRT

<213> Homo sapiens

<400> 4522

Met	Leu	Ala	Leu	Arg	Thr	Val	Lys	Gly	Phe	Lys	Arg	Lys	Ser	Thr	Pro
1			5					10					15		
Arg	Glu	Gly	Ser	Tyr	Met	Ser	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Gly
			20					25					30		
His	Thr	Glu	Thr	Ala	Ser	Ser	Phe	Gln	Pro	Ser	Pro	Phe	Ser	Ala	Asp
			35				40					45			
Phe	Glu	Leu	Gln	Ile	Ser	Leu	Leu	Tyr	Leu	Glu	Ser	Pro	Ile	Ser	Leu
			50			55				60					
Gln	Glu	Phe	Ala	Leu	Ser	Phe	Ile	Ile	Ile	Leu	Val	Tyr	Val	Leu	Asp
65				70						75				80	
Trp	Ala	Ala	Ile	Thr	Arg	Cys	His	Arg	Leu	Ser	Gly	Leu	Asn	Asn	Lys
			85					90					95		
His	Ser	Tyr	Pro	Thr	Val	Thr	Glu	Ala	Glu	Lys	Pro	Gly	Val	Lys	Val
			100				105					110			
Pro	Ala	Trp	Ser	Asp	Ser	Val	Leu	Glu	Ala	Gly	Lys	Ser	Lys	Met	Glu
			115				120					125			
Ala	Leu	Val	Gly	Leu	Val	Ser	Gly	Arg	Ala	Ser	Leu	Cys	Phe	Gln	Asp

130					135					140					
Gly	Ala	Leu	Ser	Leu	His	Leu	Pro	Glu	Gly	Arg	Asn	Ala	Val	Ser	Leu
145					150					155					160
Gln	His	Arg	Arg	Asn	Thr	Ser	Glu	Lys	Lys	Ser	Ser	Arg	Lys	Val	Glu
				165					170						175
Asn	Lys	Glu	Met	Glu	Tyr	Ile	Tyr	Glu	Asn	Tyr	Tyr	Ile			
			180					185							

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<210> 4523
<211> 1022
<212> DNA
<213> Homo sapiens
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400> 4523
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60
gacataccca ggctgagtct cntcttggtg attctgggcg tcattctcat gaatggcaac
120
cgtgccagcg aggctgtctt ctggggaggca ctacgcaaga tgggactcgc ccctggggtg
180
aggcaccatc tcctcggcga tctgaggaag ctcatcacag atgactttgt gaagcagaag
240
taccttggaa acaagaagat ccccaacagc aaccaccttg agtatgaatt cctctggggc
300
ctgcgagccc gccatgagac cagcaagatg agggctctga gattcatcgc ccagaatcag
360
aaccgagacc cccgggaatg gaaggctcat ttcttgaggg ctgtggatga tgctttcaag
420
acaaatggat tggaatagcg cgagggaact gccaggggcc agatgagggg ccagatgaat
480
atcgggggatg aagcgctgat tggacggttg agctgggatg acatacaagt cgagctcctg
540
acctgggatg aggacgggag ttttggcgat gcttgggcca ggatccccct tgctttcttg
600
gccagatacc atcagtacat tctgaatagc aaccgtgcca acaggagggg cacgtggaga
660
gctggcgctc agctgggcac caatggaggg gccagcacca gcgtctctaga tggccccagc
720
accagctcca ccatccggac cagaaatgct gccagagctg gcgccagctt ctctctcttg
780
atccagtagg agtttcggca cgttgacgca actgcagcga tcttactggc caagccagag
840
cgctctctct cagattcctt ctcgacacag caccctaggc ggctctcttc tgcagctcgg
900
aggtggcatg caagatgaag ctctcttttg tcttctctgt ttcattttgt gcttttctct
960
gtgttttcat gttttgggta tcagtgttac attaaagttg caaaattaaa aaaaaaaaaa
1020
aa
1022

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<210> 4524
<211> 262
<212> PRT
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<213> Homo sapiens

<400> 4524

Ala Leu Tyr Ile Leu Val Cys Thr Arg Asp Ser Ser Ala Arg Leu Leu
 1 5 10 15
 Gly Lys Thr Lys Asp Thr Pro Arg Leu Ser Leu Xaa Leu Val Ile Leu
 20 25 30
 Gly Val Ile Phe Met Asn Gly Asn Arg Ala Ser Glu Ala Val Leu Trp
 35 40 45
 Glu Ala Leu Arg Lys Met Gly Leu Arg Pro Gly Val Arg His Pro Phe
 50 55 60
 Leu Gly Asp Leu Arg Lys Leu Ile Thr Asp Asp Phe Val Lys Gln Lys
 65 70 75 80
 Tyr Leu Glu Tyr Lys Lys Ile Pro Asn Ser Asn Pro Pro Glu Tyr Glu
 85 90 95
 Phe Leu Trp Gly Leu Arg Ala Arg His Glu Thr Ser Lys Met Arg Val
 100 105 110
 Leu Arg Phe Ile Ala Gln Asn Gln Asn Arg Asp Pro Arg Glu Trp Lys
 115 120 125
 Ala His Phe Leu Glu Ala Val Asp Asp Ala Phe Lys Thr Met Asp Val
 130 135 140
 Asp Met Ala Glu Glu His Ala Arg Ala Gln Met Arg Ala Gln Met Asn
 145 150 155 160
 Ile Gly Asp Glu Ala Leu Ile Gly Arg Trp Trp Asp Asp Ile Gln
 165 170 175
 Val Glu Leu Leu Thr Trp Asp Glu Asp Gly Asp Phe Gly Asp Ala Trp
 180 185 190
 Ala Arg Ile Pro Phe Ala Phe Trp Ala Arg Tyr His Gln Tyr Ile Leu
 195 200 205
 Asn Ser Asn Arg Ala Asn Arg Arg Ala Thr Trp Arg Ala Gly Val Ser
 210 215 220
 Ser Gly Thr Asn Gly Gly Ala Ser Thr Ser Val Leu Asp Gly Pro Ser
 225 230 235 240
 Thr Ser Ser Thr Ile Arg Thr Arg Asn Ala Ala Arg Ala Gly Ala Ser
 245 250 255
 Phe Phe Ser Trp Ile Gln
 260

<210> 4525

<211> 1731

<212> DNA

<213> Homo sapiens

<400> 4525

nngaaccatg gcattctcca ggctctgacc acagaagctt atgaatggga gccacgtgtt
 60
 gtgagtacag aggtgggtcag agcccaagaa gaatgggaag ctgtggacac catccagcca
 120
 gagacagggga gccaaagctag ctgagagcag cctgggcagc taatctcctt cagtggaggc
 180
 ctgcagcact tccagactgt ggacctttcc cccttcaaga aaagaatcca gccaaactatt
 240
 cgaaggactg ggctcgccgc cctccgacac tacctcttcg ggcctccaaa gctccaccag
 300

cgccctcggg aagaaaggga cttggctcctg accattgtctc agtgtggcct ggatagccaa
 360
 gaccagtg c atggccgagtg cctccagacc atctataaga agctgaccgg ctccaagtgtt
 420
 gactgtgccc ttcattggaaa ccaactgggag gacctgggct ttcagggagc gaatccagcc
 480
 acagacctga gaggcgcagg cttccttgcc ctctgcac c tgctctacct agtgatggag
 540
 tcaaagaacct tgccgatggc gcaggagatt ttccgcctgt ctgcgcacca catccagcaa
 600
 ttccctttct gtttgatgtc cgtgaacatc acccacattg ccatccaggc cttgagagag
 660
 gagtgtctct ccagagagtg taatcggcag cagaaggcca tccccgtggg gaacagcttc
 720
 tatgcgcgcca cattctctca cctcgcacat gtctggaggga cacagcggaa gaccatctca
 780
 gactcgggct ttgtctctcaa aggtgtgtctc ttctctctgg ggaggcctag gctgaatgca
 840
 cagtgtctcca ggtccagaga gcccaagggtg gttgctagac tgggttttggc tgcagtctct
 900
 ccccatccac actttctcaa attccagctt accaaaatct ccatcaccga ccccttgagg
 960
 tctgctagtgt ctctcttctc tgccctgact gtccgccctt tctggtctta tacttatgac
 1020
 aagcatatat tctgatcaaa aattgggagc cagggtccaa tagttggact attcaaagtt
 1080
 gcaattgtgc agacaaggta gagtgtgtgg tccctgtggc tgtagctggc tccctagcct
 1140
 acctctctctg tgatctctcc atctgaggct ccttcacttt ctctccatgg gataggggtt
 1200
 ggggggtactc cctagagctg ctaggcttga ggccttgact gttgtgtcac ccagagcccc
 1260
 ctcaagcctt ctgctcccca attctctctg ttgcagagtt ggaagtattg gccaaaga
 1320
 gcccaagcgg ggctgtctca gacctggag ctgtacttgg ccagggtgtc aaagggacag
 1380
 gctccttgtg tgggagcaca gaagtgtat gggccagaag cccctccctt caaggatctc
 1440
 accttcacag gtgagagtga cctgcagctc cactcatccg aaggcgatg gctgatctga
 1500
 cctccagatg gaattggaggc ttaaaggctg agctgcaggg gctttcaggg ggtcagtgga
 1560
 gccatgtcag gagcctggcc aggcgcgacc cctgtctgtc tcagcagatg ggatatagga
 1620
 agctcctggg cttagctgtg ggaagccaag taccctcacc ggcatgggac atgaggggca
 1680
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 1731

<210> 4526

<211> 344

<212> PRT

<213> Homo sapiens

<400> 4526

Xaa Asn His Gly Ile Leu Gln Ala Leu Thr Thr Glu Ala Tyr Glu Trp
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 Glu Pro Arg Val Val Ser Thr Glu Val Val Arg Ala Gln Glu Glu Trp
 20 25 30
 Glu Ala Val Asp Thr Ile Gln Pro Glu Thr Gly Ser Gln Ala Ser Ser
 35 40 45
 Glu Gln Pro Gly Gln Leu Ile Ser Phe Ser Glu Ala Leu Gln His Phe
 50 55 60
 Gln Thr Val Asp Leu Ser Pro Phe Lys Lys Arg Ile Gln Pro Thr Ile
 65 70 75 80
 Arg Arg Thr Gly Leu Ala Ala Leu Arg His Tyr Leu Phe Gly Pro Pro
 85 90 95
 Lys Leu His Gln Arg Leu Arg Glu Glu Arg Asp Leu Val Leu Thr Ile
 100 105 110
 Ala Gln Cys Gly Leu Asp Ser Gln Asp Pro Val His Gly Arg Val Leu
 115 120 125
 Gln Thr Ile Tyr Lys Lys Leu Thr Gly Ser Lys Phe Asp Cys Ala Leu
 130 135 140
 His Gly Asn His Trp Glu Asp Leu Gly Phe Gln Gly Ala Asn Pro Ala
 145 150 155 160
 Thr Asp Leu Arg Gly Ala Gly Phe Leu Ala Leu Leu His Leu Leu Tyr
 165 170 175
 Leu Val Met Asp Ser Lys Thr Leu Pro Met Ala Gln Glu Ile Phe Arg
 180 185 190
 Leu Ser Arg His His Ile Gln Gln Phe Pro Phe Cys Leu Met Ser Val
 195 200 205
 Asn Ile Thr His Ile Ala Ile Gln Ala Leu Arg Glu Glu Cys Leu Ser
 210 215 220
 Arg Glu Cys Asn Arg Gln Gln Lys Val Ile Pro Val Val Asn Ser Phe
 225 230 235 240
 Tyr Ala Ala Thr Phe Leu His Leu Ala His Val Trp Arg Thr Gln Arg
 245 250 255
 Lys Thr Ile Ser Asp Ser Gly Phe Val Leu Lys Gly Val Leu Phe Leu
 260 265 270
 Leu Gly Arg Pro Arg Leu Asn Ala Gln Cys Pro Arg Ser Arg Glu Pro
 275 280 285
 Lys Val Val Ala Arg Leu Val Leu Ala Ala Val Leu Pro His Pro His
 290 295 300
 Phe Leu Lys Phe Gln Leu Thr Lys Ile Ser Ile Thr His Pro Leu Glu
 305 310 315 320
 Ser Ala Ser Ser Pro Phe Ser Ala Leu Thr Val Ala Leu Phe Trp Ser
 325 330 335
 Tyr Thr Tyr Asp Lys His Ile Phe
 340

<210> 4527

<211> 885

<212> DNA

<213> Homo sapiens

<400> 4527

nntttttttt tttttttttt tttttttttt tttttttttt tttttttttt cagagacatg
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gctgcattta ttgttcccag ccggcgaga aggtgttccc agaaagggtc cttgggtcac
 120
 ctgcccaccc agccttggtc ctgggctgcc atgtcccacc gggggcagga gagaggcaca
 180
 agtcacagtc aggcgaaggga gcctcagcgt cctgggcggt ggctgttggg gtccctccag
 240
 tcttcacctg ggaccctcgg ccaggctggg acagcatcca ggagcgaggg ctgcatggtc
 300
 cagcgggtggg tgcaggtggc aacaggtcgg cgggctgtgc aggttccaaa aggagctctc
 360
 gggttggcac tgggtgagac cagccccggg gccagcaggg gaatgagcgg tggagcaggg
 420
 gggtgtggg cactgggggtg ggccccatct cctgtccttc cctcatggct gctggaaggg
 480
 ccgcctccct ggctcagcat catctcagat tccgggactc aaacaccgtc tctctgtcgc
 540
 tgtccagcga ggccatctcc gtggggtcct cagtgttggc gaggaggcgg tatcgccctcc
 600
 gctgagggtt cttcaacctc aacgcccggg tcaggaagta gagcgcggtc aggccgcaga
 660
 agcccaggat cagtagaag gagcgcgta gcgccagacc cgacgcccc ggccgacgcg
 720
 tgtgcgtgct gttgtgtggc gcgcccggtt ggctcccgtt cgtcacggcc ggccggcgcg
 780
 acaacgtgac ctggcggggg cagcggcgag cctcttcggc accgcacggc agccgcccca
 840
 gcagcagcgc cagcaggagc agcagcagcg gcggctcgag cagcg
 885

<210> 4528

<211> 206

<212> PRT

<213> Homo sapiens

<400> 4528

Xaa Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
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 Cys Arg Asp Met Ala Ala Phe Ile Val Pro Ser Pro Ala Arg Arg Cys
 20 25 30
 Ser Gln Lys Gly Ser Leu Gly His Leu Pro Thr Gln Pro Trp Leu Trp
 35 40 45
 Ala Ala Met Ser Pro Arg Gly Gln Glu Arg Gly Thr Ser His Ser Gln
 50 55 60
 Ala Arg Glu Pro Gln Arg Pro Gly Arg Trp Leu Leu Gly Ser Leu Gln
 65 70 75 80
 Ser Ser Pro Gly Thr Leu Gly Gln Ala Gly Thr Ala Ser Arg Arg Arg
 85 90 95
 Gly Cys Met Val Gln Arg Trp Val Gln Val Ala Thr Gly Arg Arg Ala
 100 105 110
 Val Gln Val Pro Lys Gly Ala Leu Gly Leu Ala Leu Gly Glu Thr Ser
 115 120 125
 Pro Gly Ala Ser Arg Gly Met Ser Gly Gly Ala Gly Gly Cys Trp Ala
 130 135 140
 Leu Gly Trp Ala Pro Ser Pro Val Leu Pro Ser Trp Leu Leu Glu Gly

```

145              150              155              160
Pro Pro Pro Trp Leu Ser Ile Ile Ser Asp Ser Gly Thr Gln Thr Pro
              165              170              175
Ser Pro Arg Arg Cys Pro Ala Arg Pro Ser Pro Trp Gly Pro Gln Cys
              180              185              190
Trp Arg Gly Gly Arg Ile Ala Ser Ala Glu Ala Ser Ser Thr
              195              200              205

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<210> 4529
 <211> 546
 <212> DNA
 <213> Homo sapiens

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<400> 4529
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gtggcgcgcg cctaagctgc agccgcgga gccgcagaaa caagaggccg agccgtgtcg
120
aagatggagg agaaaccctc agggcccatc cgggacatgc tggccactgc agagcccagc
180
tccagtgaga cgcacaagga ggtgtgttcc ccggctgtgc cagctgcagc cccctcctcc
240
tccatgtcgg aggagccagg ccctgagcag gcagccacac cgccagtggg gaacgtggag
300
gggctggagg gatgcagcag ggctcctccc cagcccaga cagctgccag tctgtgcccc
360
gaccagccc tggcctgacc agcatagtct ccgggaccag cgaggacctg cggcctccca
420
gacgacgccc acctccaggg aagcaaatcc cttgctccag ccctggctgc tgcctcagtt
480
ttccagcgt ccgtgacctg gcacagcatc tgogaaccca ctgcccgcg agccctatgc
540
agtctc
546

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<210> 4530
 <211> 84
 <212> PRT
 <213> Homo sapiens

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<400> 4530
Met Glu Glu Lys Pro Ser Gly Pro Ile Pro Asp Met Leu Ala Thr Ala
1          5          10          15
Glu Pro Ser Ser Ser Glu Thr Asp Lys Glu Val Leu Ser Pro Ala Val
20         25         30
Pro Ala Ala Ala Pro Ser Ser Ser Met Ser Glu Glu Pro Gly Pro Glu
35         40         45
Gln Ala Ala Thr Pro Pro Val Gly Asn Val Glu Gly Leu Glu Gly Cys
50         55         60
Ser Arg Ala Pro Pro Gln Pro Gln Thr Ala Ala Ser Leu Ala Pro Asp
65         70         75         80
Pro Ala Leu Ala

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<210> 4531

<211> 1414

<212> DNA

<213> Homo sapiens

<400> 4531

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60 gccggctccct tgcaggggcg tggggcccg gccctggacc tactccgggg cctgccgcgt
120 gtgagcctgg ccaacttaaa gccgaatccc ggctccaaga aaccggagag aagaccaaga
180 ggtcggagaa gaggtagaaa atgtggcaga gcccataag gagaaagca aagaggaacc
240 cggccccgct tgggctttga gggaggccag actccatttt acatccgaat cccaaaatac
300 gggtttaacg aaggacatag ttccagacgc cagtataagc ctttgagtct caatagactg
360 cagtatctta ttgatttggg tcgtgttgat cctagtcaac ctattgactt aaccagctt
420 gtcaatggga gaggtgtgac catccagcca cttaaaaggg attatggtgt ccagctggtt
480 gaggagggtg ctgacacctt tacggcaaaa gttaatatg aagtacagtt ggcttcagaa
540 ctagctattg ctgccattga aaaaaatggt ggtgtgtgta ctacagcctt ctatgatcca
600 agaagtcctg acattgtatg caaacctggt ccattctttc ttctgggaca acccattcca
660 aaaagaatgc ttccaccaga agaactggta ccatattaca ctgatgcaaa gaaccgtggg
720 tacctggcgg atcctgccaa atttcttgaa gcacgacttg aactcgccag gaagtatggt
780 tatactctac ctgatatcac taaagatgaa ctcttcaaaa tgctctgtac taggaaggat
840 ccaaggcaga ttttctttgg tcttgcctca ggatgggtgg tgaatatggc cgataagaaa
900 atccataaac ctacagatga aaatctcctt aagtattata cctcatgaat tccggtccaa
960 ggaagcagag ttgttaaaga gtactggaat aggggctgaa ggaatctatat tccttattg
1020 catttttctt atgtataatt ttccagatgg tgatgttact ttccagtgtg ctcatatgtc
1080 tcattttcat ctaaaattaa atggcaggaa acaaggactg catagagaaa ctgagctgtg
1140 gtgggttctg tctcaaagat acaaactccc tgatagtcta tggaaggaaa atgacaacta
1200 ttttagaata tttctagtgt gttttttcag tgatcttttc atccaggcct tgttactgtt
1260 acagatcaga atgaaatgca caagtggaaat gggattgacc tgtaggcctg ctctgccgag
1320 atgagagcag atggaatgag ttggtgaccc ctcttaatct gtagcctcag ggaaacacgg
1380 ctacccaatg ccaagatggt aaacctcac gcgt
1414

<210> 4532
 <211> 296
 <212> PRT
 <213> Homo sapiens

<400> 4532
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 Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly
 20 25 30
 Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Gly Arg Lys
 35 40 45
 Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg
 50 55 60
 Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Ile Pro Lys
 65 70 75 80
 Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu
 85 90 95
 Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro
 100 105 110
 Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr
 115 120 125
 Ile Gln Pro Leu Lys Arg Asp Tyr Gly Val Gln Leu Val Glu Glu Gly
 130 135 140
 Ala Asp Thr Phe Thr Ala Lys Val Asn Ile Glu Val Gln Leu Ala Ser
 145 150 155 160
 Glu Leu Ala Ile Ala Ala Ile Glu Lys Asn Gly Gly Val Val Thr Thr
 165 170 175
 Ala Phe Tyr Asp Pro Arg Ser Leu Asp Ile Val Cys Lys Pro Val Pro
 180 185 190
 Phe Phe Leu Arg Gly Gln Pro Ile Pro Lys Arg Met Leu Pro Pro Glu
 195 200 205
 Glu Leu Val Pro Tyr Tyr Thr Asp Ala Lys Asn Arg Gly Tyr Leu Ala
 210 215 220
 Asp Pro Ala Lys Phe Pro Glu Ala Arg Leu Glu Leu Ala Arg Lys Tyr
 225 230 235 240
 Gly Tyr Ile Leu Pro Asp Ile Thr Lys Asp Glu Leu Phe Lys Met Leu
 245 250 255
 Cys Thr Arg Lys Asp Pro Arg Gln Ile Phe Phe Gly Leu Ala Pro Gly
 260 265 270
 Trp Val Val Asn Met Ala Asp Lys Lys Ile Leu Lys Pro Thr Asp Glu
 275 280 285
 Asn Leu Leu Lys Tyr Tyr Thr Ser
 290 295

<210> 4533
 <211> 968
 <212> DNA
 <213> Homo sapiens

<400> 4533
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ttgtcacacg tgtgccccgt tccggacgcc ggggctgagg cgcgtcgcgt cgggcagcgg
 120
 gcgcggcggc cccgcgcagc catggactgg ctcatgggga agtccaaagc caagcccaat
 180
 ggcaagaagc ccgctgcgga ggagaggaag gcctacatgg agcctgagca caccaaggcc
 240
 aggatcacgc acttccagtt caaggagctg gtggtgctgc cccgggagat cgacctcaac
 300
 gagtggctgg ccagcaaac aacaacattt ttccaccaca tcaacctgca gtatagcaca
 360
 atctcggagt tctgcacagg agagacgtgt cagacgatgg ccgtgtgcaa cacacagtac
 420
 tactggatg acgagcgggg gaagaaggtc aagtgcacgg cccacagta cgttgacttc
 480
 gtcatgagct ccgtgcagaa gctggtgacg gatgaggacg tgttccccac aaaatacggc
 540
 agagaattcc ccagctcctt tgagtcctgt gtgaggaaga tctgcagaca cctgttccac
 600
 gtgctggcac acatctactg ggcccacttc aaggagacgc tggccctgga gctgcacgga
 660
 cacttgaaaca cgctctacgt ccacttcate ctctttgtctc gggagttcaa cctgctggac
 720
 cccaaagaga ccgccatcat ggacgacctc accgaggtgc tatgcagcgg gcccgccggg
 780
 gtccacagtg ggggcagtggt ggatggggcc ggcagcgggg gcccgggagc acagaaccac
 840
 gtgaaggaga gatgagcccc ccgggcccga caggggcaca cgtgtgcaaa gagacggtgg
 900
 tgtgtgttct ctctctgcatc tgcgtgtgca cacatgtgct gggccctctc agacctcacc
 960
 acacgcgt
 968

<210> 4534

<211> 284

<212> PRT

<213> Homo sapiens

<400> 4534

Thr	Arg	Ala	Gln	His	Met	Cys	Ala	His	Ala	Asp	Ala	Gly	Glu	Asn	Thr
1				5					10					15	
His	His	Arg	Leu	Phe	Ala	His	Val	Cys	Pro	Cys	Pro	Asp	Ala	Gly	Ala
			20					25					30		
Glu	Ala	Asp	Arg	Val	Gly	Gln	Arg	Ala	Arg	Arg	Pro	Arg	Ala	Ala	Met
		35				40						45			
Asp	Trp	Leu	Met	Gly	Lys	Ser	Lys	Ala	Lys	Pro	Asn	Gly	Lys	Lys	Pro
	50				55					60					
Ala	Ala	Glu	Glu	Arg	Lys	Ala	Tyr	Leu	Glu	Pro	Glu	His	Thr	Lys	Ala
65				70					75					80	
Arg	Ile	Thr	Asp	Phe	Gln	Phe	Lys	Glu	Leu	Val	Val	Leu	Pro	Arg	Glu
				85				90					95		
Ile	Asp	Leu	Asn	Glu	Trp	Leu	Ala	Ser	Asn	Thr	Thr	Thr	Phe	Phe	His
		100						105					110		
His	Ile	Asn	Leu	Gln	Tyr	Ser	Thr	Ile	Ser	Glu	Phe	Cys	Thr	Gly	Glu

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      115              120              125
Thr Cys Gln Thr Met Ala Val Cys Asn Thr Gln Tyr Trp Tyr Asp
  130              135              140
Glu Arg Gly Lys Lys Val Lys Cys Thr Ala Pro Gln Tyr Val Asp Phe
  145              150              155              160
Val Met Ser Ser Val Gln Lys Leu Val Thr Asp Glu Asp Val Phe Pro
      165              170              175
Thr Lys Tyr Gly Arg Glu Phe Pro Ser Ser Phe Glu Ser Leu Val Arg
      180              185              190
Lys Ile Cys Arg His Leu Phe His Val Leu Ala His Ile Tyr Trp Ala
      195              200              205
His Phe Lys Glu Thr Leu Ala Leu Glu Leu His Gly His Leu Asn Thr
      210              215              220
Leu Tyr Val His Phe Ile Leu Phe Ala Arg Glu Phe Asn Leu Leu Asp
      225              230              235              240
Pro Lys Glu Thr Ala Ile Met Asp Asp Leu Thr Glu Val Leu Cys Ser
      245              250              255
Gly Ala Gly Gly Val His Ser Gly Gly Ser Gly Asp Gly Ala Gly Ser
      260              265              270
Gly Gly Pro Gly Ala Gln Asn His Val Lys Glu Arg
      275              280

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<210> 4535

<211> 473

<212> DNA

<213> Homo sapiens

<400> 4535

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cagtggcacg atcacagctc actgcaacct ctgcctccca ggttcaagca gttctctngc
120
ctcagcctcc cgagtagctg ggattacagg cgtccgccac cagcctccgc taatttttgc
180
atttttagta gaaacggggg ttcaccatct cggccaggct ggtcttgaac tcttgacctc
240
atgatccatc cgccttggcc tcccaaagtg ctgggattac aggcattgagc taccgcgccc
300
ggccttggct gcagattaac gggaatacct cccttgggct tcctagtgga cactgtgata
360
ttcggtatga cctcccttgc tctattcctt ggaagaagta caggcactgg tcaagagtgc
420
cggggaccca cattgcctgg ttttgaatcc cagcacctcc acatgttacg cgt
473

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<210> 4536

<211> 75

<212> PRT

<213> Homo sapiens

<400> 4536

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Arg Leu Phe Phe Phe Phe Phe Glu Met Glu Ser Arg Ser Val Thr
  1              5              10              15
Gln Ala Gly Val Gln Trp His Asp His Ser Ser Leu Gln Pro Leu Pro

```

	20		25		30										
Pro	Arg	Phe	Lys	Gln	Phe	Ser	Xaa	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp
	35		40		45										
Tyr	Arg	Arg	Pro	Pro	Pro	Arg	Pro	Ala	Asn	Phe	Cys	Ile	Phe	Ser	Arg
	50		55		60										
Asn	Gly	Val	Ser	Pro	Ser	Arg	Pro	Gly	Trp	Ser					
65			70		75										

<210> 4537

<211> 2811

<212> DNA

<213> Homo sapiens

<400> 4537

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300
gaggagngca gtagcagagg tgctagacca tcgaccatc gagccgaaac actgccctcc
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420
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480
atcctggact gtgtcaacat ggacctaaa attggaaagg caaccccaaa ggacagcaaa
540
tatgtggaga aactagaggc ccttttccca gacctacca agagaaatga tatatttgat
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tccatacaa aggcaaagtt tgatgtatca ggactgacca ctgagcagat gctgagaaaa
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720
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1080
gatgtgtcca gggagcaagt ggacaaggaa ttggacaggg caagtaactc cctgatttct
1140
ggactgagtc aagatgagga ggaccctccg ctgccccga cggccatgaa cagcttgggt
1200

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gatgagtgcc ctctagatca ggggctgcct aaactctctg ctgaggccgt cttcagaag
1260
tgcaagtcaga tctcactgtc acagtctacc acagcctccc tgtccaagaa gtgactgttg
1320
agaggcgagg aggtagtggg tgaggctacc tgactcactt caaatgcatg ttttgagatg
1380
tttgagatt cagcaattct gtcttcattg ctccaggatc tggataactg ttctcataaa
1440
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2160
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2580
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2640
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2700
agtgggtgta tcatgaacca aaggaattta tgttttgtaa cttgggtact ttattttgca
2760
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2811

<210> 4538
 <211> 437
 <212> PRT
 <213> Homo sapiens

<400> 4538

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Xaa Ala Trp His Glu Gly Asn Glu Ala Cys Asp Leu Asp Ser Thr Val
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Ser Ala Leu Ala Leu Ala Phe Tyr Leu Ala Lys Thr Thr Glu Ala Glu
      20              25              30
Glu Val Phe Val Pro Val Leu Asn Ile Lys Arg Ser Glu Leu Pro Leu
      35              40              45
Arg Gly Asp Ile Val Phe Phe Leu Gln Lys Val His Ile Pro Glu Ser
      50              55              60
Ile Leu Ile Phe Arg Asp Glu Ile Asp Leu His Ala Leu Tyr Gln Ala
      65              70              75              80
Gly Gln Leu Thr Leu Ile Leu Val Asp His His Ile Leu Ser Lys Ser
      85              90              95
Asp Thr Ala Leu Glu Glu Xaa Ser Ser Arg Gly Ala Arg Pro Ser Thr
      100             105             110
His Arg Ala Glu Thr Leu Pro Ser Leu Xaa His Val Ser Val Glu Leu
      115             120             125
Val Gly Ser Cys Ala Thr Leu Val Thr Glu Arg Ile Leu Gln Gly Ala
      130             135             140
Pro Glu Ile Leu Asp Arg Gln Thr Ala Ala Leu Leu His Gly Thr Ile
      145             150             155             160
Ile Leu Asp Cys Val Asn Met Asp Leu Lys Ile Gly Lys Ala Thr Pro
      165             170             175
Lys Asp Ser Lys Tyr Val Glu Lys Leu Glu Ala Leu Phe Pro Asp Leu
      180             185             190
Pro Lys Arg Asn Asp Ile Phe Asp Ser Leu Gln Lys Ala Lys Phe Asp
      195             200             205
Val Ser Gly Leu Thr Thr Glu Gln Met Leu Arg Lys Asp Gln Lys Thr
      210             215             220
Ile Tyr Arg Gln Gly Val Lys Val Ala Ile Ser Ala Ile Tyr Met Asp
      225             230             235             240
Leu Glu Ala Phe Leu Gln Arg Ser Asn Leu Leu Ala Asp Leu His Ala
      245             250             255
Phe Cys Gln Ala His Ser Tyr Asp Val Leu Val Ala Met Thr Ile Phe
      260             265             270
Phe Asn Thr His Asn Glu Pro Val Arg Gln Leu Ala Ile Phe Cys Pro
      275             280             285
His Val Ala Leu Gln Thr Thr Ile Cys Glu Val Leu Glu Arg Ser His
      290             295             300
Ser Pro Pro Leu Lys Leu Thr Pro Ala Ser Ser Thr His Pro Asn Leu
      305             310             315             320
His Ala Tyr Leu Gln Gly Asn Thr Gln Val Ser Arg Lys Lys Leu Leu
      325             330             335
Pro Leu Leu Gln Glu Ala Leu Ser Ala Tyr Phe Asp Ser Met Lys Ile
      340             345             350
Pro Ser Gly Gln Pro Glu Thr Ala Asp Val Ser Arg Glu Gln Val Asp
      355             360             365
Lys Glu Leu Asp Arg Ala Ser Asn Ser Leu Ile Ser Gly Leu Ser Gln

```

```

      370              375              380
Asp Glu Glu Asp Pro Pro Leu Pro Pro Thr Pro Met Asn Ser Leu Val
385              390              395              400
Asp Glu Cys Pro Leu Asp Gln Gly Leu Pro Lys Leu Ser Ala Glu Ala
              405              410              415
Val Phe Glu Lys Cys Ser Gln Ile Ser Leu Ser Gln Ser Thr Thr Ala
              420              425              430
Ser Leu Ser Lys Lys
435

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<210> 4539
<211> 331
<212> DNA
<213> Homo sapiens

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<400> 4539
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120
tcacctggaa actccagcaa gagcagagggc aggtggagga gctgaggatg cagcttcaga
180
agcagaaaaa gaataactgt tcagagaaga agccgctgcc ttctctggct gcctccatca
240
agcaagaaga ggctgtctcc agctgtcctt ttgcatccca agtacctgtg aaaagacaaa
300
gcagcagctc aaagtgtcac ccaccggctt g
331

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<210> 4540
<211> 99
<212> PRT
<213> Homo sapiens

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<400> 4540
Met Gly Ala Leu Phe Leu Leu Ser Trp Met Gly Trp Thr Pro Arg Lys
1      5      10      15
Thr Arg Ser Leu Gly Glu Asn Gln Arg Val Ile Asn Glu Leu Thr Trp
20      25      30
Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu Leu Arg Met Gln Leu
35      40      45
Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Lys Lys Pro Leu Pro Phe
50      55      60
Leu Ala Ala Ser Ile Lys Gln Glu Glu Ala Val Ser Ser Cys Pro Phe
65      70      75      80
Ala Ser Gln Val Pro Val Lys Arg Gln Ser Ser Ser Ser Lys Cys His
85      90      95
Pro Pro Ala

```

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<210> 4541
<211> 452
<212> DNA
<213> Homo sapiens

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<400> 4541
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 120
 tccagtctga gaaccataaa aaatcttcac tccagacaca aagatgtctt tctcttgaag
 180
 ggagacataa ccatttgtca tcaaatacctg agctgctttt ggaacagatt tttcctgtaa
 240
 gttcttggccc tgcgtcttga tgacaatctg gacacaaatc caaaggctaa tgctaacagc
 300
 aaagcccaaa taaatgtaaa acctgtttat ccacaatgat attaaagggtg agaagagggtc
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 420
 ctggagagcc cgatgattcg cactgggtact gc
 452

<210> 4542
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 4542
 Met Asp Pro Ser Ala Asp Thr Trp Asp Leu Phe Ser Pro Leu Ile Ser
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 Leu Trp Ile Asn Arg Phe Tyr Ile Tyr Leu Gly Phe Ala Val Ser Ile
 20 25 30
 Ser Leu Trp Ile Cys Val Gln Ile Val Ile Lys Thr Gln Gly Lys Asn
 35 40 45
 Leu Gln Glu Lys Ser Val Pro Lys Ala Ala Gln Asp Leu Met Thr Asn
 50 55 60
 Gly Tyr Val Ser Leu Gln Glu Lys Asp Ile Phe Val Ser Gly Val Lys
 65 70 75 80
 Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Lys Gly Phe Ala Thr Val
 85 90 95
 Leu Ala Glu Ala Val Thr Ser Leu Asp Leu Pro Val Ala Ile Ile Asn
 100 105 110
 Leu Lys Glu Tyr Asp Pro Asp Asp His Leu Ile Glu Glu Val Thr Ser
 115 120 125

<210> 4543
 <211> 815
 <212> DNA
 <213> Homo sapiens

<400> 4543
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 agggaggagg gagagcgagt cactgcaggt ccttggcctg cggctccgcc gtggctgcct
 120
 gaggcccccgc gcaccaatgc ttgcaacttt gctcgcgccg acaccctgcg ggccagagct
 180

cctctgccgc ccaccgggct aacccttccg ggccctacca ctcccagatg gctctgctta
 240
 tccggccact gaetccggct cctcggaagc agggccaccc tcctgaaatg gcttggaacg
 300
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 360
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 420
 gcagagggct ctgactgggg acccaagaag ggctgggtgt gccgccaccg ctgccccgtc
 480
 accatcactg tgctgaagag ctcgaggctg gggccacccg cgcgggcccc acgttctccc
 540
 ccgggctcag gtcaggggcca gggagtgacc agaaggtgct gaccctgtgg cctgactggc
 600
 ccagagctca cccctgaaca tgagcaagcg caaagaaacc cccatccctg ctccccaaaa
 660
 agggcgcccc caaggccatt ttgaaggtgg ggggaagccc ggattccgag aaaccgcaac
 720
 cagccgtcta cctcaggaag ctcgctaggg aggagcgcat tctatgtgac taatcgggac
 780
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 815

<210> 4544

<211> 150

<212> PRT

<213> Homo sapiens

<400> 4544

Met Val Thr Gly Gln Arg Trp Arg His Ser Gln Pro Phe Leu Gly Pro
 1 5 10 15
 Gln Ser Glu Pro Ser Ala Leu Pro Gly Leu Asp Leu Phe Leu Asn Ser
 20 25 30
 His Lys Leu Gln Gly Ala Ala Val Ser Leu Ala Arg His Trp Pro
 35 40 45
 Ile Thr Ser Asn Arg Leu Gly Arg Ala Pro Val Glu Ser Pro Val Pro
 50 55 60
 Ser His Phe Arg Arg Val Ala Leu Leu Pro Arg Ser Arg Ser Gln Trp
 65 70 75 80
 Pro Asp Lys Gln Ser His Ser Gly Val Val Arg Pro Gly Arg Val Ser
 85 90 95
 Pro Val Gly Gly Arg Gly Ala Leu Ala Arg Arg Val Ser Gly Glu Ala
 100 105 110
 Lys Cys Lys Ala Leu Val Arg Gly Ala Ser Gly Ser His Gly Gly Ala
 115 120 125
 Ala Gly Gln Gly Pro Ala Val Thr Arg Ser Pro Ser Ser Leu Cys Leu
 130 135 140
 Ala Leu Val Ser Thr Gly
 145 150

<210> 4545

<211> 3568

<212> DNA

<213> Homo sapiens

<400> 4545
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120
gacagaaatg cagaggagaa aaagcgttta tctcttcagc gagaaaagat tatcgcaagg
180
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240
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300
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360
gatgaaactc ttcaggctgc agtttagagaa attttggccc taattggcta tgtggatcca
420
gtgaaaagga gaggaatccg aattctctca attgatgggt gaggaacaag gggcgtgggt
480
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540
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720
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1380
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1440
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1560

cgatatgaatt ctggagaatc ctgaaaaaga cgggtgcttca accagcttgc atagcacaga
1620
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2700
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2760
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2820
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2940
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3180

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 3420
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 3480
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 3568

<210> 4546

<211> 380

<212> PRT

<213> Homo sapiens

<400> 4546

Glu	Arg	Ile	Ile	Pro	Tyr	Leu	Leu	Arg	Leu	Arg	Gln	Ile	Lys	Asp	Glu
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Thr	Leu	Gln	Ala	Ala	Val	Arg	Glu	Ile	Leu	Ala	Leu	Ile	Gly	Tyr	Val
			20						25				30		
Asp	Pro	Val	Lys	Gly	Arg	Gly	Ile	Arg	Ile	Leu	Ser	Ile	Asp	Gly	Gly
		35						40				45			
Gly	Thr	Arg	Gly	Val	Val	Ala	Leu	Gln	Thr	Leu	Arg	Lys	Leu	Val	Glu
	50					55					60				
Leu	Thr	Gln	Lys	Pro	Val	His	Gln	Leu	Phe	Asp	Tyr	Ile	Cys	Gly	Val
65					70					75				80	
Ser	Thr	Gly	Ala	Ile	Leu	Ala	Phe	Met	Leu	Gly	Leu	Phe	His	Met	Pro
			85						90					95	
Leu	Asp	Glu	Cys	Glu	Glu	Leu	Tyr	Arg	Lys	Leu	Gly	Ser	Asp	Val	Phe
			100					105					110		
Ser	Gln	Asn	Val	Ile	Val	Gly	Thr	Val	Lys	Met	Ser	Trp	Ser	His	Ala
		115					120					125			
Phe	Tyr	Asp	Ser	Gln	Thr	Trp	Glu	Asn	Ile	Leu	Lys	Asp	Arg	Met	Gly
		130				135					140				
Ser	Ala	Leu	Met	Ile	Glu	Thr	Ala	Arg	Asn	Pro	Thr	Cys	Pro	Lys	Val
145					150					155				160	
Ala	Ala	Val	Ser	Thr	Ile	Val	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Ala	Phe
			165						170					175	
Val	Phe	Arg	Asn	Tyr	Gly	His	Phe	Pro	Gly	Ile	Asn	Ser	His	Tyr	Leu
			180					185					190		
Gly	Gly	Cys	Gln	Tyr	Lys	Met	Trp	Gln	Ala	Ile	Arg	Ala	Ser	Ser	Ala
		195					200					205			
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<210> 4548

<211> 515

<212> PRT

<213> Homo sapiens

<400> 4548

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460

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<210> 4549

<211> 2927

<212> DNA

<213> Homo sapiens

<400> 4549

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<211> 908

<212> PRT

<213> Homo sapiens

<400> 4550

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Tyr	Val	Glu	Thr	Val	Asp	Ile	Asp	Gly	Glu	Thr	Asn	Leu	Lys	Phe	Arg
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Gln	Ala	Leu	Met	Val	Thr	His	Lys	Glu	Leu	Ala	Thr	Ile	Lys	Lys	Met
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Ala	Ser	Phe	Gln	Gly	Thr	Val	Thr	Cys	Glu	Ala	Pro	Asn	Ser	Arg	Met
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His	His	Phe	Val	Gly	Cys	Leu	Glu	Trp	Asn	Asp	Lys	Lys	Tyr	Ser	Leu
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Phe	Asp	Thr	Lys	Ile	Met	Lys	Asn	Cys	Gly	Lys	Ile	His	Leu	Lys	Arg
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Val	Lys	Glu	Phe	Lys	Asp	His	His	Tyr	Tyr	Leu	Ser	Gly	Val	His	Gly
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Ser	Ser	Val	Ala	Ala	Glu	Ser	Phe	Phe	Val	Phe	Trp	Ser	Phe	Leu	Ile
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Arg	Gly	Arg	Ala	Gly	Val	Leu	Ala	Pro	Ala	Gly	His	Leu	Pro	His	Gly
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 Val Lys Lys Tyr His Gln Val Val Thr Leu Ala Ile Gly Asp Gly Ala
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 Gly Gln Glu Gly Met Gln Ala Val Gln Asn Ser Asp Phe Val Leu Gly
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 Gln Phe Cys Phe Leu Gln Arg Leu Leu Val His Gly Arg Trp Ser
 740 745 750
 Tyr Val Arg Ile Cys Lys Phe Leu Arg Tyr Phe Phe Tyr Lys Ser Met
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 Ala Ser Met Met Val Gln Val Trp Phe Ala Cys Tyr Asn Gly Phe Thr

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Val Val Gly Gln Lys Asp Glu Leu Phe Asn Tyr Trp Val Phe Val Gln
      805              810              815
Ala Ile Ala His Gly Val Thr Thr Ser Leu Val Asn Phe Phe Met Thr
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Leu Trp Ile Ser Arg Asp Thr Ala Gly Pro Ala Ser Phe Ser Asp His
      835              840              845
Gln Ser Phe Ala Val Val Val Ala Leu Ser Cys Leu Leu Ser Ile Thr
      850              855              860
Met Glu Val Ile Leu Ile Ile Lys Tyr Trp Thr Ala Leu Cys Val Ala
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Thr Ile Leu Leu Ser Leu Gly Phe Tyr Ala Ile Met Thr Thr Thr Thr
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<210> 4551

<211> 361

<212> DNA

<213> Homo sapiens

<400> 4551

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<210> 4552

<211> 100

<212> PRT

<213> Homo sapiens

<400> 4552

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<210> 4554

<211> 705

<212> PRT

<213> Homo sapiens

<400> 4554

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Pro	Ala	Asn	Thr	Gln	Ile	Leu	Leu	Leu	Gln	Thr	Asn	Asn	Ile	Ala	Lys
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Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val	Lys	Lys	Met
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Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu	Thr	Glu	Leu
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Tyr	Ile	His	Pro	Asn	Ala	Phe	Phe	Arg	Leu	Pro	Lys	Leu	Glu	Ser	Leu
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Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile Arg
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Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe Gln
385          390          395          400
Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile Cys
          405          410          415
Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val Glu
          420          425          430
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465          470          475          480
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Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val Ile
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Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly Glu
          660          665          670
Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys Ser
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Ser
705

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<210> 4555

<211> 1128

<212> DNA

<213> Homo sapiens

<400> 4555

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<212> PRT

<213> Homo sapiens

<400> 4556

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Leu	Asp	Thr	Pro	Gly	Val	Leu	Ala	Pro	Arg	Ile	Glu	Ser	Val	Glu	Thr
			20					25				30			
Gly	Leu	Lys	Leu	Ala	Leu	Cys	Gly	Thr	Val	Leu	Asp	His	Leu	Val	Gly
		35				40					45				
Glu	Glu	Thr	Met	Ala	Asp	Tyr	Leu	Leu	Tyr	Thr	Leu	Asn	Lys	His	Gln
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<210> 4557

<211> 446

<212> DNA

<213> Homo sapiens

<400> 4557

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<210> 4558

<211> 148

<212> PRT

<213> Homo sapiens

<400> 4558

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Lys Ala Val Arg Cys Ala Gln Asp His Leu Gly His Ser His Pro Pro
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Glu Thr Ser Arg Ala Phe Leu Pro Pro Pro Ser Asp Val Arg Val Arg
50           55           60
Ser Cys Leu Tyr His Trp Ser Ala Thr Ala His Leu Pro Pro Leu Ser
65           70           75           80
Lys Lys Pro Pro Cys Thr Ile Ser His Leu Arg Pro Leu Leu Gly Leu
85           90           95
Pro Pro Pro Ser Asp Leu His Ile Pro Ser Ala Ala Thr Leu Gly Pro
100          105          110
Cys Met His Trp Pro Pro Pro Ser Asp Ala Pro Cys Thr Ile Ser Leu
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Thr Ser Thr Arg
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<210> 4559

<211> 919

<212> DNA

<213> Homo sapiens

<400> 4559

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<210> 4560

<211> 126

<212> PRT

<213> Homo sapiens

<400> 4560

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35          40          45
Gly Tyr Phe Glu Asn Ile Pro Lys Gly Leu Asp Gln Glu Gly Trp Thr
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Arg Gly Gly Ile Gln Pro Gln Met Pro Gly Gly Tyr Ala Leu Ser Gln
65          70          75          80
Pro Val Ser Cys Met Glu Ala Thr Pro Asn Pro Met Glu Ser Leu Arg

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<210> 4562

<211> 1182

<212> PRT

<213> Homo sapiens

<400> 4562

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 Asn Ile Ile Leu Tyr Asp Pro Ser Lys Ile Ile Ala Gly Asp Lys Glu
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 Val Val Ile Ala Gln Asn Asp Lys His Thr Gly Pro Val Arg Ala Leu
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 Pro Gly Ala Lys Thr Gln Pro Pro Glu Asp Ile Ser Cys Ile Ala Trp
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 1140 1145 1150
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<211> 2037

<212> DNA

<213> Homo sapiens

<400> 4563

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 4564

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			20					25					30		
Asp	Glu	Asp	Gly	Leu	Val	Val	Leu	Val	Phe	Asn	Lys	Lys	Glu	Thr	Glu
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Glu	Gln	Ala	Asn	Ile	Lys	Thr	Gln	Leu	Gln	Gln	Leu	Gly	Val	Thr	Leu
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Gln	Asn	Pro	Pro	Ala	Gly	Val	Asp	Pro	Ile	Ile	Trp	Glu	Gln	Ala	Lys
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Val	Asp	Asn	Pro	Asp	Ser	Glu	Lys	Leu	Ile	Pro	Val	Pro	Met	Val	Gly
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Phe	Lys	Glu	Leu	Leu	Arg	Arg	Leu	Lys	Val	Gln	Asp	Gln	Met	Thr	Lys
			180				185					190			
Gln	His	Gln	Thr	Arg	Leu	Asp	Ile	Ile	Ser	Glu	Asp	Ile	Ser	Glu	Leu
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Glu	Ile	Gln	Arg	Lys	Ser	Gly	Tyr	Ala	Ile	Gln	Ala	Asp	Glu	Glu	Gln
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Gln	Phe	Lys	Gly	Arg	Leu	Asn	Glu	Leu	Met	Ser	Gln	Ile	Arg	Met	Gln
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Asn	His	Phe	Gly	Ala	Val	Arg	Ser	Glu	Glu	Arg	Tyr	Tyr	Ile	Asp	Ala
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<211> 247

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<213> Homo sapiens

<400> 4566

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 Gln Ser Pro Pro Ile Val Glu Leu Arg Glu Lys Ile Gln Pro Glu Ile
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 65 70 75 80
 Ser Phe Arg Lys Ile Gly Asn Arg Arg Arg Gln Glu Arg Phe Trp Tyr

85 90 95
 Cys Arg Leu Ala Leu Asn His Lys Val Leu His Tyr Gly Asp Leu Asp
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 Pro Val Ala Asp Ile Lys Ala Ile Val Thr Gly Lys Asp Cys Pro His
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<210> 4567

<211> 1211

<212> DNA

<213> Homo sapiens

<400> 4567

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<400> 4568

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Leu	Arg	Gly	Gln	Ser	Val	Gln	Gln	Val	Gly	Pro	Gln	Gly	Leu	Leu	Tyr
		35					40				45				
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		50				55				60					
Ser	Ile	Leu	Gly	Ser	Asp	Ala	Thr	Thr	Cys	His	Ile	Val	Val	Leu	
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Arg	His	Thr	Gly	Asn	Gly	Ala	Thr	Cys	Leu	Thr	His	Cys	Asp	Gly	Thr
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Asp	Thr	Lys	Ala	Glu	Val	Pro	Leu	Ile	Met	Asn	Ser	Ile	Lys	Ser	Phe
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Ser	Asp	His	Ala	Gln	Cys	Gly	Arg								
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<210> 4569

<211> 1797

<212> DNA

<213> Homo sapiens

<400> 4569

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 240

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<210> 4570

<211> 141

<212> PRT

<213> Homo sapiens

<400> 4570

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      20             25             30
Gln Thr Trp His Ile Arg Phe Gly Asp Asn Gly Leu Gly Thr Leu Met
      35             40             45
Leu Leu Gly Pro Gly Glu Thr Val Leu Arg Gln Lys Leu Gly Val Gln
      50             55             60
Gly Gly Pro Arg Val Arg His Cys Gly Glu Gly Asn Ala Gly Glu Ser
65             70             75             80
Gly Pro Thr Leu Gln Leu Gly Thr Arg Gly Arg Lys Gln Arg Gly Gln
      85             90             95
Ala Ser Val Pro Leu Pro Gln Glu Gln Thr Ser Gly Pro Gln Glu Gly
      100            105            110
Leu Gln Ala Ala Arg Ser Leu Pro Ser Ala Gly Gly Ser Arg Gly Arg
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Lys Gly Trp Arg Ala Ala Gly Arg Gln Pro Ser Thr Arg
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<210> 4571

<211> 1084

<212> DNA

<213> Homo sapiens

<400> 4571

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aacgagaaga gaaaagaaat gctgggaacg cagtacggag cgccatgaag tccgaggaac
240
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720

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<210> 4572

<211> 126

<212> PRT

<213> Homo sapiens

<400> 4572

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Lys	Thr	Gln	Gln	Asn	Arg	Lys	Leu	Thr	Asp	Phe	Tyr	Pro	Val	Arg	Arg
			20					25					30		
Ser	Ser	Arg	Lys	Ser	Lys	Ala	Glu	Leu	Gln	Ser	Glu	Glu	Arg	Lys	Arg
		35					40					45			
Ile	Asp	Glu	Leu	Ile	Glu	Ser	Gly	Lys	Glu	Glu	Gly	Met	Lys	Ile	Asp
	50					55					60				
Leu	Ile	Asp	Gly	Lys	Gly	Arg	Gly	Val	Ile	Ala	Thr	Lys	Gln	Phe	Ser
65				70						75				80	
Arg	Gly	Asp	Phe	Val	Val	Glu	Tyr	His	Gly	Asp	Leu	Ile	Glu	Ile	Thr
			85					90						95	
Asp	Ala	Lys	Lys	Arg	Glu	Ala	Leu	Tyr	Ala	Gln	Asp	Pro	Ser	Thr	Gly
			100					105					110		
Cys	Tyr	Met	Tyr	Tyr	Phe	Gln	Tyr	Leu	Ser	Lys	Thr	Tyr	Trp		
		115					120						125		

<210> 4573

<211> 309

<212> DNA

<213> Homo sapiens

<400> 4573

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309

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<211> 103
<212> PRT
<213> Homo sapiens

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35 40 45
Ala Gly Ala Val Gly Thr Pro Gly Lys Arg Gly Pro Ser Gly Pro Gln
50 55 60
Gly Leu Leu Gly Pro Pro Gly Pro Pro Ala Pro Val Gly Pro Pro His
65 70 75 80
Ala Arg Ile Ser Gln His Gly Asp Pro Leu Leu Ser Asn Thr Phe Thr
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Glu Thr Asn Pro Phe Thr Arg
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<210> 4575
<211> 1068
<212> DNA
<213> Homo sapiens

<400> 4575
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240
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360
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420
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720

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<210> 4576

<211> 107

<212> PRT

<213> Homo sapiens

<400> 4576

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			20					25						30	
Pro	Ala	Arg	His	Val	Ala	Thr	Ala	Gln	Gly	Glu	Val	Leu	Pro	Pro	Gly
			35					40						45	
Gly	Leu	Gly	Gly	Ala	Ala	Gln	Arg	Ala	Arg	Gly	Gln	Ser	His	Gly	Gly
	50					55					60				
Thr	Val	Pro	Gly	Asn	Ala	Pro	Ala	Ala	Asp	Leu	Leu	Ala	Leu	Ser	Pro
65				70					75					80	
Arg	Leu	Glu	Arg	Ser	Gly	Thr	Ile	Ser	Thr	His	Cys	Lys	Leu	Arg	Leu
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<210> 4577

<211> 3525

<212> DNA

<213> Homo sapiens

<400> 4577

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<210> 4578

<211> 1007

<212> PRT

<213> Homo sapiens

<400> 4578

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 20          25          30
Leu Ala Ser Gly Asp Arg Ser Gly Asn Leu Arg Gln Val Gly Pro Gly
 35          40          45
Ser Val Gln Cys Thr Pro Pro Ser Ser Ser Ser Gly Ser Gln Gly Ser
 50          55          60
Gly Gln Lys Pro Trp Pro Trp His Leu Leu Leu Ile Gly Asn Glu
 65          70          75          80
Gly Leu Ile His Glu Leu His Phe Met Asp Glu Leu Val Lys Val Glu
 85          90          95
Ala His Asp Ala Glu Val Leu Cys Leu Glu Tyr Ser Lys Pro Glu Thr
100          105          110
Gly Leu Thr Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu Ile His Val
115          120          125
Leu Asn Val Glu Lys Asn Tyr Asn Leu Glu Gln Thr Leu Asp Asp His
130          135          140
Ser Ser Ser Ile Thr Ala Ile Lys Phe Ala Gly Asn Arg Asp Ile Gln
145          150          155          160
Met Ile Ser Cys Gly Ala Asp Lys Ser Ile Tyr Phe Arg Ser Ala Gln
165          170          175
Gln Gly Ser Asp Gly Leu His Phe Val Arg Thr His His Val Ala Glu
180          185          190
Lys Thr Thr Leu Tyr Asp Met Asp Ile Asp Ile Thr Gln Lys Tyr Val
195          200          205
Ala Val Ala Cys Gln Asp Arg Asn Val Arg Val Tyr Asn Thr Val Asn
210          215          220
Gly Lys Gln Lys Lys Cys Tyr Lys Gly Ser Gln Gly Asp Glu Gly Ser
225          230          235          240
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245          250          255
Cys Ser Asp Lys Ser Ile Ser Val Ile Asp Phe Tyr Ser Gly Glu Cys
260          265          270
Ile Ala Lys Met Phe Gly His Ser Gly Gly Cys Ala Ser Leu Leu Gly
275          280          285
Met Pro Pro His Pro Pro Thr Pro Ser Asp Ser Glu Gly Lys Cys Ser
290          295          300
Leu Ser Ala Leu Phe Ala Glu Ile Ile Thr Ser Met Lys Phe Thr Tyr
305          310          315          320
Asp Cys His His Leu Ile Thr Val Ser Gly Asp Ser Cys Val Phe Ile
325          330          335
Trp His Leu Gly Pro Glu Ile Thr Asn Cys Met Lys Gln His Leu Leu
340          345          350
Glu Ile Asp His Arg Gln Gln Gln His Thr Asn Asp Lys Lys Arg
355          360          365
Ser Gly His Pro Arg Ser Trp Gln Pro Leu Pro Val His Gln Arg Asp
370          375          380
Glu Ser Leu Pro Gly Pro His Gly Val Met Leu Gly Thr Gln Ser Ser
385          390          395          400
Leu Pro Ala Asn Gln Arg Gln Ala Ala Thr Val Gly Lys Ala Ala Gly

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Thr	Ile	Leu	Asp	Ala	Gln	Asp	Leu	Asp	Cys	Tyr	Phe	Thr	Pro	Met	Lys																		
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Pro	Glu	Ser	Leu	Glu	Asn	Ser	Ile	Leu	Asp	Ser	Leu	Glu	Pro	Gln	Ser																		
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Leu	Ala	Ser	Leu	Leu	Ser	Glu	Gln	Lys	Glu	Ser	Ser	Glu	Ala	Ser	Glu																		
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										625											630											635	
Pro	Glu	Val	Lys	Leu	Met	Asp	Arg	Gly	Gly	Ser	Gln	Pro	Arg	Ala	Gly																		
										645											650											655	
Thr	Gly	Tyr	Ala	Ser	Pro	Asp	Arg	Thr	His	Ser	Val	Pro	Ser	Ala	Ser																		
										660											665											670	
Val	Thr	Ala	Pro	Cys	Leu	Thr	Ser	Leu	Ala	Ser	Cys	Val	Pro	Ala	Ser																		
										675											680											685	
Ser	Val	Leu	Pro	Thr	Asp	Arg	Asn	Leu	Pro	Thr	Pro	Thr	Ser	Ala	Pro																		
										690											695											700	
Thr	Pro	Gly	Leu	Ala	Gln	Gly	Val	His	Ala	Pro	Ser	Thr	Cys	Ser	Tyr																		
										705											710											715	
Met	Glu	Ala	Thr	Ala	Ser	Ser	Arg	Ala	Arg	Ile	Ser	Arg	Ser	Ile	Ser																		
										725											730											735	
Leu	Gly	Asp	Ser	Glu	Gly	Pro	Ile	Val	Ala	Thr	Leu	Ala	Gln	Pro	Leu																		
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Arg	Arg	Pro	Ser	Ser	Val	Gly	Glu	Leu	Ala	Ser	Leu	Gly	Gln	Glu	Leu																		
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Gln	Ala	Ile	Thr	Thr	Ala	Thr	Thr	Pro	Ser	Leu	Asp	Ser	Glu	Gly	Gln																		
										770											775											780	
Glu	Pro	Ala	Leu	Arg	Ser	Trp	Gly	Asn	His	Glu	Ala	Arg	Ala	Asn	Leu																		
										785											790											795	
Arg	Leu	Thr	Leu	Ser	Ser	Ala	Cys	Asp	Gly	Leu	Leu	Gln	Pro	Pro	Val																		
										805											810											815	
Asp	Thr	Gln	Pro	Gly	Val	Thr	Val	Pro	Ala	Val	Ser	Phe	Pro	Ala	Pro																		
										820											825											830	
Ser	Pro	Val	Glu	Glu	Ser	Ala	Leu	Arg	Leu	His	Gly	Ser	Ala	Phe	Arg																		

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      835              840              845
Pro Ser Leu Pro Ala Pro Glu Ser Pro Gly Leu Pro Ala His Pro Ser
  850              855              860
Asn Pro Gln Leu Pro Glu Ala Arg Pro Gly Ile Pro Gly Gly Thr Ala
  865              870              875              880
Ser Leu Leu Glu Pro Thr Ser Gly Trp Gly Thr Ser Cys Thr Gly Cys
      885              890              895
Arg Pro Pro Ser Lys Lys Pro Ser Thr Phe Thr Val Cys Trp Ser Pro
      900              905              910
Val Ala Arg Trp Thr Pro Gly Ser Ser Arg His Gly Leu Ser Trp Ser
      915              920              925
Pro Pro Ser Cys Gly Ser Thr Ala Ser Trp Arg Leu Asn Ala Trp Trp
      930              935              940
Gly Leu Val Trp Pro Gln Pro Arg Leu Cys Pro Ala Gln Asp Pro Arg
      945              950              955              960
Pro His Arg Arg Cys Thr Pro Trp Pro Ala Gln Thr Cys Arg Pro Cys
      965              970              975
Trp Asn Thr Thr Arg Ser Cys Trp Cys Arg Pro Cys Gly Gly Arg His
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Gly Gly Thr Glu Gly Ala Ala Pro Pro Pro Gln Pro Cys Cys Phe
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<210> 4579

<211> 321

<212> DNA

<213> Homo sapiens

<400> 4579

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120
accaactgca tgaagcagca cttgctggag attgaccacc ggcagcagca gcagcacaca
180
aatgacaaga agcggagtgg cccccccagg caggatacgt atgtgtccac acctagtga
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<210> 4580

<211> 107

<212> PRT

<213> Homo sapiens

<400> 4580

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Tyr Asp Cys His His Leu Ile Thr Val Ser Gly Asp Ser Cys Val Phe
      20              25              30
Ile Trp His Leu Gly Pro Glu Ile Thr Asn Cys Met Lys Gln His Leu
      35              40              45
Leu Glu Ile Asp His Arg Gln Gln Gln Gln His Thr Asn Asp Lys Lys

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50					55					60					
Arg	Ser	Gly	Pro	Pro	Arg	Gln	Asp	Thr	Tyr	Val	Ser	Thr	Pro	Ser	Glu
65					70					75					80
Ile	His	Ser	Leu	Ser	Pro	Gly	Glu	Gln	Thr	Glu	Asp	Asp	Leu	Glu	Glu
				85					90					95	
Glu	Cys	Glu	Pro	Glu	Glu	Met	Leu	Lys	Thr	Pro					
			100					105							

<210> 4581

<211> 1396

<212> DNA

<213> Homo sapiens

<400> 4581

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120
cgggagcgca ggtcagattc agaggaagag cggtggcagc gctcagggat gcgaagccgg
180
agcccccccg ggcaccaagt gcactcaaga gatgggtcct ctcagtcgga ctcaggagag
240
gagcagtcac ggggccagtg ggctcgccgg cgacggcgcg cacgctcgtg gtctcctagc
300
tcctcagcat ccagctcggc gtctccaggg cgatcccaga gccccggggc ggccgcggct
360
gccctgagcc agcagcagag cctgcaggag cggtcgcggc tgcgggagga gcggaagcag
420
caggaggagc tgatgaagcg ctccgagacg cccgaggaga agcgcgcacg gcggctggcc
480
aagaaggagg ccaaggagcg caagaagcgg gagaagatgg gctgggttga ggagtacatg
540
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660
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720
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780
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840
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900
aagtacatca gcgctgagga tgacgatctg gccggggaga tgcatgagcc ctacacgttc
960
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1020
gagctggagc agggcaagaa cgccgacttc tggcgggaca tgaccacat caccgaggac
1080
gagatctcca agctccgcaa gctggaggcc tcgggcaagg ggccagggtga gcgcgcgag
1140
gggggtcaacg cctccgtcag ctctgatgtg cagtcggtgt tcaaggggaa gacatacaac
1200

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cagctgcagg tcattctcca gggcatcgag ggcaaaatcc gcgctggtgg ccccaacctg
 1260
 gacatgggct actgggagag cctcctgcag cagcttcgtg cccacatggc gcgggcccgg
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<210> 4582

<211> 354

<212> PRT

<213> Homo sapiens

<400> 4582

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		20						25				30			
Glu	Leu	Met	Lys	Ala	Phe	Glu	Thr	Pro	Glu	Glu	Lys	Arg	Ala	Arg	Arg
		35					40				45				
Leu	Ala	Lys	Lys	Glu	Ala	Lys	Glu	Arg	Lys	Lys	Arg	Glu	Lys	Met	Gly
	50					55					60				
Trp	Gly	Glu	Glu	Tyr	Met	Gly	Tyr	Thr	Asn	Thr	Asp	Asn	Pro	Phe	Gly
65				70					75					80	
Asp	Asn	Asn	Leu	Leu	Gly	Thr	Phe	Ile	Trp	Asn	Lys	Ala	Leu	Glu	Lys
			85					90						95	
Lys	Gly	Ile	Ser	His	Leu	Glu	Glu	Lys	Glu	Leu	Lys	Glu	Arg	Asn	Lys
			100					105					110		
Arg	Ile	Gln	Glu	Asp	Asn	Arg	Leu	Glu	Leu	Gln	Lys	Val	Lys	Gln	Leu
			115				120					125			
Arg	Leu	Glu	Arg	Glu	Arg	Glu	Lys	Ala	Met	Arg	Glu	Gln	Glu	Leu	Glu
	130					135					140				
Met	Leu	Gln	Arg	Val	Lys	Gly	Thr	Glu	His	Phe	Lys	Thr	Trp	Glu	Glu
145				150						155				160	
Gln	Glu	Asp	Asn	Phe	His	Leu	Gln	Gln	Ala	Lys	Leu	Arg	Ser	Lys	Ile
			165						170					175	
Arg	Ile	Arg	Asp	Gly	Arg	Ala	Lys	Pro	Ile	Asp	Leu	Leu	Ala	Lys	Tyr
			180					185					190		
Ile	Ser	Ala	Glu	Asp	Asp	Asp	Leu	Ala	Gly	Glu	Met	His	Glu	Pro	Tyr
	195						200					205			
Thr	Phe	Leu	Asn	Gly	Leu	Thr	Val	Ala	Asp	Met	Glu	Asp	Leu	Leu	Glu
	210					215					220				
Asp	Ile	Gln	Val	Tyr	Met	Glu	Leu	Glu	Gln	Gly	Lys	Asn	Ala	Asp	Phe
225				230						235				240	
Trp	Arg	Asp	Met	Thr	Thr	Ile	Thr	Glu	Asp	Glu	Ile	Ser	Lys	Leu	Arg
			245					250					255		
Lys	Leu	Glu	Ala	Ser	Gly	Lys	Gly	Pro	Gly	Glu	Arg	Arg	Glu	Gly	Val
	260							265					270		
Asn	Ala	Ser	Val	Ser	Ser	Asp	Val	Gln	Ser	Val	Phe	Lys	Gly	Lys	Thr
	275					280						285			
Tyr	Asn	Gln	Leu	Gln	Val	Ile	Phe	Gln	Gly	Ile	Glu	Gly	Lys	Ile	Arg
	290					295					300				
Ala	Gly	Gly	Pro	Asn	Leu	Asp	Met	Gly	Tyr	Trp	Glu	Ser	Leu	Leu	Gln

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305          310          315          320
Gln Leu Arg Ala His Met Ala Arg Ala Arg Leu Arg Glu Arg His Gln
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<210> 4583
<211> 3350
<212> DNA
<213> Homo sapiens

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180
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240
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300
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720
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1080
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1140
gaactatgtg aaacttttct tgaaaaaatt gtttgtactc caggccaagg tcttggggac
1200

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 3350

<210> 4584
 <211> 923
 <212> PRT
 <213> Homo sapiens

<400> 4584
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 Trp Leu Gly Glu Leu Gln Arg Ser Val His Ala Trp Glu Ile Ser Asp
 35 40 45
 Gln Leu Leu Gln Ile Arg Gln Asp Val Glu Ser Cys Tyr Phe Ala Ala
 50 55 60
 Gln Thr Met Lys Met Lys Ile Gln Thr Ser Phe Tyr Glu Leu Pro Thr
 65 70 75 80
 Asp Ser His Ala Ser Leu Arg Asp Ser Leu Leu Thr His Ile Gln Asn
 85 90 95
 Leu Lys Asp Leu Ser Pro Val Ile Val Thr Gln Leu Ala Leu Ala Ile
 100 105 110
 Ala Asp Leu Ala Leu Gln Met Pro Ser Trp Lys Gly Cys Val Gln Thr
 115 120 125
 Leu Val Glu Lys Tyr Ser Asn Asp Val Thr Ser Leu Pro Phe Leu Leu
 130 135 140
 Glu Ile Leu Thr Val Leu Pro Glu Glu Val His Ser Arg Ser Leu Arg
 145 150 155 160
 Ile Gly Ala Asn Arg Arg Thr Glu Ile Ile Glu Asp Leu Ala Phe Tyr
 165 170 175
 Ser Ser Thr Val Val Ser Leu Leu Met Thr Cys Val Glu Lys Ala Gly
 180 185 190
 Thr Asp Glu Lys Met Leu Met Lys Val Phe Arg Cys Leu Gly Ser Trp
 195 200 205
 Phe Asn Leu Gly Val Leu Asp Ser Asn Phe Met Ala Asn Asn Lys Leu
 210 215 220
 Leu Ala Leu Leu Phe Glu Val Leu Gln Gln Asp Lys Thr Ser Ser Asn

225						230										235								240
Leu	His	Glu	Ala	Ala	Ser	Asp	Cys	Val	Cys	Ser	Ala	Leu	Tyr	Ala	Ile									
				245					250						255									
Glu	Asn	Val	Glu	Thr	Asn	Leu	Pro	Leu	Ala	Met	Gln	Leu	Phe	Gln	Gly									
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Val	Leu	Thr	Leu	Glu	Thr	Ala	Tyr	His	Met	Ala	Val	Ala	Arg	Glu	Asp									
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Thr	Phe	Leu	Glu	Lys	Ile	Val	Cys	Thr	Pro	Gly	Gln	Gly	Leu	Gly	Asp									
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Leu	Arg	Thr	Leu	Glu	Leu	Leu	Ile	Cys	Ala	Gly	His	Pro	Gln	Tyr										
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Glu	Val	Val	Glu	Ile	Ser	Phe	Asn	Phe	Trp	Tyr	Arg	Leu	Gly	Glu	His									
				340					345						350									
Leu	Tyr	Lys	Thr	Asn	Asp	Glu	Val	Ile	His	Gly	Ile	Phe	Lys	Ala	Tyr									
								360							365									
Ile	Gln	Arg	Leu	Leu	His	Ala	Leu	Ala	Arg	His	Cys	Gln	Leu	Glu	Pro									
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Asp	His	Glu	Gly	Val	Pro	Glu	Glu	Thr	Asp	Asp	Phe	Gly	Glu	Phe	Arg									
						390									400									
Met	Arg	Val	Ser	Asp	Leu	Val	Lys	Asp	Leu	Ile	Phe	Leu	Ile	Gly	Ser									
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Met	Glu	Cys	Phe	Ala	Gln	Leu	Tyr	Ser	Thr	Leu	Lys	Glu	Gly	Asn	Pro									
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Pro	Trp	Glu	Val	Thr	Glu	Ala	Val	Leu	Phe	Ile	Met	Ala	Ala	Ile	Ala									
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Lys	Ser	Val	Asp	Pro	Glu	Asn	Asn	Pro	Thr	Leu	Val	Glu	Val	Leu	Glu									
						455									460									
Gly	Val	Val	Arg	Leu	Pro	Glu	Thr	Val	His	Thr	Ala	Val	Arg	Tyr	Thr									
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<211> 1952

<212> DNA

<213> Homo sapiens

<400> 4585

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120					
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<210> 4586

<211> 530

<212> PRT

<213> Homo sapiens

<400> 4586

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Ile Leu Asp Leu Ser Glu Ser Gly Leu Cys Arg Leu Glu Glu Val Phe
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Arg Ile Pro Ser Leu Gln Gln Leu His Leu Gln Arg Asn Ala Leu Cys
 65          70          75          80
Val Ile Pro Gln Asp Phe Phe Gln Leu Leu Pro Asn Leu Thr Trp Leu
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Asp Leu Arg Tyr Asn Arg Ile Lys Ala Leu Pro Ser Gly Ile Gly Ala
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His Gln His Leu Lys Thr Leu Leu Leu Glu Arg Asn Pro Ile Lys Met
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Leu Pro Val Glu Leu Gly Ser Val Thr Thr Leu Lys Ala Leu Asn Leu
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Arg His Cys Pro Leu Glu Phe Pro Pro Gln Leu Val Val Gln Lys Gly
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Leu Val Ala Ile Gln Arg Phe Leu Arg Met Trp Ala Val Glu His Ser
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Leu Pro Arg Asn Pro Thr Ser Gln Glu Ala Pro Pro Val Arg Glu Met
180          185          190
Thr Leu Arg Asp Leu Pro Ser Pro Gly Leu Glu Leu Ser Gly Asp His
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Ala Ser Asn Gln Gly Ala Val Asn Ala Gln Asp Pro Glu Gly Ala Val
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Glu Glu Ile Arg Arg Phe Trp Lys Leu Arg Gln Glu Ile Val Glu His
260          265          270
Val Lys Ala Asp Val Leu Gly Asp Gln Leu Leu Thr Arg Glu Leu Pro
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Pro Asn Leu Lys Ala Ala Leu Asn Ile Glu Lys Glu Leu Pro Lys Pro
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Arg Glu Gln Arg Arg Phe His Gly Gln Ala Pro Leu Glu Glu Met Arg
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Lys Ala Ala Glu Asp Leu Glu Ile Ala Thr Glu Leu Gln Asp Glu Val
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Leu Lys Leu Lys Leu Gly Leu Thr Leu Asn Lys Asp Arg Arg Arg Ala
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Ala Leu Thr Gly Asn Leu Ser Leu Gly Leu Pro Ala Ala Gln Pro Gln
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<210> 4587

<211> 1723

<212> DNA

<213> Homo sapiens

<400> 4587

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<210> 4588

<211> 328

<212> PRT

<213> Homo sapiens

<400> 4588

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			20					25				30			
Pro	Ser	Lys	Lys	Gly	Glu	Thr	Pro	Thr	Val	Asp	Gly	Thr	Trp	Lys	Thr
			35					40				45			
Pro	Ser	Phe	Pro	Lys	Lys	Lys	Thr	Ala	Ala	Ser	Ser	Asn	Gly	Ser	Gly
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Gln	Pro	Leu	Asp	Lys	Lys	Ala	Ala	Val	Ser	Trp	Leu	Thr	Pro	Ala	Pro
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Ser	Lys	Lys	Ala	Asp	Ser	Val	Ala	Ala	Lys	Val	Asp	Leu	Leu	Gly	Glu
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Phe	Gln	Ser	Ala	Leu	Pro	Lys	Ile	Asn	Ser	His	Pro	Thr	Arg	Ser	Gln
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Lys	Lys	Ser	Ser	Gln	Lys	Lys	Ser	Ser	Lys	Lys	Asn	His	Pro	Gln	Lys
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Met Val Gly Thr Gly Pro Lys Gly His Val Ser Ser Leu Ala Arg Cys					
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Ser Ile Val Asn Tyr Asn Gly Asp Val Leu Tyr Asp Glu Tyr Ile Leu					
	180		185		190
Pro Pro Cys His Ile Val Asp Tyr Arg Thr Arg Trp Ser Gly Ile Arg					
	195		200		205
Lys Gln His Met Val Asn Ala Thr Pro Phe Lys Ile Ala Arg Gly Gln					
	210		215		220
Ile Leu Lys Ile Leu Thr Gly Lys Ile Val Val Gly His Ala Ile His					
225		230		235	240
Asn Asp Phe Lys Ala Leu Gln Tyr Phe His Pro Lys Ser Leu Thr Arg					
	245		250		255
Asp Thr Ser His Ile Pro Pro Leu Asn Arg Lys Ala Asp Cys Pro Glu					
	260		265		270
Asn Ala Thr Met Ser Leu Lys His Leu Thr Lys Lys Leu Leu Asn Arg					
	275		280		285
Asp Ile Gln Val Gly Lys Ser Gly His Ser Ser Val Glu Asp Ala Gln					
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Ala Thr Met Glu Leu Tyr Lys Leu Val Glu Val Trp Glu Glu His					
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Leu Ala Arg Asn Pro Pro Thr Asp					
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<210> 4589

<211> 585

<212> DNA

<213> Homo sapiens

<400> 4589

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<211> 121
 <212> PRT
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 35 40 45
 His Thr Leu Ser Pro Leu Ser Phe Arg Cys Ser Gln Arg Glu Pro Gln
 50 55 60
 Gly Phe Arg Pro Gly Met Arg Cys Gly Gly Ser Ser Leu Gly Arg Thr
 65 70 75 80
 Cys Cys Ser Pro Thr Arg Arg Ala Cys Val Val Ser Arg Ala Val Thr
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<210> 4591
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 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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Ala Pro Leu Trp Pro Ser Gly His Asp Arg Leu His Glu Thr Arg Lys			
	50	55	60
Leu Arg Cys Leu Ala Asp Arg Leu Val Ser Pro His Pro Ala Ser Ser			
65	70	75	80
Pro Gly Ser Arg Tyr Leu Pro Gln Asn Ser Leu His Lys Trp Pro Gln			
	85	90	95
Ala Cys Ala Gly Leu Trp Gly Phe Leu Pro Trp Ala Val Val Leu Gly			
	100	105	110
Met Cys Ser Pro Gln Ala Asp Gly Gln Leu Trp Glu Gly Trp Ser Cys			
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Trp Ser Gln Gly Trp Ala Gly Lys			
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<210> 4593

<211> 4783

<212> DNA

<213> Homo sapiens

<400> 4593

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<210> 4594

<211> 1145

<212> PRT

<213> Homo sapiens

<400> 4594

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 35 40 45
 Thr Val Thr Ser Lys Val Ala Pro Ser Trp Pro Glu Ser His Ser Ser
 50 55 60
 Ala Asp Ser Ala Ser Leu Ala Lys Lys Lys Pro Leu Phe Ile Thr Thr
 65 70 75 80
 Asp Ser Ser Lys Leu Val Ser Gly Val Leu Gly Ser Ala Leu Thr Ser
 85 90 95
 Gly Gly Pro Ser Leu Ser Ala Met Gly Asn Gly Arg Ser Ser Ser Pro
 100 105 110
 Thr Ser Ser Leu Thr Gln Pro Ile Glu Met Pro Thr Leu Ser Ser Ser
 115 120 125
 Pro Thr Glu Glu Arg Pro Thr Val Gly Pro Gly Gln Gln Asp Asn Pro
 130 135 140
 Leu Leu Lys Thr Phe Ser Asn Val Phe Gly Arg His Ser Gly Gly Phe
 145 150 155 160
 Leu Ser Ser Pro Ala Asp Phe Ser Gln Glu Asn Lys Ala Pro Phe Glu
 165 170 175
 Ala Val Lys Arg Phe Ser Leu Asp Glu Arg Ser Leu Ala Cys Arg Gln

180										185										190																			
Asp	Ser	Asp	Ser	Ser	Thr	Asn	Ser	Asp	Leu	Ser	Asp	Leu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Leu	Ser	Asp	Ser	Asp	Leu	Ser	Asp	Ser	Asp	Leu	Ser	Asp	Ser	Asp	Leu	Ser	Asp	Ser
195										200										205																			
Glu	Glu	Gln	Leu	Gln	Ala	Lys	Thr	Gly	Leu	Lys	Gly	Ile	Pro	Glu	His																								
210										215										220																			
Leu	Met	Gly	Lys	Leu	Gly	Pro	Asn	Gly	Glu	Arg	Ser	Ala	Glu	Leu	Leu																								
225										230										235																			
Leu	Gly	Lys	Ser	Lys	Gly	Lys	Gln	Ala	Pro	Lys	Gly	Arg	Pro	Arg	Thr																								
245										250										255																			
Ala	Pro	Leu	Lys	Val	Gly	Gln	Ser	Val	Leu	Lys	Asp	Val	Ser	Lys	Val																								
260										265										270																			
Lys	Lys	Leu	Lys	Gln	Ser	Gly	Glu	Pro	Phe	Leu	Gln	Asp	Gly	Ser	Cys																								
275										280										285																			
Ile	Asn	Val	Ala	Pro	His	Leu	His	Lys	Cys	Arg	Glu	Cys	Arg	Leu	Glu																								
290										295										300																			
Arg	Tyr	Arg	Lys	Phe	Lys	Glu	Gln	Glu	Gln	Asp	Asp	Ser	Thr	Val	Ala																								
305										310										315																			
Cys	Arg	Phe	Phe	His	Phe	Arg	Arg	Leu	Ile	Phe	Thr	Arg	Lys	Gly	Val																								
325										330										335																			
Leu	Arg	Val	Glu	Gly	Phe	Leu	Ser	Pro	Gln	Gln	Ser	Asp	Pro	Asp	Ala																								
340										345										350																			
Met	Asn	Leu	Trp	Ile	Pro	Ser	Ser	Ser	Leu	Ala	Glu	Gly	Ile	Asp	Leu																								
355										360										365																			
Glu	Thr	Ser	Lys	Tyr	Ile	Leu	Ala	Asn	Val	Gly	Asp	Gln	Phe	Cys	Gln																								
370										375										380																			
Leu	Val	Met	Ser	Glu	Lys	Glu	Ala	Met	Met	Met	Val	Glu	Pro	His	Gln																								
385										390										395																			
Lys	Val	Ala	Trp	Lys	Arg	Ala	Val	Arg	Gly	Val	Arg	Glu	Met	Cys	Asp																								
405										410										415																			
Val	Cys	Glu	Thr	Thr	Leu	Phe	Asn	Ile	His	Trp	Val	Cys	Arg	Lys	Cys																								
420										425										430																			
Gly	Phe	Gly	Val	Cys	Leu	Asp	Cys	Tyr	Arg	Leu	Arg	Lys	Ser	Arg	Pro																								
435										440										445																			
Arg	Ser	Glu	Thr	Glu	Glu	Met	Gly	Asp	Glu	Glu	Val	Phe	Ser	Trp	Leu																								
450										455										460																			
Lys	Cys	Ala	Lys	Gly	Gln	Ser	His	Glu	Pro	Glu	Asn	Leu	Met	Pro	Thr																								
465										470										475																			
Gln	Ile	Ile	Pro	Gly	Thr	Ala	Leu	Tyr	Asn	Ile	Gly	Asp	Met	Val	His																								
485										490										495																			
Ala	Ala	Arg	Gly	Lys	Trp	Gly	Ile	Lys	Ala	Asn	Cys	Pro	Cys	Ile	Ser																								
500										505										510																			
Arg	Gln	Asn	Lys	Ser	Val	Leu	Arg	Pro	Ala	Val	Thr	Asn	Gly	Met	Ser																								
515										520										525																			
Gln	Leu	Pro	Ser	Ile	Asn	Pro	Ser	Ala	Ser	Ser	Gly	Asn	Glu	Thr	Thr																								
530										535										540																			
Phe	Ser	Gly	Gly	Gly	Gly	Pro	Ala	Pro	Val	Thr	Thr	Pro	Glu	Pro	Asp																								
545										550										555																			
His	Val	Pro	Lys	Ala	Asp	Ser	Thr	Asp	Ile	Arg	Ser	Glu	Glu	Pro	Leu																								
565										570										575																			
Lys	Thr	Asp	Ser	Ser	Ala	Ser	Asn	Ser	Asn	Ser	Glu	Leu	Lys	Ala	Ile																								
580										585										590																			
Arg	Pro	Pro	Cys	Pro	Asp	Thr	Ala	Pro	Pro	Ser	Ser	Ala	Leu	His	Trp																								
595										600										605																			
Leu	Ala	Asp	Leu	Ala	Thr	Gln	Lys	Ala	Lys	Glu	Glu	Thr	Lys	Glu	Ala																								

610	615	620
Gly Ser Leu Arg Ser Val Leu Asn Lys Glu Ser His Ser Pro Phe Gly		
625	630	635
Leu Asp Ser Phe Asn Ser Thr Ala Lys Val Ser Pro Leu Thr Pro Lys		
	645	650
Leu Phe Asn Ser Leu Leu Leu Gly Pro Thr Ala Ser Asn Asn Lys Thr		
	660	665
Glu Gly Ser Ser Leu Arg Asp Leu Leu His Ser Gly Pro Gly Lys Leu		
	675	680
Pro Gln Thr Pro Leu Asp Thr Gly Ile Pro Phe Pro Pro Val Phe Ser		
	690	695
Thr Ser Ser Ala Gly Val Lys Ser Lys Ala Ser Leu Pro Asn Phe Leu		
	705	710
Asp His Ile Ile Ala Ser Val Val Glu Asn Lys Lys Thr Ser Asp Ala		
	725	730
Ser Lys Arg Ala Cys Asn Leu Thr Asp Thr Gln Lys Glu Val Lys Glu		
	740	745
Met Val Met Gly Leu Asn Val Leu Asp Pro His Thr Ser His Ser Trp		
	755	760
Leu Cys Asp Gly Arg Leu Leu Cys Leu His Asp Pro Ser Asn Lys Asn		
	770	775
Asn Trp Lys Ile Phe Arg Glu Cys Trp Lys Gln Gly Gln Pro Val Leu		
	785	790
Val Ser Gly Val His Lys Lys Leu Lys Ser Glu Leu Trp Lys Pro Glu		
	805	810
Ala Phe Ser Gln Glu Phe Gly Asp Gln Asp Val Asp Leu Val Asn Cys		
	820	825
Arg Asn Cys Ala Ile Ile Ser Asp Val Lys Val Arg Asp Phe Trp Asp		
	835	840
Gly Phe Glu Ile Ile Cys Lys Arg Leu Arg Ser Glu Asp Gly Gln Pro		
	850	855
Met Val Leu Lys Leu Lys Asp Trp Pro Pro Gly Glu Asp Phe Arg Asp		
	865	870
Met Met Pro Thr Arg Phe Glu Asp Leu Met Glu Asn Leu Pro Leu Pro		
	885	890
Glu Tyr Thr Lys Arg Asp Gly Arg Leu Asn Leu Ala Ser Arg Leu Pro		
	900	905
Ser Tyr Phe Val Arg Pro Asp Leu Gly Pro Lys Met Tyr Asn Ala Tyr		
	915	920
Gly Leu Ile Thr Ala Glu Asp Arg Arg Val Gly Thr Asn Leu His		
	930	935
Leu Asp Val Ser Asp Ala Val Asn Val Met Val Tyr Val Gly Ile Pro		
	945	950
Ile Gly Glu Gly Ala His Asp Glu Glu Val Leu Lys Thr Ile Asp Glu		
	965	970
Gly Asp Ala Asp Glu Val Thr Lys Gln Arg Ile His Asp Gly Lys Glu		
	980	985
Lys Pro Gly Ala Leu Trp His Ile Tyr Ala Ala Lys Asp Ala Glu Lys		
	995	1000
Ile Arg Glu Leu Leu Arg Lys Val Gly Glu Glu Gln Gly Gln Glu Asn		
	1010	1015
Pro Pro Asp His Asp Pro Ile His Asp Gln Ser Trp Tyr Leu Asp Gln		
	1025	1030
Thr Leu Arg Lys Arg Leu Tyr Glu Glu Tyr Gly Val Gln Gly Trp Ala		
	1035	1040

<211> 169
 <212> PRT
 <213> Homo sapiens

<400> 4596
 Asp Cys Gly Gly Thr Val Pro Ala Val Pro Val Ser Ser Leu Gly
 1 5 10 15
 Arg Lys Gln Arg Ala Val Ser Gln Leu Ser Arg Gly Leu Thr Asp Ile
 20 25 30
 Phe Leu Gly Thr Ser Ile Ser Ser Ser Ser Trp Ala Pro Leu Arg
 35 40 45
 Gly Arg Glu Ala Ala Leu Pro Gly Pro Ala Gly Asp Xaa Ala Val Lys
 50 55 60
 Gly Pro Ala Asp Pro Ala Ala Gln His Ser Arg Asp Gly Gln Gly Gly
 65 70 75 80
 Trp Pro Pro Ala Gln Gly Thr Ala Ser Thr Ala Gly Lys Ser Gly Ala
 85 90 95
 Pro Gly Ala Trp Ser Val Gly Gly Ala Thr Gly Pro Arg Gly Ala Lys
 100 105 110
 Gly Pro Arg Thr Gly Arg Pro Ala Pro Ser Pro Gly Ser Pro Pro Arg
 115 120 125
 Glu Ser Arg Cys Leu Ala Pro Gly Pro Ser Arg Leu Asp Pro Gly Pro
 130 135 140
 Ala Xaa Ala Ala Ala Pro Gly Ala Leu Arg Pro Pro Ala Asp Pro Ser
 145 150 155 160
 Gln Ala Arg Pro Arg Gly Ser Asn
 165

<210> 4597
 <211> 515
 <212> DNA
 <213> Homo sapiens

<400> 4597
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 ctgcaggggc ggtgcagaca gagctgcagg acctgcttcc ctgcaggcaa tgtcctcctg
 120
 gggacactca tgcctcagtga ctgatgggat ggggggtaca aagtcaccagc cactgtattc
 180
 tgggaggcca ttccagctca caactcctgg gccctgggga gtcggccctg ggacctgcct
 240
 cacagctcag ctctcctctc cggcccccatt ctgcctcctc ccggcccttt cccaggcagt
 300
 aagcccaagg aactccttaa gaaacatcct cactctgaac tccactgcag agcctctctc
 360
 ctgggaaagc agggagcgcc ccttgcaatc acgtaattgt tactcatccg cctccttctc
 420
 ggagcacctt gacggaggat gctccccact agtgetacaa agcctagcac gtgaataaag
 480
 ctcaacatgg ttggttgacc agagtctgag ggaac
 515

<210> 4598

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 4598
 Met Ser Ser Trp Gly His Ser Cys Ser Val Thr Asp Gly Met Gly Gly
 1 5 10 15
 Thr Lys Ser Gln Pro Arg Asp Ser Gly Arg Pro Phe Gln Leu Thr Thr
 20 25 30
 Pro Gly Pro Trp Gly Val Gly Arg Gly Thr Cys Leu Thr Ala Gln Leu
 35 40 45
 Leu Leu Ser Ala Pro Phe Cys Leu Leu Pro Ala Leu Ser Gln Ala Val
 50 55 60
 Ser Pro Arg Asn Ser Leu Arg Asn Ile Leu Thr Leu Asn Ser Thr Ala
 65 70 75 80
 Glu Pro Ser Ser Trp Glu Ser Arg Glu Arg Pro Leu Gln Ser Arg Asn
 85 90 95
 Val Tyr Ser Ser Ala Ser Phe Ser Glu His Leu Asp Gly Gly Cys Ser
 100 105 110
 Pro Leu Val Leu Gln Ser Leu Ala Arg Arg Ile Ser Ser Thr Trp Leu
 115 120 125
 Val Asp Gln Ser Leu Arg Glu
 130 135

<210> 4599
 <211> 2314
 <212> DNA
 <213> Homo sapiens

<400> 4599
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 ccacctctcc ccagccccgg agaggctgag gagccgcagc cccccagacc gcgcagcgcg
 120
 ggaggcaggt tccgcacgaa ataaatcaga atgagttatg cagaaaaacc cgatgaaatc
 180
 acgaaagatg agtggatgga aaagctcaat aacttgcagc tcagagagac agacatgaac
 240
 cgctcatca tgaactacct ggtcacagag ggctttaagg aagcagcgga gaagtctcga
 300
 atggaatctg gaatcgaacc tagtgtggat ctggaacac ttgatgaacg aatcaagatc
 360
 cgggagatga tactgaaagg tcagattcag gaggccatcg ccttgatcaa cagcctccac
 420
 ccagagctct tggacacaaa ccggtatctt tacttccatt tgcagcaaca gcatttgatc
 480
 gagctgatcc gccagcggga gacagaggcg gcgctggagt ttgcacagac tcagctggcg
 540
 gagcaggcg aggagagcgg agagtgcctc acagagatgg agcgtaccct ggcactgctg
 600
 gcctttgaca gtcccgagga gtcgcctctc ggagacctcc tccaccatc gcagaggcag
 660
 aaggtgtgga gtgaagttaa ccaagctgtg ctgattatg aaaatcgcga gtcaacaccc
 720

aaactggcaa aattactgaa actactactt tgggctcaga acgagctgga ccagaagaaa
780
gtaaaataac ccaaaaatgac agacctcagc aagggtgtga ttgaggagcc caagtagcgc
840
ctgcgcttgc gtgtgggtgac caacaccagc cctgcgctgt gggacttgcc tcagatcagc
900
ctgcgactgc aagattctta ctgcagtaga gaactctttt tctcccttgt actttttttt
960
gacctggcat ctttttatag ggaaaaatgg cctttgtagg cagtggaaaaa cttgcaagga
1020
aagctgccgt ctcttttgca gtctgatgca gagcctgcac tctggcactc gctgaagaat
1080
ctggaaggtt gcggttttgt cttccagtgt tcgggggacct ctggctgctg aaggattcgg
1140
tctaccacgg agggctgtgc tgttaggctg catccactc aaaatacagg aaagcacga
1200
atcatgatcc tgcctttctgt tagcttaggc agacattggg ccttcaccta caagtttttc
1260
cttaccctgt tgggttttgt gttttttttt ttttctttt ccataggaaa gaatatataa
1320
atttgtaaat cctaattcaa agatggctca tgtgtgaggg cattgagttt gatttgtttt
1380
ccctttggct tgggttgtgt ggcttttggg ggaatgctgt gagggggcta tgtgtttttt
1440
aattttttta atatatattt tgggtgctgtg tgtggtaaga gacttggtcc tagtggaatca
1500
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1560
tgacccaaaat ggcctctaaa agatgttaat catctcaaat gaccttttgt ctttggggcg
1620
ttcttcccc tgtgatagcg gcagtggtct tttctggtac ctgcagctgg aaaggccact
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tggccctgtg ctgagtgagc ggcctccatt agagcgaggc agcccttgcc cgggtggggac
1740
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1800
gatctgccct ccagcatctc ggcagcatct catcctccat cgtcagccgg ctctgccgat
1860
gtcctgcttc tgttactca cagaactgtc cctgctccg tgggtgggag gaggggaagt
1920
gtgcagggtc gcgtgcattg cctgcgagtc gggacagttg atgggcacat ggccttgtag
1980
ctctggggac agatgtgttt ggattcattg cagcggacca ccgggcaactg ttgacccac
2040
tgagcagctg taagtgttgg tttagtggat gttcgtgaa ttgctgatcc atcaaggggc
2100
gtcctttgga gccagtggag cctgcggcgg catctgaggg gcagaatgct gctagcactt
2160
gaatctggga tctcgcctta ttctcaagta gcaaggcatc tcgacaagca tggctaggt
2220
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2280
tcaccgagct cctgcacccc ttgagtgttg atca
2314

<210> 4600
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 4600
 Met Ser Tyr Ala Glu Lys Pro Asp Glu Ile Thr Lys Asp Glu Trp Met
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 Glu Lys Leu Asn Asn Leu His Val Gln Arg Ala Asp Met Asn Arg Leu
 20 25 30
 Ile Met Asn Tyr Leu Val Thr Glu Gly Phe Lys Glu Ala Ala Glu Lys
 35 40 45
 Phe Arg Met Glu Ser Gly Ile Glu Pro Ser Val Asp Leu Glu Thr Leu
 50 55 60
 Asp Glu Arg Ile Lys Ile Arg Glu Met Ile Leu Lys Gly Gln Ile Gln
 65 70 75 80
 Glu Ala Ile Ala Leu Ile Asn Ser Leu His Pro Glu Leu Leu Asp Thr
 85 90 95
 Asn Arg Tyr Leu Tyr Phe His Leu Gln Gln His Leu Ile Glu Leu
 100 105 110
 Ile Arg Gln Arg Glu Thr Glu Ala Ala Leu Glu Phe Ala Gln Thr Gln
 115 120 125
 Leu Ala Glu Gln Gly Glu Glu Ser Arg Glu Cys Leu Thr Glu Met Glu
 130 135 140
 Arg Thr Leu Ala Leu Leu Ala Phe Asp Ser Pro Glu Glu Ser Pro Phe
 145 150 155 160
 Gly Asp Leu Leu His Thr Met Gln Arg Gln Lys Val Trp Ser Glu Val
 165 170 175
 Asn Gln Ala Val Leu Asp Tyr Glu Asn Arg Glu Ser Thr Pro Lys Leu
 180 185 190
 Ala Lys Leu Leu Lys Leu Leu Trp Ala Gln Asn Glu Leu Asp Gln
 195 200 205
 Lys Lys Val Lys Tyr Pro Lys Met Thr Asp Leu Ser Lys Gly Val Ile
 210 215 220
 Glu Glu Pro Lys
 225

<210> 4601
 <211> 916
 <212> DNA
 <213> Homo sapiens

<400> 4601
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 120
 tttctaaaga gtgaccaggt ggccagaatg gtacagagtg gaggggtgttc tgctaatagac
 180
 ttcagagaag tatttaagaa aaacatagaa aaacgtgtgc ggagtttgcc agaaatagat
 240
 ggcttgagca aagagacagt gttgagctca tggatagcca aatatgatgc catttacaga
 300

ggtgaagagg acttgtgcaa acagccaaat agaattggccc taagtgcagt gtctgaactt
 360
 attcttgagca aggaacaact ctatgaaatg ttctcagcaga ttctgggtat taaaaaacta
 420
 gaaccaccagc tcctttataa tgcattgtcag ctggataacg cagatgaaca agcagcccag
 480
 atcagaaggg aacttgatgg ccggctgcaa ttggcagata aaatggcaaa ggaagaaaaa
 540
 ttccccaaat ttatagcaaa agatatggag aatatgtata tagaagagtt gcggtcttca
 600
 gtgaatttgc taatggccaa ttggaaaagt cttccagttt cgaaagggtg tccggaattt
 660
 aaattacaaa aattaaaacg ttcacagaac tctgcatttt tggacatagg agatgagaat
 720
 gagattcagc tgtcaaaagc cgacgtggta ctgtcattca ccttagagat tgtcataatg
 780
 gaagtgaag gcctgaagtc agttgctccc aatcgaattg ttactgtac aatggaagtg
 840
 gaaggagaaa aacttcagac agaccaggcc gaagcctcaa ggccacaatg gggggactca
 900
 ggggaatttc accccc
 916

<210> 4602

<211> 305

<212> PRT

<213> Homo sapiens

<400> 4602

Lys Leu Asn Lys Gln Gln Leu Gln Leu Leu Lys Glu Arg Phe Gln Ala
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 Phe Leu Asn Gly Glu Thr Gln Ile Val Ala Asp Glu Ala Phe Cys Asn
 20 25 30
 Ala Val Arg Ser Tyr Tyr Glu Val Phe Leu Lys Ser Asp Arg Val Ala
 35 40 45
 Arg Met Val Gln Ser Gly Gly Cys Ser Ala Asn Asp Phe Arg Glu Val
 50 55 60
 Phe Lys Lys Asn Ile Glu Lys Arg Val Arg Ser Leu Pro Glu Ile Asp
 65 70 75 80
 Gly Leu Ser Lys Glu Thr Val Leu Ser Ser Trp Ile Ala Lys Tyr Asp
 85 90 95
 Ala Ile Tyr Arg Gly Glu Glu Asp Leu Cys Lys Gln Pro Asn Arg Met
 100 105 110
 Ala Leu Ser Ala Val Ser Glu Leu Ile Leu Ser Lys Glu Gln Leu Tyr
 115 120 125
 Glu Met Phe Gln Gln Ile Leu Gly Ile Lys Lys Leu Glu His Gln Leu
 130 135 140
 Leu Tyr Asn Ala Cys Gln Leu Asp Asn Ala Asp Glu Gln Ala Ala Gln
 145 150 155 160
 Ile Arg Arg Glu Leu Asp Gly Arg Leu Gln Leu Ala Asp Lys Met Ala
 165 170 175
 Lys Glu Arg Lys Phe Pro Lys Phe Ile Ala Lys Asp Met Glu Asn Met
 180 185 190
 Tyr Ile Glu Glu Leu Arg Ser Ser Val Asn Leu Leu Met Ala Asn Leu

acagatagga atctcccaac gccacatct gacccaccc caggcctggc tcagggtgtc
 1020
 catgccccct ccacctgttc ctacatggag gccactgcc gctcccgctg caggatatca
 1080
 cgcagcatct ccctcggtga cagttagggc cctatcgtgg ccacactggc ccagcccctc
 1140
 cgtaggccat cgtccgttgg ggagctggcc tccttggggc agggagcttca ggccatcacc
 1200
 accgcgacaa caccagttt ggacagttag ggccaagagc ctgccctgcg ttctctggggc
 1260
 aaccacgagg cccggggcaa cctgagactg accctgtcaa gtgcctgtga tgggctcctg
 1320
 ctgcccccg tggtataccca gcttggcgtc accgtccctg cagttagctt cccagccccct
 1380
 agccctgtgg aagagagcgc cctgaggttc cagggtctg cctttcgccc aagtctccca
 1440
 gctcctgagt ccctggcct tcctgccac ccagtaacc cccagcttcc agaggcccgg
 1500
 cctggcatcc ctggcggcac tgctccctc ctggagccca cctccggtgc acttggtctg
 1560
 ttccagggca gcctgcccg ctggagttag ccctgggtgc cgggtgaagc cctgccccca
 1620
 tctcccttg agctgagcgg gtgggaaca tcttgacag gctgcagacc acctccaag
 1680
 aagccctcga cctttaccgt gtgttggtct ccagtgccca ggtggacacc gggcagcagc
 1740
 aggcacggac tgagctgggtc tccaccttc tgtggatcca cagccagctg gaggtgaat
 1800
 gccttggtgg gactagtgtg gcccagccc aggtctctgc cagcccagga ccccgctccc
 1860
 caccgacgt gtacccccg gccagcccag acctgcaggc cctgttgga cactactcgg
 1920
 agctgctggt gcaggccgtg cggaggaagg caccggggca ctgagggcgc agcccccca
 1980
 ccgcagccct gctgcttctg aggaacttag tattttaagc gaataaactg acagctttga
 2040
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 2090

<210> 4604

<211> 666

<212> PRT

<213> Homo sapiens

<400> 4604

Ala Glu Arg Ala Gly Gln Glu Pro Leu Lys Thr Ile Leu Asp Ala Gln
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 Asp Leu Asp Cys Tyr Phe Thr Pro Met Lys Pro Glu Ser Leu Glu Asn
 20 25 30
 Ser Ile Leu Asp Ser Leu Glu Pro Gln Ser Leu Ala Ser Leu Leu Ser
 35 40 45
 Glu Ser Glu Ser Pro Gln Glu Ala Gly Arg Gly His Pro Ser Phe Leu
 50 55 60
 Pro Gln Gln Lys Glu Ser Ser Glu Ala Ser Glu Leu Ile Leu Tyr Ser

65					70					75				80
Leu	Glu	Ala	Glu	Val	Thr	Val	Thr	Gly	Thr	Asp	Ser	Gln	Tyr	Cys
														Arg
														95
Lys	Glu	Val	Glu	Ala	Gly	Pro	Gly	Asp	Gln	Gln	Gly	Asp	Ser	Tyr
														Leu
														110
Arg	Val	Ser	Ser	Asp	Ser	Pro	Lys	Asp	Gln	Ser	Pro	Pro	Glu	Asp
														Ser
														125
Gly	Glu	Ser	Glu	Ala	Asp	Leu	Glu	Cys	Ser	Phe	Ala	Ala	Ile	His
														Ser
														140
Pro	Ala	Pro	Pro	Pro	Asp	Pro	Ala	Pro	Arg	Phe	Ala	Thr	Ser	Leu
														Pro
														160
His	Phe	Pro	Gly	Cys	Ala	Gly	Pro	Thr	Glu	Asp	Glu	Leu	Ser	Leu
														Pro
														175
Glu	Gly	Pro	Ser	Val	Pro	Ser	Ser	Ser	Leu	Pro	Gln	Thr	Pro	Glu
														Gln
														190
Glu	Lys	Phe	Leu	Arg	His	His	Phe	Glu	Thr	Leu	Thr	Glu	Ser	Pro
														Cys
														205
Arg	Ala	Leu	Gly	Asp	Val	Glu	Ala	Ser	Glu	Ala	Glu	Asp	His	Phe
														Phe
														220
Asn	Pro	Arg	Leu	Ser	Ile	Ser	Thr	Gln	Phe	Leu	Ser	Ser	Leu	Gln
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														240
Ala	Ser	Arg	Phe	Thr	His	Thr	Phe	Pro	Pro	Arg	Ala	Thr	Gln	Cys
														Leu
														255
Val	Lys	Ser	Pro	Glu	Val	Lys	Leu	Met	Asp	Arg	Gly	Gly	Ser	Gln
														Pro
														270
Arg	Ala	Gly	Thr	Gly	Tyr	Ala	Ser	Pro	Asp	Arg	Thr	His	Val	Leu
														Ala
														285
Ala	Gly	Lys	Ala	Glu	Glu	Thr	Leu	Glu	Ala	Trp	Arg	Pro	Pro	Pro
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														300
Cys	Leu	Thr	Ser	Leu	Ala	Ser	Cys	Val	Pro	Ala	Ser	Ser	Val	Leu
														Pro
														320
Thr	Asp	Arg	Asn	Leu	Pro	Thr	Pro	Thr	Ser	Ala	Pro	Thr	Pro	Gly
														Leu
														335
Ala	Gln	Gly	Val	His	Ala	Pro	Ser	Thr	Cys	Ser	Tyr	Met	Glu	Ala
														Thr
														350
Ala	Ser	Ser	Arg	Ala	Arg	Ile	Ser	Arg	Ser	Ile	Ser	Leu	Gly	Asp
														Ser
														365
Glu	Gly	Pro	Ile	Val	Ala	Thr	Leu	Ala	Gln	Pro	Leu	Arg	Arg	Pro
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														380
Ser	Val	Gly	Glu	Leu	Ala	Ser	Leu	Gly	Gln	Glu	Leu	Gln	Ala	Ile
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														430
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														445
Gly	Val	Thr	Val	Pro	Ala	Val	Ser	Phe	Pro	Ala	Pro	Ser	Pro	Val
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														Leu
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3805

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<210> 4606

<211> 584

<212> PRT

<213> Homo sapiens

<400> 4606

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 20 25 30
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 35 40 45
 Asp Ser Gly Gly Arg Thr Lys Arg Tyr Val Val Phe Asn Asn Gly Thr
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 Leu Tyr Phe Asn Glu Val Gly Met Arg Glu Glu Gly Asp Tyr Thr Cys
 65 70 75 80
 Phe Ala Glu Asn Gln Val Gly Lys Asp Glu Met Arg Val Arg Val Lys
 85 90 95
 Val Val Thr Ala Pro Ala Thr Ile Arg Asn Lys Thr Cys Leu Ala Val
 100 105 110
 Gln Val Pro Tyr Gly Asp Val Val Thr Val Ala Cys Glu Ala Lys Gly
 115 120 125
 Glu Pro Met Pro Lys Val Thr Trp Leu Ser Pro Thr Asn Lys Val Ile
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 Pro Thr Ser Ser Glu Lys Tyr Gln Ile Tyr Gln Asp Gly Thr Leu Leu
 145 150 155 160
 Ile Gln Lys Ala Gln Arg Ser Asp Ser Gly Asn Tyr Thr Cys Leu Val
 165 170 175
 Arg Asn Ser Ala Gly Glu Asp Arg Lys Thr Val Trp Ile His Val Asn
 180 185 190
 Val Gln Pro Pro Lys Ile Asn Gly Asn Pro Asn Pro Ile Thr Thr Val
 195 200 205
 Arg Glu Ile Ala Ala Gly Gly Ser Arg Lys Leu Ile Asp Cys Lys Ala

210 215 220
 Glu Gly Ile Pro Thr Pro Arg Val Leu Trp Ala Phe Pro Glu Gly Val
 225 230 235 240
 Val Leu Pro Ala Pro Tyr Tyr Gly Asn Arg Ile Thr Val His Gly Asn
 245 250 255
 Gly Ser Leu Asp Ile Arg Ser Leu Arg Lys Ser Asp Ser Val Gln Leu
 260 265 270
 Val Cys Met Ala Arg Asn Glu Gly Gly Glu Ala Arg Leu Ile Leu Gln
 275 280 285
 Leu Thr Val Leu Glu Pro Met Glu Lys Pro Ile Phe His Asp Pro Ile
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 Ser Glu Lys Ile Thr Ala Met Ala Gly His Thr Ile Ser Leu Asn Cys
 305 310 315 320
 Ser Ala Ala Gly Thr Pro Thr Pro Ser Leu Val Trp Val Leu Pro Asn
 325 330 335
 Gly Thr Asp Leu Gln Ser Gly Gln Gln Leu Gln Arg Phe Tyr His Lys
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 Ala Asp Gly Met Leu His Ile Ser Gly Leu Ser Ser Val Asp Ala Gly
 355 360 365
 Ala Tyr Arg Cys Val Ala Arg Asn Ala Ala Gly His Thr Glu Arg Leu
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 Val Ser Leu Lys Val Gly Leu Lys Pro Glu Ala Asn Lys Gln Tyr His
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 Asn Leu Val Ser Ile Ile Asn Gly Glu Thr Leu Lys Leu Pro Cys Thr
 405 410 415
 Pro Pro Gly Ala Gly Gln Gly Arg Phe Ser Trp Thr Leu Pro Asn Gly
 420 425 430
 Met His Leu Glu Gly Pro Gln Thr Leu Gly Arg Val Ser Leu Leu Asp
 435 440 445
 Asn Gly Thr Leu Thr Val Arg Glu Ala Ser Val Phe Asp Arg Gly Thr
 450 455 460
 Tyr Val Cys Arg Met Glu Thr Glu Tyr Gly Pro Ser Val Thr Ser Ile
 465 470 475 480
 Pro Val Ile Val Ile Ala Tyr Pro Pro Arg Ile Thr Ser Glu Pro Thr
 485 490 495
 Pro Val Ile Tyr Thr Arg Pro Gly Asn Thr Val Lys Leu Asn Cys Met
 500 505 510
 Ala Met Gly Ile Pro Lys Ala Asp Ile Thr Trp Glu Leu Pro Asp Lys
 515 520 525
 Ser His Leu Lys Ala Gly Val Gln Ala Arg Leu Tyr Gly Asn Arg Phe
 530 535 540
 Leu His Pro Gln Gly Ser Leu Thr Ile Gln His Ala Thr Gln Arg Asp
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<210> 4607

<211> 456

<212> DNA

<213> Homo sapiens

<400> 4607

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<210> 4608

<211> 107

<212> PRT

<213> Homo sapiens

<400> 4608

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			20				25					30			
Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu	Cys	Pro	Asn	Val	Lys
			35				40				45				
Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val	Glu	Ile	Glu	Pro	Gly	Val
			50			55				60					
Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile	Gly	Glu	Gly	Glu	Pro	His	Val
65				70				75						80	
Asp	Gly	Xaa	Pro	Gly	Asp	Leu	Arg	Phe	Arg	Ile	Lys	Val	Val	Lys	His
			85					90			95				
Pro	Ile	Phe	Glu	Arg	Arg	Gly	Asp	Asp	Leu	Tyr					
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<210> 4609

<211> 904

<212> DNA

<213> Homo sapiens

<400> 4609

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<210> 4610

<211> 250

<212> PRT

<213> Homo sapiens

<400> 4610

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			20					25					30		
Ala	Ala	Arg	Leu	Gly	Ala	Gln	Gly	Arg	Arg	Val	Val	Leu	Val	Thr	Ser
		35				40						45			
Gly	Gly	Thr	Lys	Val	Pro	Leu	Glu	Ala	Arg	Pro	Val	Arg	Phe	Leu	Asp
		50				55					60				
Asn	Phe	Ser	Ser	Gly	Arg	Arg	Gly	Ala	Thr	Ser	Ala	Glu	Ala	Phe	Leu
65				70				75						80	
Ala	Ala	Gly	Tyr	Gly	Val	Leu	Phe	Leu	Tyr	Arg	Ala	Arg	Ser	Ala	Phe
			85					90						95	
Pro	Tyr	Ala	His	Arg	Phe	Pro	Pro	Gln	Thr	Trp	Leu	Ser	Ala	Leu	Arg
			100					105					110		
Pro	Ser	Gly	Pro	Ala	Leu	Ser	Gly	Leu	Leu	Ser	Leu	Glu	Ala	Glu	Glu
		115				120					125				
Asn	Ala	Leu	Pro	Gly	Phe	Ala	Glu	Ala	Leu	Arg	Ser	Tyr	Gln	Glu	Ala
		130				135					140				
Ala	Ala	Ala	Gly	Thr	Phe	Leu	Ala	Val	Glu	Phe	Thr	Thr	Leu	Ala	Asp
145				150					155					160	
Tyr	Leu	His	Leu	Leu	Gln	Ala	Ala	Ala	Gln	Ala	Leu	Asn	Pro	Leu	Gly
			165					170						175	
Pro	Ser	Ala	Met	Phe	Tyr	Leu	Ala	Ala	Val	Ser	Asp	Phe	Tyr	Val	
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Leu Gln Gly Lys Val Gln	Leu Glu Asp Ile Leu	His His Leu Glu Lys
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Glu Glu Ile Asn Pro Leu	Ala Thr Thr Glu Glu	Gln Leu Cys Leu Val
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<210> 4611

<211> 1946

<212> DNA

<213> Homo sapiens

<400> 4611

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<210> 4612

<211> 532

<212> PRT

<213> Homo sapiens

<400> 4612

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 35 40 45
 Arg Gln Arg Asn Arg Leu Arg Leu Glu Glu Asp Lys Pro Ala Val Glu
 50 55 60
 Arg Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp
 65 70 75 80
 Ala Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp
 85 90 95
 Ser Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro
 100 105 110
 Gln Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Met
 115 120 125
 Val Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala
 130 135 140
 Ser Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu
 145 150 155 160
 Glu Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr

165 170 175
 Lys Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp
 180 185 190
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 195 200 205
 Arg Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg
 210 215 220
 Pro Thr Val Ala Arg Ile Ser Ser Val Gln Phe His Pro Gly Ala Gln
 225 230 235 240
 Ile Val Met Val Ala Gly Leu Asp Asn Ala Val Ser Leu Phe Gln Val
 245 250 255
 Asp Gly Lys Thr Asn Pro Lys Ile Gln Ser Ile Tyr Leu Glu Arg Phe
 260 265 270
 Pro Ile Phe Lys Ala Cys Phe Ser Ala Asn Gly Glu Glu Val Leu Ala
 275 280 285
 Thr Ser Thr His Ser Lys Val Leu Tyr Val Tyr Asp Met Leu Ala Gly
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 Lys Leu Ile Pro Val His Gln Val Arg Gly Leu Lys Glu Lys Ile Val
 305 310 315 320
 Arg Ser Phe Glu Val Ser Pro Asp Gly Ser Phe Leu Leu Ile Asn Gly
 325 330 335
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 340 345 350
 Gly Ser Met Lys Ile Asn Gly Arg Val Ala Ala Ser Thr Phe Ser Ser
 355 360 365
 Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly Asp Gly Glu Val Tyr Val
 370 375 380
 Trp Asp Val Asn Ser Arg Lys Cys Leu Asn Arg Phe Val Asp Glu Gly
 385 390 395 400
 Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser Arg Asn Gly Gln Tyr Val
 405 410 415
 Ala Cys Gly Ser Asn Cys Gly Val Val Asn Ile Tyr Asn Gln Asp Ser
 420 425 430
 Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile Lys Ala Ile Met Asn Leu
 435 440 445
 Val Thr Gly Val Thr Ser Leu Thr Phe Asn Pro Thr Thr Glu Ile Leu
 450 455 460
 Ala Ile Ala Ser Glu Lys Met Lys Glu Ala Val Arg Leu Val His Leu
 465 470 475 480
 Pro Ser Cys Thr Val Phe Ser Asn Phe Pro Val Ile Lys Asn Lys Asn
 485 490 495
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<210> 4613
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 4613

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<210> 4614

<211> 117

<212> PRT

<213> Homo sapiens

<400> 4614

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			20					25					30		
Glu	Phe	Thr	Asn	Gly	Asn	Leu	Thr	Met	Ser	Asn	Glu	Phe	His	Cys	Lys
		35					40					45			
Asp	Phe	Leu	Ile	Phe	Thr	Thr	Gln	Ile	Leu	Thr	Ile	Leu	Gln	Leu	Arg
	50					55				60					
Ser	Leu	Asn	Ile	Ile	Tyr	Asn	Lys	Gln	Asn	Leu	Val	Asn	Leu	Gln	Lys
65				70					75					80	
Ser	Asn	Ala	Leu	Lys	Lys	His	Gln	Ser	Leu	Cys	Met	Cys	Arg	Thr	Asp
			85					90						95	
Pro	Ala	Pro	Gln	Gly	Asn	Thr	Ala	Gly	Thr	Val	Pro	Arg	Thr	Leu	Thr
		100						105					110		
Ser	Val	Ser	Leu	Leu											
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<210> 4615

<211> 1350

<212> DNA

<213> Homo sapiens

<400> 4615

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<210> 4616

<211> 188

<212> PRT

<213> Homo sapiens

<400> 4616

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 20 25 30
 Arg Lys Asp Met Asp Glu Val Glu Glu Lys Ser Lys Asp Val Ile Asn
 35 40 45
 Phe Thr Ala Glu Lys Leu Ser Val Asp Glu Val Ser Gln Leu Val Ile
 50 55 60
 Ser Pro Leu Cys Gly Ala Ile Ser Leu Phe Val Gly Thr Thr Arg Asn

65		70		75		80									
Asn	Phe	Glu	Gly	Lys	Lys	Val	Ile	Ser	Leu	Glu	Tyr	Glu	Ala	Tyr	Leu
			85					90						95	
Pro	Met	Ala	Glu	Asn	Glu	Val	Arg	Lys	Ile	Cys	Ser	Asp	Ile	Arg	Gln
			100					105					110		
Lys	Trp	Pro	Val	Lys	His	Ile	Ala	Val	Phe	His	Leu	Leu	Gly	Leu	Val
			115				120					125			
Pro	Val	Ser	Glu	Ala	Ser	Thr	Val	Ile	Ala	Val	Ser	Ser	Ala	His	Arg
			130				135				140				
Ala	Ala	Ser	Leu	Glu	Ala	Val	Ser	Tyr	Ala	Ile	Asp	Ser	Leu	Lys	Ala
			145			150				155				160	
Lys	Val	Pro	Ile	Trp	Lys	Lys	Glu	Ile	Tyr	Glu	Glu	Ser	Ser	Thr	Trp
			165					170						175	
Lys	Gly	Asn	Lys	Glu	Cys	Phe	Trp	Ala	Ser	Asn	Ser				
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<210> 4617

<211> 2266

<212> DNA

<213> Homo sapiens

<400> 4617

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<210> 4618

<211> 197

<212> PRT

<213> Homo sapiens

<400> 4618

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1

5

10

15

Asp Pro Thr Ala Ala Ala Ala Ala Leu Asn Gly Gly His Cys Leu Ala

<400> 4620

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          20          25          30
Leu Gln Ala Arg Pro Asn Pro Arg Phe Pro Gly Arg Cys Thr Pro Gly
          35          40          45
Trp Glu Lys Leu Thr Asn Glu Ser Ser Trp Gln Pro Pro Gln Ala Pro
          50          55          60
Pro Asp Trp Ala Ser Trp Leu Cys Cys Gln Asp Tyr Asp Pro Leu Pro
65          70          75          80
Glu Ser Arg Arg Ser Pro Gln Ala Glu Arg Tyr Arg His Leu Cys Pro
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Tyr Leu Asn Gln Glu Val Pro
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<210> 4621

<211> 2588

<212> DNA

<213> Homo sapiens

<400> 4621

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960

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2588

<210> 4622
<211> 403
<212> PRT
<213> Homo sapiens

<400> 4622
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35 40 45
Ala Arg Ile Thr Ile Ser Glu Gly Ser Cys Pro Glu Arg Ile Thr Thr
50 55 60
Ile Thr Gly Ser Thr Ala Ala Val Phe His Ala Val Ser Met Ile Ala
65 70 75 80
Phe Lys Leu Asp Glu Asp Leu Cys Ala Ala Pro Ala Asn Gly Gly Asn
85 90 95
Val Ser Arg Pro Pro Val Thr Leu Arg Leu Val Ile Pro Ala Ser Gln
100 105 110
Cys Gly Ser Leu Ile Gly Lys Ala Gly Thr Lys Ile Lys Glu Ile Arg
115 120 125
Glu Thr Thr Gly Ala Gln Val Gln Val Ala Gly Asp Leu Leu Pro Asn
130 135 140
Ser Thr Glu Arg Ala Val Thr Val Ser Gly Val Pro Asp Ala Ile Ile
145 150 155 160
Leu Cys Val Arg Gln Ile Cys Ala Val Ile Leu Glu Ser Pro Pro Lys
165 170 175
Gly Ala Thr Ile Pro Tyr His Pro Ser Leu Ser Leu Gly Thr Val Leu
180 185 190
Leu Ser Ala Asn Gln Gly Phe Ser Val Gln Gly Gln Tyr Gly Ala Val
195 200 205
Thr Pro Ala Glu Val Thr Lys Leu Gln Gln Leu Ser Ser His Ala Val
210 215 220
Pro Phe Ala Thr Pro Ser Val Val Pro Gly Leu Asp Pro Gly Thr Gln
225 230 235 240
Thr Ser Ser Gln Glu Phe Leu Val Pro Asn Asp Leu Ile Gly Cys Val
245 250 255
Ile Gly Arg Gln Gly Ser Lys Ile Ser Glu Ile Arg Gln Met Ser Gly
260 265 270
Ala His Ile Lys Ile Gly Asn Gln Ala Glu Gly Ala Gly Glu Arg His
275 280 285
Val Thr Ile Thr Gly Ser Pro Val Ser Ile Ala Leu Ala Gln Tyr Leu
290 295 300
Ile Thr Ala Cys Leu Glu Thr Ala Lys Ser Thr Ser Gly Gly Thr Pro
305 310 315 320
Gly Ser Ala Pro Ala Asp Leu Pro Thr Pro Phe Ser Pro Pro Leu Thr
325 330 335
Ala Leu Pro Thr Ala Pro Pro Gly Leu Leu Gly Thr Pro Tyr Ala Ile
340 345 350
Ser Leu Ser Asn Phe Ile Gly Leu Lys Pro Val Pro Phe Leu Ala Leu

	355					360						365			
Pro	Pro	Ala	Ser	Pro	Gly	Pro	Pro	Pro	Gly	Leu	Ala	Ala	Tyr	Thr	Ala
	370					375					380				
Lys	Met	Ala	Ala	Ala	Asn	Gly	Ser	Lys	Lys	Ala	Glu	Arg	Gln	Lys	Phe
385					390					395					400
Ser	Pro	Tyr													

<210> 4623

<211> 2220

<212> DNA

<213> Homo sapiens

<400> 4623

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<210> 4624

<211> 189

<212> PRT

<213> Homo sapiens

<400> 4624

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			20					25					30		
Asp	Pro	Trp	Lys	Glu	Glu	Thr	Asp	Thr	Asp	Leu	Glu	Val	Val	Leu	Glu
			35				40					45			
Lys	Lys	Gly	Asn	Met	Asp	Glu	Ala	His	Ile	Asp	Gln	Val	Arg	Arg	Lys
			50			55				60					
Ala	Leu	Gln	Glu	Glu	Ile	Asp	Arg	Glu	Ser	Gly	Lys	Thr	Glu	Ala	Ser
65					70				75					80	
Glu	Thr	Arg	Lys	Trp	Thr	Gly	Thr	Gln	Phe	Gly	Gln	Trp	Asp	Thr	Ala
					85				90					95	
Gly	Phe	Glu	Asn	Glu	Asp	Gln	Lys	Leu	Lys	Phe	Leu	Arg	Leu	Met	Gly

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Gly Phe Lys Asn Leu Ser Pro Ser Phe Ser Arg Pro Ala Ser Thr Ile
          115              120              125
Ala Arg Pro Asn Met Ala Leu Gly Lys Lys Ala Ala Asp Ser Leu Gln
          130              135              140
Gln Asn Leu Gln Arg Asp Tyr Asp Arg Ala Met Ser Trp Lys Tyr Ser
          145              150              155              160
Arg Gly Ala Gly Leu Gly Phe Ser Thr Ala Pro Asn Lys Ile Phe Tyr
          165              170              175
Ile Asp Arg Asn Ala Ser Lys Ser Val Lys Leu Glu Asp
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<210> 4625

<211> 334

<212> DNA

<213> Homo sapiens

<400> 4625

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334

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<210> 4626

<211> 111

<212> PRT

<213> Homo sapiens

<400> 4626

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20          25          30
Glu Gln Glu Tyr Lys Arg Lys Gln Leu Glu Glu Gln Arg Gln Ser Glu
35          40          45
Arg Leu Gln Arg Gln Leu Gln Gln Glu His Ala Tyr Leu Lys Ser Leu
50          55          60
Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Lys Gln Gln Gln Gln Gln
65          70          75          80
Leu Leu Pro Gly Asp Arg Lys Pro Leu Tyr His Tyr Gly Arg Gly Met
85          90          95
Asn Pro Ala Asp Lys Pro Ala Trp Ala Arg Glu Gly Glu Glu Arg
100          105          110

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<210> 4627

<211> 1736

<212> DNA

<213> Homo sapiens

<400> 4627

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180
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1080
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1140
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1320
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1500

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 1680
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 1736

<210> 4628

<211> 469

<212> PRT

<213> Homo sapiens

<400> 4628

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 Pro Glu Ala Lys Gln Glu Ile Leu Glu Asn Lys Asp Val Val Val Gln
 35 40 45
 His Val His Phe Asp Gly Leu Gly Arg Thr Lys Asp Asp Ile Ile Ile
 50 55 60
 Cys Glu Ile Gly Asp Val Phe Lys Ala Lys Asn Leu Ile Glu Val Met
 65 70 75 80
 Arg Lys Ser His Glu Ala Arg Glu Lys Leu Leu Arg Leu Gly Ile Phe
 85 90 95
 Arg Gln Val Asp Val Leu Ile Asp Thr Cys Gln Gly Asp Gly Ala Leu
 100 105 110
 Pro Asn Gly Leu Asp Val Thr Phe Glu Val Thr Glu Leu Arg Arg Leu
 115 120 125
 Thr Gly Ser Tyr Asn Thr Met Val Gly Asn Asn Glu Gly Ser Met Val
 130 135 140
 Leu Gly Leu Lys Leu Pro Asn Leu Leu Gly Arg Ala Glu Lys Val Thr
 145 150 155 160
 Phe Gln Phe Ser Tyr Gly Thr Lys Glu Thr Ser Tyr Gly Leu Ser Phe
 165 170 175
 Phe Lys Pro Arg Pro Gly Asn Phe Glu Arg Asn Phe Ser Val Asn Leu
 180 185 190
 Tyr Lys Val Thr Gly Gln Phe Pro Trp Ser Ser Leu Arg Glu Thr Asp
 195 200 205
 Arg Gly Met Ser Ala Glu Tyr Ser Phe Pro Ile Trp Lys Thr Ser His
 210 215 220
 Thr Val Lys Trp Glu Gly Val Trp Arg Glu Leu Gly Cys Leu Ser Arg
 225 230 235 240
 Thr Ala Ser Phe Ala Val Arg Lys Glu Ser Gly His Ser Leu Lys Ser
 245 250 255
 Ser Leu Ser His Ala Met Val Ile Asp Ser Arg Asn Ser Ser Ile Leu
 260 265 270
 Pro Arg Arg Gly Ala Leu Leu Lys Val Asn Gln Glu Leu Ala Gly Tyr
 275 280 285
 Thr Gly Gly Asp Val Ser Phe Ile Lys Glu Asp Phe Glu Leu Gln Leu
 290 295 300
 Asn Lys Gln Leu Ile Phe Asp Ser Val Phe Ser Ala Ser Phe Trp Gly

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305          310          315          320
Gly Met Leu Val Pro Ile Gly Asp Lys Pro Ser Ser Ile Ala Asp Arg
          325          330          335
Phe Tyr Leu Gly Gly Pro Thr Ser Val Arg Gly Phe Ser Met His Ser
          340          345          350
Ile Gly Pro Gln Ser Glu Gly Asp Tyr Leu Gly Gly Glu Ala Tyr Trp
          355          360          365
Ala Gly Gly Leu His Leu Tyr Thr Pro Leu Pro Phe Arg Pro Gly Gln
          370          375          380
Gly Gly Phe Gly Glu Leu Phe Arg Thr His Phe Phe Leu Asn Ala Gly
385          390          395          400
Asn Leu Cys Asn Leu Asn Tyr Gly Glu Gly Pro Lys Ala His Ile Arg
          405          410          415
Lys Leu Ala Glu Cys Ile Arg Trp Ser Tyr Gly Ala Gly Ile Val Leu
          420          425          430
Arg Leu Gly Asn Ile Ala Arg Leu Glu Leu Asn Tyr Cys Val Pro Met
          435          440          445
Gly Val Gln Thr Gly Asp Arg Ile Cys Asp Gly Val Gln Phe Gly Ala
          450          455          460
Gly Ile Arg Phe Leu
465

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<210> 4629
<211> 706
<212> DNA
<213> Homo sapiens

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<400> 4629
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cctgatctct agcctagctc aaagcctcca ccaggatcgg gtggcagctt ccatttgagg
240
ccatttctag gccagcggcc cagctgccag cttcacgtct cctgagttgg gggatctctg
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360
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420
accctcccca cctccggctc caagcccggc tccaagagga ccaggggctg agcagaggct
480
tgtcccctat atcctccctc gccctctcct ttctctattt gagggagac tgacacctc
540
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600
ctcgaggaat ctgccctcag ctccccccat tctgggggtc caccacacac ccacacacac
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706

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<210> 4630

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<211> 140
 <212> PRT
 <213> Homo sapiens

<400> 4630
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 Leu Gly Gly Pro Pro Glu Trp Gly Glu Leu Arg Ala Asp Ser Ser Ser
 20 25 30
 Arg Asp Gln Gly Ala Leu Ser Leu Ser Arg Met Gly Arg Asp Ala Ser
 35 40 45
 Ser Trp Ala Leu Arg Val Ser Val Phe Pro Gln Ile Gly Lys Met Arg
 50 55 60
 Gly Arg Gly Gly Tyr Trp Gly Gln Ala Ser Ala Gln Pro Trp Val Leu
 65 70 75 80
 Leu Glu Pro Gly Leu Glu Pro Glu Val Gly Arg Val Ser Lys Leu Ser
 85 90 95
 Ser Trp Ile Pro Ile Cys Arg Thr Ala Pro Arg Thr Arg Ser Gly Val
 100 105 110
 Arg Ala His Pro Leu Ala Arg Ile Leu Gly Ser Leu Gly His Lys Ala
 115 120 125
 Gly Gln Gly Thr Arg Asp Pro Pro Thr Gln Glu Thr
 130 135 140

<210> 4631
 <211> 2756
 <212> DNA
 <213> Homo sapiens

<400> 4631
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 120
 gagtcggccg gctgggactt gcagatcgcg ctacgagact tttatgagga cggaggggat
 180
 gaagacattg tgaccatttc gcaggcaacc ccaggttcag tgtccagagg cacagcccc
 240
 agtgataata gaggacatc cttcagagac ctcattcatg accaagatga agatgaggag
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 gaagaggaag gccagaggag caggttttat gctgggggct cagagagaag tggacagcag
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 420
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 480
 aaaccgagac catttgcagg aggtggctac cgccttgggg cagcaccaga ggaagagtct
 540
 gcctatgtgg caggagaaaa gaggcagcat tccagccaag atgttcatgt agtattgaaa
 600
 ctctggaaga gtggattcag cctggataat ggagaactca gaagctacca agacccatcc
 660
 aatgcccagt ttctggagtc tatccgcaga ggggaggtgc cagcagagct tcggaggcta
 720

gctcacggtg gacaggtgaa cttggatatg gaggaccatc gggacgagga ctttgtgaag
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gtggatgccc ggccagccat ggctgccacc agctttatcc tcatgactac tttcccgaac
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aaagagcttg ctgatgagag ccagaccctg aaggaagcca acctgctcaa tgetgtcatc
1140
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1320
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1380
aaaacaacca aaaaattga agaatatca ccagcatggt gtacggaac tctccactg
1440
aagcaggctt taattgcttt aaaattatat ttatcttggg gcctgtggga ggaacttcc
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1560
cgcacagccc cacagatgac tggaggaagg aggggaaatg ttagaaaaga ggcttcgcca
1620
ccacttgttc ccacgagaat atgtcacttg ccagataaa actgggcggc agccagagtt
1680
cctgaagtg ggaagtca ga gctccatgca cacagtgtct tcagaagggt aaaataaata
1740
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1980
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2280
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2340

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 2460
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 2520
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 2580
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 2640
 ggtgttttct ccagcagggt gagattatgg aacctacata tgggtctgga aaaactgtac
 2700
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 2756

<210> 4632

<211> 372

<212> PRT

<213> Homo sapiens

<400> 4632

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		20						25					30		
Asp	Leu	Gln	Ile	Ala	Leu	Ala	Ser	Phe	Tyr	Glu	Asp	Gly	Gly	Asp	Glu
		35					40					45			
Asp	Ile	Val	Thr	Ile	Ser	Gln	Ala	Thr	Pro	Ser	Ser	Val	Ser	Arg	Gly
		50				55					60				
Thr	Ala	Pro	Ser	Asp	Asn	Arg	Val	Thr	Ser	Phe	Arg	Asp	Leu	Ile	His
65				70						75				80	
Asp	Gln	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Gly	Gln	Arg	Ser	Arg	Phe
			85				90						95		
Tyr	Ala	Gly	Gly	Ser	Glu	Arg	Ser	Gly	Gln	Gln	Ile	Val	Gly	Pro	Pro
		100					105					110			
Arg	Lys	Lys	Ser	Pro	Asn	Glu	Leu	Val	Asp	Asp	Leu	Phe	Lys	Gly	Ala
		115				120						125			
Lys	Glu	His	Gly	Ala	Val	Ala	Val	Glu	Arg	Val	Thr	Lys	Ser	Pro	Gly
		130				135					140				
Glu	Thr	Ser	Lys	Pro	Arg	Pro	Phe	Ala	Gly	Gly	Gly	Tyr	Arg	Leu	Gly
145				150					155					160	
Ala	Ala	Pro	Glu	Glu	Glu	Ser	Ala	Tyr	Val	Ala	Gly	Glu	Lys	Arg	Gln
			165					170						175	
His	Ser	Ser	Gln	Asp	Val	His	Val	Val	Leu	Lys	Leu	Trp	Lys	Ser	Gly
		180					185					190			
Phe	Ser	Leu	Asp	Asn	Gly	Glu	Leu	Arg	Ser	Tyr	Gln	Asp	Pro	Ser	Asn
		195					200					205			
Ala	Gln	Phe	Leu	Glu	Ser	Ile	Arg	Arg	Gly	Glu	Val	Pro	Ala	Glu	Leu
		210				215					220				
Arg	Arg	Leu	Ala	His	Gly	Gly	Gln	Val	Asn	Leu	Asp	Met	Glu	Asp	His
225				230						235				240	
Arg	Asp	Glu	Asp	Phe	Val	Lys	Pro	Lys	Gly	Ala	Phe	Lys	Ala	Phe	Thr
			245					250						255	
Gly	Glu	Gly	Gln	Lys	Leu	Gly	Ser	Thr	Ala	Pro	Gln	Val	Leu	Ser	Thr

<211> 242
 <212> PRT
 <213> Homo sapiens

<400> 4634
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 Arg Ile Cys Ile Gln Ala Ile Leu Gln Asp Lys Pro Lys Ile Ala Thr
 20 25 30
 Ala Asn Leu Gly Lys Phe Leu Glu Leu Arg Ser His Gln Ser Arg
 35 40 45
 Pro Ala Lys Cys Leu Thr Ile Met Trp Ala Leu Gly Gln Ala Gly Phe
 50 55 60
 Ala Asn Leu Thr Glu Gly Leu Lys Val Trp Leu Gly Ile Met Leu Pro
 65 70 75 80
 Val Leu Gly Ile Lys Ser Leu Ser Pro Phe Ala Ile Thr Tyr Leu Asp
 85 90 95
 Arg Leu Leu Leu Met His Pro Asn Leu Thr Lys Gly Phe Gly Met Ile
 100 105 110
 Gly Pro Lys Asp Phe Phe Pro Leu Leu Asp Phe Ala Tyr Met Pro Asn
 115 120 125
 Asn Ser Leu Thr Pro Ser Leu Gln Glu Gln Leu Cys Gln Leu Tyr Pro
 130 135 140
 Arg Leu Lys Val Leu Ala Phe Gly Ala Lys Pro Asp Ser Thr Leu His
 145 150 155 160
 Thr Tyr Phe Pro Ser Phe Leu Ser Arg Ala Thr Pro Ser Cys Pro Pro
 165 170 175
 Glu Met Lys Lys Glu Leu Leu Ser Ser Leu Thr Glu Cys Leu Thr Val
 180 185 190
 Asp Pro Leu Ser Ala Ser Val Trp Arg Gln Leu Tyr Pro Lys His Leu
 195 200 205
 Ser Gln Ser Ser Leu Leu Leu Glu His Leu Leu Ser Ser Trp Glu Gln
 210 215 220
 Ile Pro Lys Lys Val Gln Lys Ser Leu Gln Glu Thr Ile Gln Ser Leu
 225 230 235 240
 Lys Leu

<210> 4635
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 4635
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 120
 agtggggccc gaggaggaag gccggtggtg tgtgggcaga gccagccagt ggtggccttc
 180
 ctctcccca agatgagttt ttagcccgag gtgtttgcac actcacactt gctcactccc
 240
 tcacacaaa aacctcact ctttgctttt tctggggaga gggaggccac tggcagaagc
 300

gcctaccctg gccacagtca gttcccatc tcattttcta agaattttat cacaaaacag
 360
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 384

<210> 4636
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 4636
 Met Leu Gly Gly Pro Val Cys Ser Tyr Glu Leu Gly Gly Cys Pro Val
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 Thr Arg Val Leu Gly Gln Pro Arg Lys Leu Phe Ser Ile Gly Trp Gly
 20 25 30
 Lys Glu Val Lys Trp Gly Pro Arg Arg Lys Ala Gly Gly Val Trp Ala
 35 40 45
 Glu Pro Ala Ser Gly Gly Leu Pro Pro Pro Glu Asp Glu Phe Cys Ser
 50 55 60
 Pro Gly Val Cys Thr Leu Thr Leu Ala His Ser Leu Thr His Lys Thr
 65 70 75 80
 Leu Thr Leu Cys Phe Phe Trp Gly Glu Gly Gly His Trp Gln Lys Arg
 85 90 95
 Leu Pro Trp Pro Gln Ser Val Pro Ile Leu Ile Phe
 100 105

<210> 4637
 <211> 2162
 <212> DNA
 <213> Homo sapiens

<400> 4637
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 120
 agctgcttct ctttcaacca ggactgcaca tccctagcaa ttggaactaa agccgggtat
 180
 aagctgtttt ctctgagttc tgtggagcag ctggatcaag tccacggaag caatgaaatc
 240
 ccggacgtct acatcgtgga gcgcctcttc tccagcagcc tgggtgggtgt agtcagtcac
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 360
 agctactcca gcaacatctt gtccataagg ctgaaccggc aaaggctgct ggtttgccta
 420
 gaagagtcca tttatattca caacattaaa gacatgaagc tgttgaagac cctcctggat
 480
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 660

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720
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780
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1680
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1740
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1980
cagtcatttc acccttaaaa ggagaggaag gggattgggc cacagactta tccatggact
2040
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2160
ga
2162

<210> 4638

<211> 446

<212> PRT

<213> Homo sapiens

<400> 4638

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Thr Lys Ala Gly Tyr Lys Leu Phe Ser Leu Ser Ser Val Glu Gln Leu
 35          40          45
Asp Gln Val His Gly Ser Asn Glu Ile Pro Asp Val Tyr Ile Val Glu
 50          55          60
Arg Leu Phe Ser Ser Ser Leu Val Val Val Val Ser His Thr Lys Pro
 65          70          75          80
Arg Gln Met Asn Val Tyr His Phe Lys Lys Gly Thr Glu Ile Cys Asn
          85          90          95
Tyr Ser Tyr Ser Ser Asn Ile Leu Ser Ile Arg Leu Asn Arg Gln Arg
          100          105          110
Leu Leu Val Cys Leu Glu Glu Ser Ile Tyr Ile His Asn Ile Lys Asp
 115          120          125
Met Lys Leu Leu Lys Thr Leu Leu Asp Ile Pro Ala Asn Pro Thr Gly
 130          135          140
Leu Cys Ala Leu Ser Ile Asn His Ser Asn Ser Tyr Leu Ala Tyr Pro
 145          150          155          160
Gly Ser Leu Thr Ser Gly Glu Ile Val Leu Tyr Asp Gly Asn Ser Leu
          165          170          175
Lys Thr Val Cys Thr Ile Ala Ala His Glu Gly Thr Leu Ala Ala Ile
          180          185          190
Thr Phe Asn Ala Ser Gly Ser Lys Leu Ala Ser Ala Ser Glu Lys Gly
 195          200          205
Thr Val Ile Arg Val Phe Ser Val Pro Asp Gly Gln Lys Leu Tyr Glu
 210          215          220
Phe Arg Arg Gly Met Lys Arg Tyr Val Thr Ile Ser Ser Leu Val Phe
 225          230          235          240
Ser Met Asp Ser Gln Phe Leu Cys Ala Ser Ser Asn Thr Glu Thr Val
          245          250          255
His Ile Phe Lys Leu Glu Gln Val Thr Asn Ser Arg Pro Glu Glu Pro
 260          265          270
Ser Thr Trp Ser Gly Tyr Met Gly Lys Met Phe Met Ala Ala Thr Asn
 275          280          285
Tyr Leu Pro Thr Gln Val Ser Asp Met Met His Gln Asp Arg Ala Phe
 290          295          300
Ala Thr Ala Arg Leu Asn Phe Ser Gly Gln Arg Asn Ile Cys Thr Leu
 305          310          315          320
Ser Thr Ile Gln Lys Leu Pro Arg Leu Leu Val Ala Ser Ser Ser Gly
          325          330          335
His Leu Tyr Met Tyr Asn Leu Asp Pro Gln Asp Gly Gly Glu Cys Val
          340          345          350
Leu Ile Lys Thr His Ser Leu Leu Gly Ser Gly Thr Thr Glu Glu Asn
 355          360          365
Lys Glu Asn Asp Leu Arg Pro Ser Leu Pro Gln Ser Tyr Ala Ala Thr
 370          375          380
Val Ala Arg Pro Ser Ala Ser Ser Ala Ser Thr Val Pro Gly Tyr Ser

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385          390          395          400
Glu Asp Gly Gly Ala Leu Arg Gly Glu Val Ile Pro Glu His Glu Phe
          405          410          415
Ala Thr Gly Pro Val Cys Leu Asp Glu Asn Glu Phe Pro Pro Ile
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Ile Leu Cys Arg Gly Asn Gln Lys Gly Lys Thr Lys Gln Ser
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<210> 4639
 <211> 1007
 <212> DNA
 <213> Homo sapiens

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<400> 4639
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120
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ccactagat cccacaaagg gcaaaactcaa agatgaaaca aaggcaacgc catcaataac
240
caccatattc cacaggcttt ctcccctagg acgtactaac agggagtttc cacaggga
300
aattctcttt taaaaaatta acagtaaaaa taggagttac ttactatcta gatgaacaca
360
attgggtttc acaaaagctt ttgctgctgt ctggactcac catgcttttt tcttgagaga
420
aacataccaa actttttgtt gttgtgtgtg agacggagtt tcgctcttgt tgcccaggct
480
agagtgcatt ggcgtgatct cagctcactg caacctcgc ctcccaggct caagcgattc
540
tcccactca gcctcccaag tagctaggac tacagggtgtg tgccaccaca cccagctaat
600
tttnnctgta gagacggttn ttccaccatgt tgcccagact ggtctcaaat tcttgggctc
660
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720
ccagctacaa agactctttt cccacataag gtcacattca cagggtccaa gtagacatct
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840
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900
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1007

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<210> 4640
 <211> 71
 <212> PRT
 <213> Homo sapiens

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<400> 4640
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Pro Cys Phe Phe Leu Glu Arg Asn Ile Pro Asn Phe Leu Leu Leu
 20           25           30
Leu Arg Arg Ser Phe Ala Leu Val Ala Gln Ala Arg Val Gln Trp Arg
 35           40           45
Asp Leu Ser Ser Leu Gln Pro Pro Pro Arg Leu Lys Arg Phe Ser
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His Leu Ser Leu Pro Ser Ser
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<210> 4641

<211> 1873

<212> DNA

<213> Homo sapiens

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<400> 4641
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 240
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 300
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 360
cctgcctggg aaggggataa aggaaacact aaaggtgaca agcacgatga cctccagcgg
 420
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 480
cttcggtgct gcggctgtgt gttttctgag cgagccttga aagagataaa agcgggaagt
 540
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 600
gaggatgtgg acgtgctgaa gacaaggatg gaggagagaa ggctgagagc gaagctggaa
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 780
gagaagaaaa ccaacttggc tcccaaaagc acagcaatga atgagagctc ttctggaaaa
 840
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gcctacaagt cctcttttac cactcacagc tccgccaaag gctccaagga ggagtctgcc
 960
cactgggtca cccacacgtc ctactgcttc tgaagcccg actgccaccg ctccctgccc
 1020
agaaggttgt ttagtttcca cgtaggcagg tcgctttgtg cctctgagtg cgctgctgtg
 1080

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tgttctctct atagtctctgt gtcataaagc tgcctctggcc agccttcaag ctggtgtggc
 1140
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 1260
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 1320
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 1440
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 1680
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 1740
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 1873

<210> 4642

<211> 306

<212> PRT

<213> Homo sapiens

<400> 4642

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 Gln Trp Asn Tyr Cys Thr Leu Ser Gln Glu Ile Leu Arg Arg Pro Ile
 35 40 45
 Val Ala Cys Glu Leu Gly Arg Leu Tyr Asn Lys Asp Ala Val Ile Glu
 50 55 60
 Phe Leu Leu Asp Lys Ser Ala Glu Lys Ala Leu Gly Lys Ala Ala Ser
 65 70 75 80
 His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
 85 90 95
 Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
 100 105 110
 Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
 115 120 125
 Asn Gly Arg His Arg Phe Cys Phe Leu Arg Cys Cys Gly Cys Val Phe
 130 135 140
 Ser Glu Arg Ala Leu Lys Glu Ile Lys Ala Glu Val Cys His Thr Cys

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145              150              155              160
Gly Ala Ala Phe Gln Glu Asp Asp Val Ile Met Leu Asn Gly Thr Lys
              165              170              175
Glu Asp Val Asp Val Leu Lys Thr Arg Met Glu Glu Arg Arg Leu Arg
              180              185              190
Ala Lys Leu Glu Lys Lys Thr Lys Lys Pro Lys Ala Ala Glu Ser Val
              195              200              205
Ser Lys Pro Asp Val Ser Glu Glu Ala Pro Gly Pro Ser Lys Val Lys
              210              215              220
Thr Gly Lys Pro Glu Glu Ala Ser Leu Asp Ser Arg Glu Lys Lys Thr
              225              230              235
Asn Leu Ala Pro Lys Ser Thr Ala Met Asn Glu Ser Ser Ser Gly Lys
              245              250              255
Ala Gly Lys Pro Pro Cys Gly Ala Thr Lys Arg Ser Ile Ala Asp Ser
              260              265              270
Glu Glu Ser Glu Ala Tyr Lys Ser Leu Phe Thr Thr His Ser Ser Ala
              275              280              285
Lys Arg Ser Lys Glu Glu Ser Ala His Trp Val Thr His Thr Ser Tyr
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Cys Phe
305

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<210> 4643

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 4643

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120
acgggaacgc gctatgccgg gaaggtggtg gtcgtgacgg gggcgggcgc cggcatcgga
180
gctgggatcg tgcgcgcctt cgtggacagc gggggcccgag tgggttatctg cgacaaggat
240
gagtcctggg gccggggcct ggagcaggag ctccctggag ctgtctttat cctctgtgat
300
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360
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420
tctgcccagg gattccgccg gctgctggag ctgaacctac tggggacgta caccttgacc
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600
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660
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720
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780

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 840
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 960
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 1125

<210> 4644

<211> 270

<212> PRT

<213> Homo sapiens

<400> 4644

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			20					25				30			
Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly	Gly	Arg	Ala
		35					40					45			
Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu	Cys	Asp	Val	Thr
	50				55					60					
Gln	Glu	Asp	Asp	Met	Lys	Thr	Leu	Val	Ser	Glu	Thr	Ile	Arg	Arg	Phe
	65			70					75					80	
Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala	Gly	His	His	Pro	Pro	Pro
			85					90					95		
Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln	Gly	Phe	Arg	Gln	Leu	Leu	Glu
		100						105					110		
Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr	Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr
	115					120					125				
Leu	Arg	Lys	Ser	Gln	Gly	Asn	Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly
	130				135					140					
Ala	Ile	Gly	Gln	Ala	Gln	Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala
	145			150					155				160		
Val	Thr	Ala	Met	Thr	Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly
			165					170					175		
Val	Arg	Val	Asn	Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp
		180						185				190			
Glu	Glu	Leu	Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu
	195					200						205			
Gly	Met	Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val
	210				215						220				
Gly	Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
	225			230					235					240	
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	Lys
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Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser		
			260				265					270			

<210> 4645

<211> 1725

<212> DNA

<213> Homo sapiens

<400> 4645

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120
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180
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240
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300
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360
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420
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540
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600
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720
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780
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1380
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1440

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 1725

<210> 4646

<211> 358

<212> PRT

<213> Homo sapiens

<400> 4646

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			20					25					30		
Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr	Arg	Lys	Leu
		35					40						45		
Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp	Pro	Gln	Ala	Gln
		50				55					60				
Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Ser
65				70						75				80	
Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly	Glu	Glu	Gly	Leu	Lys	Asp
				85					90					95	
Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile	Phe	Ser	His	Phe	Phe	Gly	Asp
			100					105					110		
Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr	Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile
			115				120					125			
Pro	Arg	Gly	Ser	Asp	Ile	Ile	Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu
			130				135					140			
Val	Tyr	Ala	Gly	Asn	Phe	Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala
145				150						155					160
Arg	Gln	Ala	Pro	Gly	Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg
				165				170						175	
Thr	Thr	Gln	Leu	Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val
			180					185					190		
Cys	Asp	Glu	Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu
		195					200					205			
Glu	Val	Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe
		210				215						220			
Ile	Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
225					230					235				240	
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly	Asp
			245					250						255	
Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu	Val	Gly
			260					265					270		
Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val	His	Ile	Ser
		275					280						285		
Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp	Lys	Lys	Gly	Glu

290		295		300
Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile				
305		310	315	320
Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg				
	325		330	335
Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr				
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Asn Gly Leu Gln Gly Tyr				
355				

<210> 4647

<211> 791

<212> DNA

<213> Homo sapiens

<400> 4647

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120
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180
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240
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300
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360
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420
tcaaaaatgt ccatgaagac agaatgtccc ttcggtgttt tctcattcag gctggcagga
480
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600
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<210> 4648

<211> 188

<212> PRT

<213> Homo sapiens

<400> 4648

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Leu Ser Ser Asp Gly Thr Tyr Phe Tyr Trp Ile Trp Ser Pro Ala Ser

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Leu	Asn	Glu	Lys	Thr	Pro	Lys	Gly	His	Ser	Val	Phe	Met	Asp	Ile	Phe				
35										40					45				
Glu	Leu	Val	Val	Glu	Asn	Gly	Val	Phe	Val	Ala	Asn	Pro	Leu	Gln	Glu				
50										55					60				
Arg	Thr	Ile	Leu	Met	Arg	Lys	Glu	Gly	Glu	Ser	Ala	Lys	Ser	Ile	Asn				
65										70					75				
Glu	Met	Leu	Leu	Ser	Arg	Leu	Ser	Arg	Tyr	Arg	Ala	Ser	Pro	Ser	Ala				
85										90					95				
Thr	Leu	Ala	Ala	Leu	Thr	Gly	Ser	Thr	Ile	Ser	Asn	Thr	Leu	Lys	Glu				
100										105					110				
Asp	Gln	Ala	Ala	Asn	Thr	Ser	Cys	Gly	Leu	Pro	Leu	Lys	Met	Leu	Arg				
115										120					125				
Lys	Thr	Pro	Ile	Tyr	Thr	Cys	Gly	Thr	Tyr	Leu	Val	Met	Leu	Val	Pro				
130										135					140				
Pro	Pro	Gly	Gly	Ser	Gly	Ser	Ser	Ala	Thr	Arg	Ser	Leu	Phe	Gly	Gly				
145										150					155				
Thr	Ser	Gly	Leu	Ser	Ser	Leu	Lys	Ile	Leu	Ala	Ser	Ser	Leu	Val	Tyr				
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<210> 4649
<211> 3276
<212> DNA
<213> Homo sapiens
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120						
gggcaggcca	ataaatggat	taagaacatg	gagaaggcga	ataaactggc	tgatcatcaag	
180						
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240						
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300						
acattcaaac	agcaaggagt	tgagtacatg	aggctgggtg	aaaacatcat	tgaatatctc	
360						
agggatttta	agttatacat	cacaaaccgt	ttgaggaaatc	cacattacct	cccagaagtt	
420						
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480						
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540						
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600						
ctctccatgt	ccaagggtaa	catcctggag	gatgaaacgg	ccatcaaaat	tctgtcctcc	
660						
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<210> 4650

<211> 965

<212> PRT

<213> Homo sapiens

<400> 4650

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Leu Tyr Met His Ser Leu Thr His Ser Thr Lys Ser Glu Glu Leu Asn
              180              185              190
Leu Arg Ile Lys Tyr Ile Ile Asp His Phe Thr Leu Ser Ile Tyr Asn
              195              200              205
Asn Val Cys Arg Ser Leu Phe Glu Lys Asp Lys Leu Leu Phe Ser Leu
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225              230              235              240
Val Trp Tyr Phe Leu Leu Thr Gly Gly Ile Ala Leu Asp Asn Pro Tyr
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Pro Asn Pro Ala Pro Gln Trp Leu Ser Glu Lys Ala Trp Ala Glu Ile
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Thr Asn Glu Pro Pro Lys Gly Leu Arg Ala Asn Leu Leu Arg Ser Tyr
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Ala Val Met Trp Gln Lys Met Leu Phe Gly Leu Cys Phe Phe His Ala
              515              520              525
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 850 855 860
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<210> 4651

<211> 869

<212> DNA

<213> Homo sapiens

<400> 4651

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<210> 4652

<211> 289

<212> PRT

<213> Homo sapiens

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65     70     75     80
Leu Met Lys Pro Asp Gly Arg Glu Phe Phe Gln Gln Ile Ile Glu Tyr
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Thr Glu Glu Tyr Arg His Met Pro Leu Leu Lys Leu Trp Val Gly Pro

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<212> DNA

<213> Homo sapiens

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<211> 255

<212> PRT

<213> Homo sapiens

<400> 4654

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 35 40 45
 Lys Glu Arg Pro Ser Arg Arg Ala Arg Gly Ser Pro Phe Val Arg Ser
 50 55 60
 Gly Thr Ile Val Arg Ser Gln Thr Phe Ser Pro Gly Ala Arg Ser Gln
 65 70 75 80
 Tyr Val Cys Arg Leu Tyr Arg Ser Asp Ser Asp Ser Ser Thr Leu Pro
 85 90 95
 Arg Lys Ser Pro Phe Val Arg Asn Thr Leu Glu Arg Arg Thr Leu Arg
 100 105 110
 Tyr Lys Gln Ser Cys Arg Ser Ser Leu Ala Glu Leu Met Ala Arg Thr
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 165 170 175
 Arg Asp Glu Arg Leu Arg Gly Leu Leu Arg Glu Ala Glu Arg Gln Thr
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 Asn Leu Tyr Glu Asp Arg Gln Val Pro Glu Ala Ser Ala Arg Leu Thr
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35 40 45
Pro Ser Val Asp Ile Ser Leu Asp Leu Ala Lys Ser Thr Met Arg Thr
50 55 60
Ala Lys Ser Cys His Ile Val Ile Thr Asn Arg Ser Arg Asp Ala Ile
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Lys Cys Ala Thr Glu Thr Asp Ser Ala Val Ala Glu Thr Val Thr His
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<212> DNA
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<212> PRT
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<210> 4663

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<212> DNA

<213> Homo sapiens

<400> 4663

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 1380
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 1440
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<210> 4664

<211> 347

<212> PRT

<213> Homo sapiens

<400> 4664

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Ser	Asp	Glu	Ser	Asp	Glu	Val	Ile	Leu	Lys	Asp	Leu	Glu	Val	Leu	Ala
			20					25					30		
Glu	Ile	Ala	Ser	Ser	Pro	Ala	Gly	Gln	Thr	Asp	Asp	Pro	Gly	Pro	Leu
		35					40					45			
Asp	Gly	Pro	Asp	Leu	Gln	Ala	Ser	His	Ser	Glu	Leu	Gln	Val	Pro	Thr
	50				55					60					
Pro	Gly	Arg	Ala	Gly	Leu	Leu	Asn	Thr	Ser	Gly	Thr	Lys	Gly	Leu	Glu
65				70					75					80	
Cys	Ser	Pro	Ser	Thr	Pro	Thr	Met	Asn	Ser	Tyr	Phe	Tyr	Lys	Phe	Met
			85					90					95		
Ile	Asn	Leu	Leu	Lys	Arg	Phe	Ser	Ser	Glu	Arg	Lys	Leu	Leu	Glu	Val
		100					105						110		
Arg	Gly	Pro	Phe	Ile	Ile	Arg	Gln	Leu	Cys	Leu	Leu	Leu	Asn	Ala	Glu
		115					120					125			
Asn	Ile	Phe	His	Ser	Met	Ala	Asp	Ile	Leu	Leu	Arg	Glu	Glu	Asp	Leu
		130				135					140				
Lys	Phe	Ala	Ser	Thr	Met	Val	His	Ala	Leu	Asn	Thr	Ile	Leu	Leu	Thr
145				150					155					160	
Ser	Thr	Glu	Leu	Phe	Gln	Leu	Arg	Asn	Gln	Leu	Lys	Asp	Leu	Lys	Thr
			165					170						175	
Leu	Glu	Ser	Gln	Asn	Leu	Phe	Cys	Cys	Leu	Tyr	Arg	Ser	Trp	Cys	His
		180					185						190		
Asn	Pro	Val	Thr	Thr	Val	Ser	Leu	Cys	Phe	Leu	Thr	Gln	Asn	Tyr	Arg
		195				200						205			
His	Ala	Tyr	Asp	Leu	Ile	Gln	Lys	Phe	Gly	Asp	Leu	Glu	Val	Thr	Val
		210				215				220					
Asp	Phe	Leu	Ala	Glu	Val	Asp	Lys	Leu	Val	Gln	Leu	Ile	Glu	Cys	Pro
225				230					235					240	
Ile	Phe	Thr	Tyr	Leu	Arg	Leu	Gln	Leu	Leu	Asp	Val	Lys	Asn	Asn	Pro
			245				250							255	
Tyr	Leu	Ile	Lys	Ala	Leu	Tyr	Gly	Leu	Leu	Met	Leu	Leu	Pro	Gln	Ser
		260					265					270			
Ser	Ala	Phe	Gln	Leu	Leu	Ser	His	Arg	Leu	Gln	Cys	Val	Pro	Asn	Pro

275		280		285
Glu Leu Leu Gln Thr Glu Asp Ser Leu Lys Ala Ala Pro Lys Ser Gln				
290		295	300	
Lys Ala Asp Ser Pro Ser Ile Asp Tyr Ala Glu Leu Leu Gln His Phe				
305		310	315	320
Glu Lys Val Gln Asn Lys His Leu Glu Val Arg His Gln Arg Ser Gly				
	325	330		335
Arg Gly Asp His Leu Asp Arg Arg Val Val Leu				
340		345		

<210> 4665

<211> 1043

<212> DNA

<213> Homo sapiens

<400> 4665

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120
aaagagaaa agccagtggg tgttgagaca gtagaagaga aaaaggaacc tatcctagtg
180
tggtccacct tacgaagccg agcatcacaca ccacctgaag atctccagag tcgtttggaa
240
tcttacgtta aagaagtgtt tgggttcacct ctctcctagta attggcaaga catctccctg
300
gaagatagtc gtctaaagtt caatcttctg gctcatttag ctgatgacct ggggtcatgta
360
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420
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480
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540
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600
cagaactgtt ctctaaaccc actttttctg tagaggaatg tatcatcttt ttttttctca
660
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720
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780
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1043

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<210> 4666

<211> 167

<212> PRT

<213> Homo sapiens

<400> 4666

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Gly Ile Thr Arg Arg Val Phe Met Trp Thr Val Ser Gly Thr Pro Cys
          20           25           30
Arg Glu Phe Trp Ser Arg Phe Arg Lys Glu Lys Glu Pro Val Val Val
          35           40           45
Glu Thr Val Glu Glu Lys Lys Glu Pro Ile Leu Val Cys Pro Pro Leu
          50           55           60
Arg Ser Arg Ala Tyr Thr Pro Pro Glu Asp Leu Gln Ser Arg Leu Glu
65          70          75          80
Ser Tyr Val Lys Glu Val Phe Gly Ser Ser Leu Pro Ser Asn Trp Gln
          85          90          95
Asp Ile Ser Leu Glu Asp Ser Arg Leu Lys Phe Asn Leu Leu Ala His
          100          105          110
Leu Ala Asp Asp Leu Gly His Val Val Pro Asn Ser Arg Leu His Gln
          115          120          125
Met Cys Arg Val Arg Asp Val Leu Asp Phe Tyr Asn Val Pro Ile Gln
          130          135          140
Asp Arg Ser Lys Phe Asp Glu Leu Ser Ala Ser Asn Leu Pro Pro Asn
145          150          155          160
Leu Lys Ile Thr Trp Ser Tyr
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<210> 4667

<211> 1031

<212> DNA

<213> Homo sapiens

<400> 4667

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120
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tcagatgcca ccaacattga ggcttccatc agagaggagg acagcttcta tgtcataaac
240
ggtcacaaat ggtggatcac aggcacctcg gatcctcggt gccaaactctg tgtgtttatg
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420
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480
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540
tgcatgaggg tcatcggggt ctacagagagg gccctggcac tcatgaaggc ccgctgaggt
600

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gctttccccc gcacccagca ctgactcaga accaccacct tctgctttgc tgtcggactt
 660
 caattcctac ctgtttttctg agtgcagtc tagcagggtga agcaagggtga tgcctttgcc
 720
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 780
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 900
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 1031

<210> 4668

<211> 207

<212> PRT

<213> Homo sapiens

<400> 4668

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		20					25						30		
Ala	Gln	Lys	Ala	Arg	Trp	Leu	Ile	Pro	Leu	Leu	Glu	Gly	Lys	Ala	Arg
		35				40						45			
Ser	Cys	Phe	Ala	Met	Thr	Glu	Pro	Gln	Val	Ala	Ser	Ser	Asp	Ala	Thr
	50				55					60					
Asn	Ile	Glu	Ala	Ser	Ile	Arg	Glu	Glu	Asp	Ser	Phe	Tyr	Val	Ile	Asn
65				70					75					80	
Gly	His	Lys	Trp	Trp	Ile	Thr	Gly	Ile	Leu	Asp	Pro	Arg	Cys	Gln	Leu
			85					90						95	
Cys	Val	Phe	Met	Gly	Lys	Thr	Asp	Pro	His	Ala	Pro	Arg	His	Arg	Gln
		100					105						110		
Gln	Ser	Val	Leu	Leu	Val	Pro	Met	Asp	Thr	Pro	Gly	Ile	Lys	Ile	Ile
		115					120					125			
Arg	Pro	Leu	Thr	Val	Tyr	Gly	Leu	Glu	Asp	Ala	Pro	Gly	Gly	His	Gly
		130				135					140				
Glu	Val	Arg	Phe	Glu	His	Val	Arg	Val	Pro	Lys	Glu	Asn	Met	Val	Leu
145				150						155					160
Gly	Pro	Gly	Arg	Gly	Phe	Glu	Ile	Ala	Gln	Gly	Arg	Leu	Gly	Pro	Gly
			165					170						175	
Arg	Ile	His	His	Cys	Met	Arg	Leu	Ile	Gly	Phe	Ser	Glu	Arg	Ala	Leu
		180					185					190			
Ala	Leu	Met	Lys	Ala	Arg	Val	Ser	Ala	Phe	Pro	Arg	Thr	Gln	His	
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<210> 4669

<211> 683

<212> DNA

<213> Homo sapiens

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 120
 gacatgaaca taaaaaaca gattcaggaa cagcaccagg ctgccattat tattcagaag
 180
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 240
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 360
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 420
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 480
 aacttttttag cagttcagaa atctgtccga actattcagg ctgcttttag aggcatagaa
 540
 gttagacaaa aattgaaaaa atgtatcaga ggaaaagatg gcagccattg ttaaccaatc
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<210> 4670
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 4670
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 Thr Cys Val Gln Ala Gly Phe Gln Asp Met Asn Ile Lys Lys Gln Ile
 35 40 45
 Gln Glu Gln His Gln Ala Ala Ile Ile Ile Gln Lys His Cys Lys Ala
 50 55 60
 Phe Lys Ile Arg Lys His Tyr Leu His Ile Arg Ala Thr Val Val Ser
 65 70 75 80
 Ile Gln Arg Arg Tyr Arg Lys Leu Thr Ala Val Arg Thr Gln Ala Val
 85 90 95
 Ile Cys Ile Gln Ser Tyr Tyr Arg Gly Phe Lys Val Arg Lys Asp Ile
 100 105 110
 Gln Asn Met His Arg Ala Ala Thr Leu Ile Gln Ser Phe Tyr Arg Met
 115 120 125
 His Arg Ala Lys Val Asp Tyr
 130 135

<210> 4671
 <211> 657

<212> DNA

<213> Homo sapiens

<400> 4671

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 120
 ggggctcggc aggggctacc cggtccgct tccgccagt aatggagact gcagccacgt
 180
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 240
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 300
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 360
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 480
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<210> 4672

<211> 152

<212> PRT

<213> Homo sapiens

<400> 4672

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 20 25 30
 Lys Leu Met Leu Asp His Met Thr Asn Thr Thr Asn Ala Ser His Val
 35 40 45
 Pro Val Gln Pro Gly Ser Ser Val Val Met Met Val Asn Asn Leu Gly
 50 55 60
 Gly Leu Ser Phe Leu Glu Leu Gly Ile Ile Ala Asp Ala Thr Val Arg
 65 70 75 80
 Ser Leu Glu Gly Arg Gly Val Lys Ile Ala Arg Ala Leu Val Gly Thr
 85 90 95
 Phe Met Ser Ala Leu Glu Met Pro Gly Ile Ser Leu Thr Leu Leu Leu
 100 105 110
 Val Asp Glu Pro Leu Leu Lys Leu Ile Asp Ala Glu Thr Thr Ala Ala
 115 120 125
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 130 135 140
 Leu Ser Trp Ala Trp Arg Asn Thr
 145 150

<210> 4673

<211> 1335

<212> DNA

<213> Homo sapiens

<400> 4673

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120
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360
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420
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480
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<210> 4674

<211> 402
 <212> PRT
 <213> Homo sapiens

<400> 4674

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              20              25              30
Ala Asn Ser Leu Ala Ser Ser Gly Pro His Asn Leu Thr Tyr Pro Leu
              35              40              45
Gly Pro Arg Asn Glu Asp Leu Ser Leu Asp Tyr Ala Ser Gln Pro Ala
              50              55              60
Asn Leu Gln Phe Pro His Ile Met Pro Leu Ala Glu Asp Ile Lys Gly
65              70              75              80
Ser Cys Phe Gln Ser Gly Asn Lys Arg Asn His Glu Pro Phe Ile Ala
              85              90              95
Pro Glu Arg Phe Gly Asn Ser Ser Val Gly Phe Gly Ser Asn Ser His
              100              105              110
Ser Gln Ala Pro Glu Lys Val Thr Leu Leu Val Asp Gly Thr Arg Phe
              115              120              125
Val Val Asn Pro Gln Ile Phe Thr Ala His Pro Asp Thr Met Leu Gly
130              135              140
Arg Met Phe Gly Pro Gly Arg Glu Tyr Asn Phe Thr Arg Pro Asn Glu
145              150              155              160
Lys Gly Glu Tyr Glu Ile Ala Glu Gly Ile Ser Ala Thr Val Phe Arg
              165              170              175
Thr Val Leu Asp Tyr Tyr Lys Thr Gly Ile Ile Asn Cys Pro Asp Gly
              180              185              190
Ile Ser Ile Pro Asp Leu Arg Asp Thr Cys Asp Tyr Leu Cys Ile Asn
              195              200              205
Phe Asp Phe Asn Thr Ile Arg Cys Gln Asp Leu Ser Ala Leu Leu His
              210              215              220
Glu Leu Ser Asn Asp Gly Ala His Lys Gln Phe Asp His Tyr Leu Glu
225              230              235              240
Glu Leu Ile Leu Pro Ile Met Val Gly Cys Ala Lys Lys Gly Glu Arg
              245              250              255
Glu Cys His Ile Val Val Leu Thr Asp Glu Asp Ser Val Asp Trp Asp
              260              265              270
Glu Asp His Pro Pro Pro Met Gly Glu Glu Tyr Ser Gln Ile Leu Tyr
              275              280              285
Ser Ser Lys Leu Tyr Arg Phe Phe Lys Tyr Ile Glu Asn Arg Asp Val
              290              295              300
Ala Lys Thr Val Leu Lys Glu Arg Gly Leu Lys Asn Ile Arg Ile Gly
305              310              315              320
Ile Glu Gly Tyr Pro Thr Cys Lys Glu Lys Ile Lys Arg Arg Pro Gly
              325              330              335
Gly Arg Ser Glu Val Ile Tyr Asn Tyr Val Gln Arg Pro Phe Ile Gln
              340              345              350
Met Ser Trp Glu Lys Glu Glu Gly Lys Ser Arg His Val Asp Phe Gln
              355              360              365
Cys Val Arg Ser Lys Ser Leu Thr Asn Leu Val Ala Ala Gly Asp Asp
              370              375              380
Val Leu Glu Asp Gln Glu Ile Leu Met His His Pro Pro Gln Val Asp

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385	390	395	400
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<210> 4675			
<211> 2868			
<212> DNA			
<213> Homo sapiens			
<400> 4675			
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120			
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180			
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240			
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300			
ggaagcattc	agtcctctcg	atataagaag	gaatcaaagt caggccttgt gaaaccagggt
360			
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420			
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480			
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660			
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720			
ccagagcagt	atttgactcc	atgcgcagcg	aaagagggtga cagtgcagaca cctcaaaaacc
780			
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840			
tcccagctgg	cccgcgatcg	agaggactgg	attgaggagg agtgtcaccg ggtagaggcc
900			
cagttggcac	tcaaagaagc	caggaaagag	attaaacagc tcaaacagggt catcgaaaacc
960			
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<400> 4676

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<211> 940

<212> DNA

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<400> 4678

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 3240
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 3246

<210> 4684
 <211> 385
 <212> PRT
 <213> Homo sapiens

<400> 4684
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 20 25 30
 Pro His Ala Arg Ser Arg Val Arg Pro Ala Pro Lys Thr Ile Pro Gln
 35 40 45
 Gln Thr His Gly Thr Ala Arg Ile Gly Thr His Asn Gly Thr Phe His
 50 55 60
 Cys Asp Glu Ala Leu Ala Cys Ala Leu Leu Arg Leu Leu Pro Glu Tyr
 65 70 75 80
 Arg Asp Ala Glu Ile Val Arg Thr Arg Asp Pro Glu Lys Leu Ala Ser
 85 90 95
 Cys Asp Ile Val Val Asp Val Gly Gly Glu Tyr Asp Pro Arg Arg His
 100 105 110
 Arg Tyr Asp His His Gln Arg Ser Phe Thr Glu Thr Met Ser Ser Leu
 115 120 125
 Ser Pro Gly Lys Pro Trp Gln Thr Lys Leu Ser Ser Ala Gly Leu Ile
 130 135 140
 Tyr Leu His Phe Gly His Lys Leu Leu Ala Gln Leu Leu Gly Thr Ser
 145 150 155 160
 Glu Glu Asp Ser Met Val Gly Thr Leu Tyr Asp Lys Met Tyr Glu Asn
 165 170 175
 Phe Val Glu Glu Val Asp Ala Val Asp Asn Gly Ile Ser Gln Trp Ala
 180 185 190
 Glu Gly Glu Pro Arg Tyr Ala Leu Thr Thr Thr Leu Ser Ala Arg Val
 195 200 205
 Ala Arg Leu Asn Pro Thr Trp Asn His Pro Asp Gln Asp Thr Glu Ala
 210 215 220
 Gly Phe Lys Arg Ala Met Asp Leu Val Gln Glu Glu Phe Leu Gln Arg
 225 230 235 240
 Leu Asp Phe Tyr Gln His Ser Trp Leu Pro Ala Arg Ala Leu Val Glu
 245 250 255
 Glu Ala Leu Ala Gln Arg Phe Gln Val Asp Pro Ser Gly Glu Ile Val
 260 265 270
 Glu Leu Ala Lys Gly Ala Cys Pro Trp Lys Glu His Leu Tyr His Leu
 275 280 285
 Glu Ser Gly Leu Ser Pro Pro Val Ala Ile Phe Phe Val Ile Tyr Thr
 290 295 300
 Asp Gln Ala Gly Gln Trp Arg Ile Gln Cys Val Pro Lys Glu Pro His

```

305          310          315          320
Ser Phe Gln Ser Arg Leu Pro Leu Pro Glu Pro Trp Arg Gly Leu Arg
          325          330          335
Asp Glu Ala Leu Asp Gln Val Ser Gly Ile Pro Gly Cys Ile Phe Val
          340          345          350
His Ala Ser Gly Phe Ile Gly Gly His Arg Thr Arg Glu Gly Ala Leu
          355          360          365
Ser Met Ala Arg Ala Thr Leu Ala Gln Arg Ser Tyr Leu Pro Gln Ile
          370          375          380

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Ser

385

<210> 4685

<211> 618

<212> DNA

<213> Homo sapiens

<400> 4685

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240
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300
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360
gtccagaaga actatgaaca cttatttaag gtgaatgata aatccgtggg tggctccttc
420
tacctgcagt caaaggtggt ccgcgcaaag gagcgcttgg atgaggaact caaaatccag
480
gcccaggagg acagagaaaa agggcagatg ccccatcgt gactgctcgg ctccccccgc
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gctggagtgt gctcgcga
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<210> 4686

<211> 106

<212> PRT

<213> Homo sapiens

<400> 4686

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Gly Leu Ser Asp His Pro His Val His Thr Ala Ser Arg Ala Ala Ala
1          5          10          15
Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ser Asn Leu
20          25          30
Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn Val Ser Lys
35          40          45
Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu Phe Lys Val

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```

      50              55              60
Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser Lys Val Val
65              70              75              80
Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln Ala Gln Glu
      85              90              95
Asp Arg Glu Lys Gly Gln Met Pro His Thr
      100              105

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<210> 4687
<211> 309
<212> DNA
<213> Homo sapiens

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<400> 4687
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cggcgcgtctc gcaccccccgt tgggtggcat tgatgagcgc cctaactctg ggtctgtctt
180
tcgtggcggt ctacagcttg tcccatggcg aggtctccta tgaccactc tatgctgggt
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300
atgggggggg
309

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<210> 4688
<211> 90
<212> PRT
<213> Homo sapiens

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<400> 4688
Met Asp Ile Pro Pro Leu Ala Gly Lys Ile Ala Ala Leu Ser Leu Ser
1      5      10      15
Ala Leu Pro Val Ser Tyr Ala Leu Asn His Val Ser Ala Leu Ser His
      20      25      30
Pro Leu Trp Val Ala Leu Met Ser Ala Leu Ile Leu Gly Leu Leu Phe
      35      40      45
Val Ala Val Tyr Ser Leu Ser His Gly Glu Val Ser Tyr Asp Pro Leu
      50      55      60
Tyr Ala Gly Phe Ala Val Phe Ala Phe Thr Ser Gly Gly Asp Leu Ile
65      70      75      80
Ile Ala Leu Gln Glu Asp Ser Tyr Gly Gly
      85      90

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```

<210> 4689
<211> 898
<212> DNA
<213> Homo sapiens

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<400> 4689
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60

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 120
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 180
 gggcagctgg tggctccact gccctggcca ccgngggccc tgcgtgccag tctggtgcac
 240
 gtgggcagtc ggccatacac cgagttcccc ttcggccagc acagctcggg tgaggctgcc
 300
 caggatgcgg tgcgtgcttc tgcccagcgc atgggtgaca cccacactgg cctggcgctg
 360
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 420
 gtgctggtgt ggggtgacaga tggcggtctc agcgaccctg tgggcccccc catgcaggag
 480
 ctcaaggacc tgggcgtcac cgtgttcatt gtcagaccg gccgaggcaa ctctctggag
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 720
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 780
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 898

<210> 4690

<211> 299

<212> PRT

<213> Homo sapiens

<400> 4690

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 20 25 30
 Ser Ala Pro Glu Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val
 35 40 45
 Ser His Tyr Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val
 50 55 60
 Ala Pro Leu Pro Leu Ala Pro Xaa Ala Leu Arg Ala Ser Leu Val His
 65 70 75 80
 Val Gly Ser Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser
 85 90 95
 Gly Glu Ala Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly
 100 105 110
 Asp Thr His Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe
 115 120 125
 Ala Glu Ala Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp
 130 135 140
 Val Thr Asp Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu

```

145              150              155              160
Leu Lys Asp Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly
              165              170              175
Asn Phe Leu Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His
              180              185              190
Leu His Phe Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu
              195              200              205
Arg Gly Ser Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr
              210              215              220
Glu Ile Thr Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr
225              230              235              240
Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro
              245              250              255
Gly Ala Ala Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile
              260              265              270
Trp Ala Gly Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro
275              280              285
Glu Ser Asn Val Arg Leu Leu Arg Pro Gln Ile
290              295

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<210> 4691

<211> 2375

<212> DNA

<213> Homo sapiens

<400> 4691

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ccaaatgctc ctatctggct catactcaat gaagctggac tatactggag agcagtagga
180
aatagcactt ttgctattgc ctgtcttcag agggctttga atttagctcc acttcaatac
240
caagatgttc ctcttgtcaa cttggccaac cttttgattc attacggcct tcactctgat
300
gccactaagc tgctacttca agctttggcc atcaatagct ctgagcctct gacctttttg
360
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480
tgtatgcagt ttatctcttt tctgtacaac atcactctct ctgtttgcag tggtaattgt
540
catgagaaaa ccctggacaa cagccatgac aaacagaaat attttgacaa ctcacagtca
600
ctggatgctg ctgaagaaga gccctctgag agaggaacag aggaggaccc tgtattctct
660
gttgagaatt cagggaggga ctcagatgcc cttagacttg aaagtacggt ggttgaggag
720
agcaatggtt ctgatgatag ggagaattca gatgaaacca aaatgtcaga agaatactg
780
gctttggttg atgaatttca acaggcatgg cctttggaag gctttggggg tgcaactagag
840

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atgaaagggc ggcgtctaga cttacaagga atacgggtgc tgaagaaagg tccccaggat
900
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960
tggattacat tccagggtcaa acgtgtaaag aaacccaag gagatcataa gaaaactcct
1020
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1080
atcactggcc ccaagggtggc atctcctggg ccacaagggc tactagactg gaagaccagg
1140
aaagtgccat agacataatg taactggatt tcagcaaggc atttaacaga gcctcttatg
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1260
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1320
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1380
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1440
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2100
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2160
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2280
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2340
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2375

<211> 383

<212> PRT

<213> Homo sapiens

<400> 4692

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Xaa Asp Leu Lys Ala Lys Met Pro Asp Asp His Ala Arg Lys Ile Leu
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Leu Ser Arg Ile Asn Asn Tyr Thr Ile Pro Glu Glu Glu Ile Gly Ser
 20          25          30
Phe Leu Phe His Ala Ile Asn Lys Pro Asn Ala Pro Ile Trp Leu Ile
 35          40          45
Leu Asn Glu Ala Gly Leu Tyr Trp Arg Ala Val Gly Asn Ser Thr Phe
 50          55          60
Ala Ile Ala Cys Leu Gln Arg Ala Leu Asn Leu Ala Pro Leu Gln Tyr
 65          70          75          80
Gln Asp Val Pro Leu Val Asn Leu Ala Asn Leu Leu Ile His Tyr Gly
 85          90          95
Leu His Leu Asp Ala Thr Lys Leu Leu Leu Gln Ala Leu Ala Ile Asn
 100          105          110
Ser Ser Glu Pro Leu Thr Phe Leu Ser Leu Gly Asn Ala Tyr Leu Ala
 115          120          125
Leu Lys Asn Ile Ser Gly Ala Leu Glu Ala Phe Arg Gln Ala Leu Lys
 130          135          140
Leu Thr Thr Lys Cys Pro Glu Cys Glu Asn Ser Leu Lys Leu Ile Arg
 145          150          155          160
Cys Met Gln Phe Tyr Pro Phe Leu Tyr Asn Ile Thr Ser Ser Val Cys
 165          170          175
Ser Gly Asn Cys His Glu Lys Thr Leu Asp Asn Ser His Asp Lys Gln
 180          185          190
Lys Tyr Phe Asp Asn Ser Gln Ser Leu Asp Ala Ala Glu Glu Glu Pro
 195          200          205
Ser Glu Arg Gly Thr Glu Glu Asp Pro Val Phe Ser Val Glu Asn Ser
 210          215          220
Gly Arg Asp Ser Asp Ala Leu Arg Leu Glu Ser Thr Val Val Glu Glu
 225          230          235          240
Ser Asn Gly Ser Asp Glu Met Glu Asn Ser Asp Glu Thr Lys Met Ser
 245          250          255
Glu Glu Ile Leu Ala Leu Val Asp Glu Phe Gln Gln Ala Trp Pro Leu
 260          265          270
Glu Gly Phe Gly Gly Ala Leu Glu Met Lys Gly Arg Arg Leu Asp Leu
 275          280          285
Gln Gly Ile Arg Val Leu Lys Lys Gly Pro Gln Asp Gly Val Ala Arg
 290          295          300
Ser Ser Cys Tyr Gly Asp Cys Arg Ser Glu Asp Asp Glu Ala Thr Glu
 305          310          315          320
Trp Ile Thr Phe Gln Val Lys Arg Val Lys Lys Pro Lys Gly Asp His
 325          330          335
Lys Lys Thr Pro Gly Lys Lys Val Glu Thr Gly Gln Ile Glu Asn Gly
 340          345          350
His Arg Tyr Gln Ala Asn Leu Glu Ile Thr Gly Pro Lys Val Ala Ser
 355          360          365
Pro Gly Pro Gln Gly Leu Leu Asp Trp Lys Thr Arg Lys Val Pro
 370          375          380

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<210> 4693
 <211> 794
 <212> DNA
 <213> Homo sapiens

<400> 4693
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 360
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 780
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 794

<210> 4694
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 4694
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 20 25 30
 Asn Ser Gly Val Gly Gln Asp Gly Ser Leu Leu Ser Ser Pro Phe Leu
 35 40 45
 Lys Gly Phe Leu Ala Gly Tyr Val Val Ala Lys Leu Arg Ala Ser Ala
 50 55 60
 Val Leu Gly Phe Ala Val Gly Thr Cys Thr Gly Ile Tyr Ala Ala Gln
 65 70 75 80
 Ala Tyr Ala Val Pro Asn Val Glu Lys Thr Leu Arg Asp Tyr Leu Gln
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 Leu Leu Arg Lys Gly Pro Asp

100

<210> 4695

<211> 2209

<212> DNA

<213> Homo sapiens

<400> 4695

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1380

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<210> 4696

<211> 302

<212> PRT

<213> Homo sapiens

<400> 4696

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Arg	Gly	Val	Lys	Ile	Ala	Arg	Ala	Leu	Val	Gly	Thr	Phe	Met	Ser	Ala
			20					25					30		
Leu	Glu	Met	Pro	Gly	Ile	Ser	Leu	Thr	Leu	Leu	Leu	Val	Asp	Glu	Pro
		35					40					45			
Leu	Leu	Lys	Leu	Ile	Asp	Ala	Glu	Thr	Thr	Ala	Ala	Ala	Trp	Pro	Asn
		50				55				60					
Val	Ala	Ala	Val	Ser	Ile	Thr	Gly	Arg	Lys	Arg	Ser	Arg	Val	Ala	Pro
65				70				75						80	
Ala	Glu	Pro	Gln	Glu	Ala	Pro	Asp	Ser	Thr	Ala	Ala	Xaa	Glu	Ala	Gln
			85					90					95		
Pro	Arg	Ser	Xaa	Met	Ala	Leu	Val	Leu	Glu	Arg	Val	Cys	Ser	Thr	Leu
		100						105					110		
Leu	Gly	Leu	Glu	Glu	His	Leu	Asn	Ala	Leu	Asp	Arg	Ala	Ala	Gly	Asp
		115					120					125			
Gly	Asp	Cys	Gly	Thr	Thr	His	Ser	Arg	Ala	Ala	Arg	Ala	Ile	Gln	Glu
130						135					140				
Trp	Leu	Lys	Glu	Gly	Pro	Pro	Pro	Ala	Ser	Pro	Ala	Gln	Leu	Leu	Ser

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145             150             155             160
Lys Leu Ser Val Leu Leu Leu Glu Lys Met Gly Gly Ser Ser Gly Ala
165             170             175
Leu Tyr Gly Leu Phe Leu Thr Ala Ala Ala Gln Pro Leu Lys Ala Lys
180             185             190
Thr Ser Leu Pro Ala Trp Ser Ala Ala Met Asp Ala Gly Leu Glu Ala
195             200             205
Met Gln Lys Tyr Gly Lys Ala Ala Pro Gly Asp Arg Thr Met Leu Asp
210             215             220
Ser Leu Trp Ala Ala Glu Gln Glu Leu Gln Ala Trp Lys Ser Pro Gly
225             230             235             240
Ala Asp Leu Leu Gln Val Leu Thr Lys Ala Val Lys Ser Ala Glu Ala
245             250             255
Ala Ala Glu Ala Thr Lys Asn Met Glu Ala Gly Ala Gly Arg Ala Ser
260             265             270
Tyr Ile Ser Ser Ala Arg Leu Glu Gln Pro Asp Pro Gly Ala Val Ala
275             280             285
Ala Ala Ala Ile Leu Arg Ala Ile Leu Glu Val Leu Gln Ser
290             295             300

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<210> 4697

<211> 1047

<212> DNA

<213> Homo sapiens

<400> 4697

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180
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420
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780
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840

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<210> 4698

<211> 182

<212> PRT

<213> Homo sapiens

<400> 4698

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 20 25 30
 Asp Ala Asp Ile Pro Leu Glu Leu Val Phe His Leu Pro Val Asn Tyr
 35 40 45
 Pro Ser Cys Leu Pro Gly Ile Ser Ile Asn Ser Glu Gln Leu Thr Arg
 50 55 60
 Ala Gln Cys Val Thr Val Lys Glu Lys Leu Leu Glu Gln Ala Glu Ser
 65 70 75 80
 Leu Leu Ser Glu Pro Met Val His Glu Leu Val Leu Trp Ile Gln Gln
 85 90 95
 Asn Leu Arg His Ile Leu Ser Gln Pro Glu Thr Gly Ser Gly Ser Glu
 100 105 110
 Lys Cys Thr Phe Ser Thr Ser Thr Thr Met Asp Asp Gly Leu Trp Ile
 115 120 125
 Thr Leu Leu His Leu Asp His Met Arg Ala Lys Thr Lys Tyr Val Lys
 130 135 140
 Ile Val Glu Lys Trp Ala Ser Asp Leu Arg Leu Thr Gly Arg Leu Met
 145 150 155 160
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 165 170 175
 Leu Lys Val Pro Lys Ser
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<210> 4699

<211> 1441

<212> DNA

<213> Homo sapiens

<400> 4699

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 taagtcattt cacctcggag accgaaaaaa tgaatcaaaaa gaaactatga gtaacaagct
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 ataacatagt tcaccacaat gggaccccc ccccttttt ctcaccctac agttagtaat
 240

attacaatta aaataactat attcttctat attttttctg ttaaaatcat ctcataaatt
 300
 tacaatgcta ttattagttt ccaagactaa tataaattca ctccattttt ctacaacgaa
 360
 aatgattaat ttagaagcac acgacgtcat gatgaaaaac acaagcattt tagtagcaag
 420
 gacttgatca gttaagaatt agttttcttg taaaacattc taaagccaag taaaatatcc
 480
 attcttataa catacctata atatgagact aaggaatagg ttacatatag gtctacaaca
 540
 cattgggttg tctttaaaaa aacaaaagta gacatttata aataaaaaag agggacaatt
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 660
 taacatggat taacactttt tattacagaa accgtacggt gaaggaacac aacagaccag
 720
 ggctttcata gggttattga gattgagctg agatgacctg ggagagaaag atctaggtga
 780
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 960
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 1441

<210> 4700

<211> 116

<212> PRT

<213> Homo sapiens

<400> 4700

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 Ser Thr Arg Gly Gln Ser Lys Thr Gly Trp Lys Leu Pro Val Thr Leu
 20 25 30
 Ile Cys Cys Pro Arg His Pro Leu Met Arg Leu Lys Leu Gly Pro Ser

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      35              40              45
Glu Thr Ala Ala Ala Pro Tyr Arg Ala Cys Trp Leu Cys Arg Gly Glu
  50              55              60
Val Asp Asp Lys Gly Thr Arg His Ala Ser Ala Pro Cys Val Arg Ser
  65              70              75              80
Gly Leu Gly His Ser Pro Cys Thr Ser Lys Thr Pro Val Leu Thr Pro
      85              90              95
Thr Ser Lys Glu Leu Leu Leu Leu Ile Cys Lys Ala Ile Leu Leu Leu
  100              105              110
Ser Asn Leu Val
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<210> 4701

<211> 812

<212> DNA

<213> Homo sapiens

<400> 4701

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  120
cctggccatt tttttcttga gacaaggctct tattctctcg ccaagaatgg agtgcagtgg
  180
tgcaatgttg gctcactgca gcccaaacct cctgggctta agtgcctctc ctacctcagc
  240
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  300
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  420
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  480
tgctgcctct cagccacctg ccagccctgt tttatgaata tgtttaccgt ggctgtcact
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  600
atggaactcca agacggtctg acggtgctcg gacgccttca ggcggaatctg ctgcgggatg
  660
atgtctgcat tctccgcctc ggcccttggtg cgcgcccggt cctcggtctc cactgcagc
  720
atctcattct tgtgcgcagc ctccatctcc cgtctccagc tggctcgcgc catggcttcc
  780
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  812

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<210> 4702

<211> 69

<212> PRT

<213> Homo sapiens

<400> 4702

Arg Gln Gly Phe Thr Leu Thr Arg Met Ile Ser Ile Ser Gly Pro Arg


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      1             5             10             15
Asp Pro Pro Thr Ser Ala Ser Glu Asn Ala Gly Ile Thr Gly Leu Ser
      20
His Xaa Pro Pro Gly His Phe Phe Leu Glu Thr Arg Ser Tyr Ser Leu
      35             40             45
Ala Lys Asn Gly Val Gln Trp Cys Asn Val Gly Ser Leu Gln Pro Lys
      50             55             60
Pro Pro Gly Leu Lys
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<210> 4703

<211> 513

<212> DNA

<213> Homo sapiens

<400> 4703

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cgaagagtct tcgaagggtt gccgcttttc ggtggcgagc ttctcgcgag aaggaaaatg
180
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240
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300
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360
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513

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<210> 4704

<211> 112

<212> PRT

<213> Homo sapiens

<400> 4704

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Met Ala Ala Pro Glu Gln Pro Leu Ala Ile Ser Arg Gly Cys Thr Ser
      1             5             10             15
Ser Ser Ser Leu Ser Pro Pro Arg Ala Asp Arg Thr Leu Leu Val Arg
      20
His Leu Pro Ala Glu Leu Thr Ala Glu Glu Lys Glu Asp Leu Leu Lys
      35             40             45
Tyr Phe Gly Ala Gln Ser Val Arg Val Leu Ser Asp Lys Gly Arg Leu
      50             55             60
Lys His Thr Ala Phe Ala Thr Phe Pro Asn Glu Lys Ala Ala Ile Lys
      65             70             75             80
Ala Leu Thr Arg Leu His Gln Leu Lys Leu Leu Gly His Thr Leu Val
      85             90             95
Val Glu Phe Ala Lys Glu Gln Asp Arg Val His Ser Pro Cys Pro Thr

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100

105

110

<210> 4705
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 4705
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 180
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 240
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 360
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 420
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<210> 4706
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 4706
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 20 25 30
 Thr Glu Leu Arg Glu Tyr Phe Lys Lys Phe Gly Val Val Thr Glu Val
 35 40 45
 Val Met Ile Tyr Asp Ala Glu Lys Gln Arg Pro Arg Gly Lys Gly Arg
 50 55 60
 Ser Ser Leu Thr Ser Ala Phe Ser Leu Leu Leu Pro Gln Met Ala Asn
 65 70 75 80
 Tyr Leu Thr Arg Gln Ala His Thr Gly Gly Gly Cys Ser Lys Gln Pro
 85 90 95
 Gln Glu Gly Thr Ile Trp Arg Gln Met Thr Lys Thr Trp Ala Pro His
 100 105 110
 Val His Pro Ile Gln Pro Val Cys Ala Ser Arg Gly Gln Thr Ser His
 115 120 125
 Ile Val Phe Trp Leu Val Leu Leu Lys Phe Leu Arg Leu Val Met Ser
 130 135 140
 Leu Gly Leu Ala Ser Val Phe His Cys Pro

145

150

<210> 4707

<211> 748

<212> DNA

<213> Homo sapiens

<400> 4707

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 120
 gtctttccgg agacccctgg aatttaaattc attagcaccg cgccttcccc cgaagagtct
 180
 tcgaagggtt gccgcttttc ggtggcgag ttctcgcgag aagggtgactt tctttctcgg
 240
 tatttctcgg ttccagaat ccttagcgcg agggcgaaaa aatatttctc ccagcttggtg
 300
 ttgatgccgc gattttgact gagacttctt cccacgattt ctgtttttgc ttctccaagg
 360
 aaaatggcag ctccccgagc gccgcttgcg atatcaagg gatgcacgag ctctctctcg
 420
 ctttccccgc ctccggggcga ccgaaccctt ctggtcaggc acctgccggc tgagcttact
 480
 gctgaggaga aagaggactt gctgaagtac ttccggggcgc agtctgtgcy ggtcctgtca
 540
 gataaggggc gactgaaaca tacagctttt gccacattcc ctaatgaaaa agcagctata
 600
 aaggcattga caagactcca tcaactgaaa cttttaggtc atactttagt cgttgaaatt
 660
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 720
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 748

<210> 4708

<211> 128

<212> PRT

<213> Homo sapiens

<400> 4708

Met Ala Ala Pro Glu Gln Pro Leu Ala Ile Ser Arg Gly Cys Thr Ser
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 Ser Ser Ser Leu Ser Pro Pro Arg Gly Asp Arg Thr Leu Leu Val Arg
 20 25 30
 His Leu Pro Ala Glu Leu Thr Ala Glu Lys Glu Asp Leu Leu Lys
 35 40 45
 Tyr Phe Gly Ala Gln Ser Val Arg Val Leu Ser Asp Lys Gly Arg Leu
 50 55 60
 Lys His Thr Ala Phe Ala Thr Phe Pro Asn Glu Lys Ala Ala Ile Lys
 65 70 75 80
 Ala Leu Thr Arg Leu His Gln Leu Lys Leu Leu Gly His Thr Leu Val
 85 90 95
 Val Glu Phe Ala Lys Glu Gln Asp Arg Val His Ser Pro Cys Pro Thr

aaaaaaaaattt attaaaaaaat tctattatttt t
1351

<210> 4710

<211> 304

<212> PRT

<213> Homo sapiens

<400> 4710

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Leu Asp Trp Ser Thr Thr Gln Glu Thr Leu Arg Ser Tyr Phe Ser Gln
 20          25          30
Tyr Gly Glu Val Val Asp Cys Val Ile Met Lys Asp Lys Thr Thr Asn
 35          40          45
Gln Ser Arg Gly Phe Gly Phe Val Lys Phe Lys Asp Pro Asn Cys Val
 50          55          60
Gly Thr Val Leu Ala Ser Arg Pro His Thr Leu Asp Gly Arg Asn Ile
 65          70          75          80
Asp Pro Lys Pro Cys Thr Pro Arg Gly Met Gln Pro Glu Arg Thr Arg
 85          90          95
Pro Lys Glu Gly Trp Gln Lys Gly Pro Arg Ser Asp Asn Ser Lys Ser
100          105          110
Asn Lys Ile Phe Val Gly Gly Ile Pro His Asn Cys Gly Glu Thr Glu
115          120          125
Leu Arg Glu Tyr Phe Lys Lys Phe Gly Val Val Thr Glu Val Val Met
130          135          140
Ile Tyr Asp Ala Glu Lys Gln Arg Pro Arg Gly Phe Gly Phe Ile Thr
145          150          155          160
Phe Glu Asp Glu Gln Ser Val Asp Gln Ala Val Asn Met His Phe His
165          170          175
Asp Ile Met Gly Lys Lys Val Glu Val Lys Arg Ala Glu Pro Arg Asp
180          185          190
Ser Lys Ser Gln Ala Pro Gly Gln Pro Gly Ala Ser Gln Trp Gly Ser
195          200          205
Arg Val Val Pro Asn Ala Ala Asn Gly Trp Ala Gly Gln Pro Pro Pro
210          215          220
Thr Trp Gln Gln Gly Tyr Gly Pro Gln Gly Met Trp Val Pro Ala Gly
225          230          235          240
Gln Ala Ile Gly Gly Tyr Gly Pro Pro Pro Ala Gly Arg Gly Ala Pro
245          250          255
Pro Pro Pro Pro Pro Phe Thr Ser Tyr Ile Val Ser Thr Pro Pro Gly
260          265          270
Gly Phe Pro Pro Pro Gln Gly Phe Pro Gln Gly Tyr Gly Ala Pro Pro
275          280          285
Gln Phe Ser Phe Gly Tyr Gly Pro Pro Pro Pro Pro Gly Ser Arg
290          295          300
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<210> 4711

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 4711

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120
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600
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720
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840
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1620

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 1740
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 1920
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 2040
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<210> 4712

<211> 187

<212> PRT

<213> Homo sapiens

<400> 4712

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Leu	Gln	Met	Asp	Val	Met	Pro	Gly	Glu	Gly	Asp	Leu	Pro	Gln	Met	Glu
		20						25				30			
Val	Gly	Ser	Gly	Ser	Arg	Glu	Leu	Ser	Leu	Arg	Pro	Ser	Arg	Ser	Gly
		35					40				45				
Ala	Gln	Gln	Leu	Glu	Glu	Glu	Gly	Pro	Met	Glu	Glu	Glu	Glu	Ala	Gln
	50					55				60					
Pro	Met	Ala	Ala	Pro	Glu	Gly	Lys	Arg	Ser	Leu	Ala	Asn	Gly	Pro	Asn
	65				70				75					80	
Ala	Gly	Glu	Gln	Pro	Gly	Gln	Val	Ala	Gly	Ala	Asp	Phe	Glu	Ser	Glu
			85					90					95		
Asp	Glu	Gly	Glu	Glu	Phe	Asp	Asp	Trp	Glu	Asp	Asp	Tyr	Asp	Tyr	Pro
		100					105					110			
Glu	Glu	Glu	Gln	Leu	Ser	Gly	Ala	Gly	Tyr	Arg	Val	Ser	Ala	Ala	Leu
		115				120					125				
Glu	Glu	Ala	Asp	Lys	Met	Phe	Leu	Arg	Thr	Arg	Glu	Pro	Ala	Leu	Asp
		130				135					140				
Gly	Gly	Phe	Gln	Met	His	Tyr	Glu	Lys	Thr	Pro	Phe	Asp	Gln	Leu	Ala
	145				150				155					160	
Phe	Ile	Glu	Glu	Leu	Phe	Ser	Leu	Met	Val	Val	Asn	Arg	Leu	Thr	Glu
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<210> 4713

<211> 1324

<212> DNA

<213> Homo sapiens

<400> 4713

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120
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180
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240
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<211> 145

<212> PRT

<213> Homo sapiens

<400> 4714

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Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln			
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Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn			
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<212> DNA

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<400> 4715

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<211> 239

<212> PRT

<213> Homo sapiens

<400> 4716

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<212> DNA

<213> Homo sapiens

<400> 4717

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<212> PRT

<213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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<210> 4720
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 <212> PRT
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 Glu Glu Asn Gln His Ser Asp Ser Cys Tyr Lys Leu Gly Ala Tyr Tyr
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 Cys Phe Leu Met Ala Cys Glu Lys Pro Gly Lys Lys Ser Ile Ala Ala
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 Cys His Asn Val Gly Leu Leu Ala His Asp Gly Gln Val Asn Glu Asp
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<210> 4721

<211> 1385

<212> DNA

<213> Homo sapiens

<400> 4721

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<213> Homo sapiens

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Val	Met	Cys	Thr	Glu	Cys	Ser	Thr	Glu	Val	Ala	Val	Tyr	Asp	Lys	Asp
			260					265					270		
Glu	Val	Phe	His	Phe	Phe	Asn	Val	Leu	Ala	Ser	His	Ser			
		275					280					285			

<210> 4723
 <211> 1213
 <212> DNA
 <213> Homo sapiens

<400> 4723
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 60
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 120
 ggctggggagc tgcacctccc tcctactcat ggtggacagc agtggggact agggaggggc
 180
 aggagaggtg gctgacgccca ggcagcagca gcagtgatgg ggccacgacg ccacagagca
 240
 agctccatcc tccccagac cctgggtggga gtccctgtgg gttgggggtg ggagtgggga
 300
 gaaccacccc caggccctcc ctctcccttc cccagacagt ctcttttcgg gctcaaccca
 360
 tttttctcgg caggagactg aggcacacag agaggaggaa gtgggagagg aggacgaggg
 420
 aggggcaggn gtggcagcac aaatgaaggc agaggtgaga ggcgtgggca aggccactcc
 480
 acccccacac ccaccccaga gggggcgag gaagccacac catcacgacg catgtcgggg
 540
 ggacaaggcg gggtttaagg ctgagggggc cggggcgagg cgggcctcgg gcctcagtca
 600
 aagccgtgcc cagtcgctgt gctctgagtc gtattccagc tcggcgccca cacacttgac
 660
 accatccagc agcatgggag tgccgtggtg cgggtccatg acgcgggcct gcaccgtcac
 720
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 780
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 840
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 1020
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 1080
 ccggactctg ggctgtgtgc ccttgttggc tgcagccatg gacgcccccc ctgccacgca
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 1200
 ggagccttgc tgt
 1213

<210> 4724
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 4724

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Met Gly Pro Arg Arg His Arg Ala Ser Ser Ile Leu Pro Gln Thr Leu
 1           5           10           15
Val Gly Val Pro Val Gly Trp Gly Gly Glu Trp Gly Glu Pro Thr Pro
          20           25           30
Gly Pro Pro Ser Pro Phe Pro Arg Gln Ser Pro Phe Gly Leu Asn Pro
          35           40           45
Phe Leu Pro Ala Gly Asp
          50

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<210> 4725

<211> 366

<212> DNA

<213> Homo sapiens

<400> 4725

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120
tgccgatgtg cagctgtgta tatgcatatg tgcacaggtg cctgtgcctg tgtgaacaca
180
tgttctcagc tgtgtacctg cntctcttgc ccatgcctgt acgtgcacac gtgcctctgt
240
atgcatgcat gtagatctgt gtgccatcac cctcacgtga gaatacatat gcgcttgtgc
300
cttcacctct gcattgatgc tagtgtgtgc ctgcgtgcat gggtgtgcat ctgtgcctgc
360
acgcgt
366

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<210> 4726

<211> 122

<212> PRT

<213> Homo sapiens

<400> 4726

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Xaa Phe Leu Glu Gly Glu Leu Gly Arg Ser Arg Arg Thr Pro Ala Gly
 1           5           10           15
Gly Arg Gly Ala Met Leu Ala Ile Asp Thr Ala Ser Asp Ile Leu Ala
          20           25           30
His Val His Val Tyr Ser Arg Leu Cys Ala Cys Ala Arg Val Tyr Met
          35           40           45
His Met Cys Thr Gly Ala Cys Ala Cys Val Asn Thr Cys Ser His Val
          50           55           60
Cys Thr Cys Xaa Ser Cys Pro Cys Xaa Tyr Val His Thr Cys Leu Cys
          65           70           75           80
Met His Ala Cys Ile Ala Val Cys Pro Tyr Pro His Val Arg Ile His
          85           90           95
Met Arg Leu Cys Leu His Leu Cys Met His Ala Ser Val Leu Leu Arg
          100          105          110
Ala Trp Val Cys Ile Cys Ala Cys Thr Arg
          115          120

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<210> 4727

<211> 2031

<212> DNA

<213> Homo sapiens

<400> 4727

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120
tagctgggat tacagggacc caccaccaca ccgggctaatt tttttttgta tttttactag
180
agacgggggtt tcaactatgtt ggccagactg gtctcgaaact cctaacctca tgatccgctc
240
actttggcct cccaaagtgc tgggattaca gccgtgagcc accgcacctg gtctcgcttc
300
acttaacttct tcaattcttc gatggcctcc ggcaaccggc ggaggtgggt aagtagcagg
360
gagactgcga gttcggcggt ggtatctgtc aggacatctg ggggtgtagcc aactcggatc
420
ccagcttctt tgatttcctc caaagccaag tggtcgatgc ccacagacat ggtgctgatg
480
actttgagat tggccccggc ccagctacat tcccgggcca gcttctgtac tgcagggtcc
540
gggtcggcgg ctgcactcgc gatgagaccg gtgcgactca tgaagtggtt cgtcaccgcg
600
aggatacccg ccgagggtag ggtcgcgctc gcccgggcgg cagactgtga ggtggagcag
660
tgggactcgg atgagcccat ccctgccaaag gagctagagc gaggtgtggc gggggccac
720
ggctgctctt gctcctcttc cgaccacgtg gacaagagga tcttgatgc tgcaggggct
780
aatctcaaa gcatcagcac catgtctgtg ggcatcgacc acttggtctt ggatgaaatc
840
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900
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960
aagaatgggt gctggacctc gtggaagccc ctctggctgt gtggctatgg actcacgcag
1020
agcactgtcg gcatcactcg gctggggcgc ataggccagg ccattgctcg gcgtctgaaa
1080
ccattcggtg tccagagatt tctgtacaca gggcgccagc ccaggcctga ggaagcagcg
1140
gaattccagg cagagtttgt gtctaccctt gagctggctg cccaatctga tttcatcgct
1200
gtggcctgct ccttaacacc tgcaaccogag ggactctgca acaaggactt cttccagaag
1260
atgaaggaaa cagctgtgtt catcaacatc agcagggggc acgtcgtaaa ccaggacgac
1320
ctgtaccagg ccttgggcag tggtaagatt gcagctgctg gactggatgt gacgagccca
1380
gaaccactgc ctacaaacca cctctcctcg accctgaaga actgtgtgat tctgccccac
1440

attggcagtg ccaccacag aaccgcaac accatgtcct tgttggcagc taacaacttg
 1500
 ctggctggcc tgagagggga gccgatgcct agtgaactca agctgtagcc aaacagtaga
 1560
 gatggagggc cgggaagcaa accgtgccct ggtattgtca gacacacca ggcttgattt
 1620
 ggatccacag gcagagccaa gggaaggtgt gattctctga ggaaagagtg attctgatat
 1680
 atgtacttgg cgcaaattgtg tccaacacca atgtgacaga ctgaccccaa caccctccag
 1740
 tcacaacaac tcacgtggac tgctctcct cagggcttcc aggatagcct tcttttcttc
 1800
 gggcaagccc tagcccaaga ccttgctctc ttggatcttt cccccagccg ccttcttcaa
 1860
 tatctagatg acctcttctt ctgtagcccc tccctaaaaa actcccaaac tcacactgcc
 1920
 acccttctga atttcttac taataaaggc tatagggtct cccctttaa gaacagcttt
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 2031

<210> 4728

<211> 328

<212> PRT

<213> Homo sapiens

<400> 4728

Met	Arg	Pro	Val	Arg	Leu	Met	Lys	Val	Phe	Val	Thr	Arg	Arg	Ile	Pro
1				5					10					15	
Ala	Glu	Gly	Arg	Val	Ala	Leu	Ala	Arg	Ala	Ala	Asp	Cys	Glu	Val	Glu
			20					25					30		
Gln	Trp	Asp	Ser	Asp	Glu	Pro	Ile	Pro	Ala	Lys	Glu	Leu	Glu	Arg	Gly
	35					40					45				
Val	Ala	Gly	Ala	His	Gly	Leu	Leu	Cys	Leu	Leu	Ser	Asp	His	Val	Asp
	50					55					60				
Lys	Arg	Ile	Leu	Asp	Ala	Ala	Gly	Ala	Asn	Leu	Lys	Val	Ile	Ser	Thr
	65				70				75					80	
Met	Ser	Val	Gly	Ile	Asp	His	Leu	Ala	Leu	Asp	Glu	Ile	Lys	Lys	Arg
			85						90					95	
Gly	Ile	Arg	Val	Gly	Tyr	Thr	Pro	Asp	Val	Leu	Thr	Asp	Thr	Thr	Ala
			100					105					110		
Glu	Leu	Ala	Val	Ser	Leu	Leu	Leu	Thr	Thr	Cys	Arg	Arg	Leu	Pro	Glu
			115					120					125		
Ala	Ile	Glu	Glu	Val	Lys	Asn	Gly	Gly	Trp	Thr	Ser	Trp	Lys	Pro	Leu
	130					135					140				
Trp	Leu	Cys	Gly	Tyr	Gly	Leu	Thr	Gln	Ser	Thr	Val	Gly	Ile	Ile	Gly
	145				150					155				160	
Leu	Gly	Arg	Ile	Gly	Gln	Ala	Ile	Ala	Arg	Arg	Leu	Lys	Pro	Phe	Gly
			165						170					175	
Val	Gln	Arg	Phe	Leu	Tyr	Thr	Gly	Arg	Gln	Pro	Arg	Pro	Glu	Glu	Ala
			180					185					190		
Ala	Glu	Phe	Gln	Ala	Glu	Phe	Val	Ser	Thr	Pro	Glu	Leu	Ala	Ala	Gln
	195						200					205			
Ser	Asp	Phe	Ile	Val	Val	Ala	Cys	Ser	Leu	Thr	Pro	Ala	Thr	Glu	Gly

```

      210              215              220
Leu Cys Asn Lys Asp Phe Phe Gln Lys Met Lys Glu Thr Ala Val Phe
225              230              235              240
Ile Asn Ile Ser Arg Gly Asp Val Val Asn Gln Asp Asp Leu Tyr Gln
      245              250              255
Ala Leu Ala Ser Gly Lys Ile Ala Ala Gly Leu Asp Val Thr Ser
      260              265              270
Pro Glu Pro Leu Pro Thr Asn His Pro Leu Leu Thr Lys Asn Cys
      275              280              285
Val Ile Leu Pro His Ile Gly Ser Ala Thr His Arg Thr Arg Asn Thr
      290              295              300
Met Ser Leu Leu Ala Ala Asn Asn Leu Leu Ala Gly Leu Arg Gly Glu
305              310              315              320
Pro Met Pro Ser Glu Leu Lys Leu
      325

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<210> 4729

<211> 753

<212> DNA

<213> Homo sapiens

<400> 4729

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ngctagcagc agcccgacca cgcgttacgc cgcgtcgcg cctttccctt gacacggcgg
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120
cctgtgtgtg gatttgggga aattttttgt ttgtttttta tgatttgtat ttgactgaga
180
gaaacccact gaagacgtct cgttgagaat agagaccacc gaggcgcgact cgcggggccgc
240
tgcaaccacc gccagggaca aaaggagccc agcgtacta gctgcaccgc attcctccca
300
gtgcttagca tgaagaaggc cgaaatggga cgattcagta tttccccgga tgaagacagc
360
agcagctaca gttccaacag cgacttcaac tactcctacc ccaccaagca agctgctctg
420
aaaagccatt atgcagatgt agatcctgaa aaccagaact ttttacttga atcgaatttg
480
gggaagaaga agtatgaaac agaatttcat ccagggtacta cttccttttg aatgtcagta
540
tttaattctg gcaatgcgat tgtgggcagt ggaatccttg ggctttctta tgccatgggt
600
aatactggaa ttgctctttt tataattctc ttgacatttg tgtcaatatt ttcctgtgat
660
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753

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<210> 4730

<211> 148

<212> PRT

<213> Homo sapiens

<400> 4730

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Met Lys Lys Ala Glu Met Gly Arg Phe Ser Ile Ser Pro Asp Glu Asp
 1           5           10           15
Ser Ser Ser Tyr Ser Ser Asn Ser Asp Phe Asn Tyr Ser Tyr Pro Thr
 20           25           30
Lys Gln Ala Ala Leu Lys Ser His Tyr Ala Asp Val Asp Pro Glu Asn
 35           40           45
Gln Asn Phe Leu Leu Glu Ser Asn Leu Gly Lys Lys Tyr Glu Thr
 50           55           60
Glu Phe His Pro Gly Thr Thr Ser Phe Gly Met Ser Val Phe Asn Leu
 65           70           75           80
Ser Asn Ala Ile Val Gly Ser Gly Ile Leu Gly Leu Ser Tyr Ala Met
 85           90           95
Ala Asn Thr Gly Ile Ala Leu Phe Ile Ile Leu Leu Thr Phe Val Ser
100           105           110
Ile Phe Ser Leu Tyr Ser Val His Leu Leu Leu Lys Thr Ala Asn Glu
115           120           125
Gly Gly Ser Leu Leu Tyr Glu Gln Leu Gly Tyr Lys Ala Ser Gly Leu
130           135           140
Val Gly Lys Leu
145

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<210> 4731

<211> 2417

<212> DNA

<213> Homo sapiens

<400> 4731

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tttttttttt tttttcagac aaggtacat tttattcctt ataaaatata tttcatattg
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ttgctgtaaa aacattacat ttcacatttt taaaaaat ttaacagta aaaataatac
120
ttggaagaca gctgaggaaa aaggcgcaa taagacaaac tcacagatgg gatttatctc
180
cctcttgctt tttttttttt tttttgcccc tggtaaaagt cagaacctgg gatgaccaga
240
aagtaacagg acagatttct ccagcaaat cagtcctcac aacaaatga atattgttct
300
ccaaggagtc aagctataga ctcaaatga caacgtggcc atggctcaaa acactctctg
360
aaattacaaa attgctttct gagccaattt aaagtcaca tgattgaatc caagctattt
420
tactttaaat ggtccttttg ctttgcaact gagacctcgc ttggccacag acgtcattcg
480
ctggactccc tgggcaacta atgagtgtct agcatcctta aggetgtctc acacacagcc
540
ccagactctg aatatgattc caagaaatat tctgaaaaaa gtcacatcgc tgggaataac
600
agtttcccaa gataactgct ttgaaaacca gtcccgtagg tttctaaaag cccacctacg
660
gcaccttctt tccatcagag tctgctgccc ggggtgggctg ggaaggaggg agatacaaa
720
aagaaagtag gcatgatcac tgggtcggtt cccaagccac cctcaccttc caagaaggca
780

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tgaatggaac aaccccagaga acagagcacg tgtgaagaac caacacgaca ggcacgggat
840
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900
agcgcaggga ggggaaggtgg caccaaaacc tagtaagaac aaagcaaac caccgtggtt
960
tccacactgc tctctccctt tattcctctc ttctctgccc tgtataccaa cggcataaga
1020
agcctgcaca aagagaaaaa tccgtatatc cagttatatc tacacggtcc aaactggggg
1080
cggggggaat tcaaacagct ttctaaagac gagacggcag tgaaaactct gagggagagg
1140
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1320
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1920
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1980
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2040
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2100
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2160
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2220
cttctgaata catcgtaaaa gaaaacaaag catttctgag gcgtccttcc aataaccgga
2280
ggaaggcggc gtcaggaggg tgcttcctcg ggtcagagca gagagtttcc agacgtctaa
2340
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2400

cattccaaaa agtgaat
2417

<210> 4732

<211> 129

<212> PRT

<213> Homo sapiens

<400> 4732

Met	Ser	Ile	Ser	Arg	Ala	Val	Leu	Gly	Glu	Lys	Glu	Gly	Gly	Leu	Gly
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Ser	Val	Ala	Pro	Cys	Gln	Pro	Ala	Leu	Arg	Glu	Asp	Arg	Val	Ser	His
			20					25					30		
Ala	Arg	Met	Ala	Gly	His	Val	Ser	Val	Leu	Val	Ser	His	Phe	Pro	Pro
		35				40						45			
Ser	Val	Thr	Tyr	Leu	Gly	Ile	Pro	Gln	Gly	Leu	Glu	Cys	Asp	Cys	
	50				55					60					
Pro	Leu	Pro	Ser	Cys	Leu	Gly	Tyr	Lys	Ser	Trp	Pro	Tyr	Val	Pro	Ala
65					70				75					80	
Val	Arg	Gly	Ser	Gly	Asn	Pro	Thr	Gln	Pro	Pro	Val	Leu	Gly	Trp	Ser
			85					90					95		
Val	Ser	Ile	His	Pro	Leu	Val	Val	Ile	Glu	Ala	Ala	Leu	Pro	Val	Leu
			100					105					110		
Gly	Glu	Asp	Ile	Trp	Ala	Thr	Arg	Ala	Pro	Leu	Ala	Pro	Ser	Arg	Arg
		115					120						125		

Lys

<210> 4733

<211> 543

<212> DNA

<213> Homo sapiens

<400> 4733

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120
tccattccca ataactgtaa gctgcagtgt gtatcctgga acaaggaaca agggttcata
180
gcatgcggtg gtgaagatgg attactgaaa gttttgaaat tagagacgca gacagatgat
240
gcaaaattga ggggccttgc agccccagt aacctttcta tgaatcagac tcttgaaggt
300
catagtgtgt ctgttcaagt tgtaacatgg aatgagcagt atcagaagtt gactaccagt
360
gatgaaaacg ggcttatcat tgtgtggatg ttatataaag gctcttggat tgaggagatg
420
atcaacaatc gaaataaatc agttgttcgc agtatgagct ggaatgctga cggacagaag
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540
tgg
543

<210> 4734
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 4734
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 1 5 10 15
 Val Glu Gly Leu Ser Gly Arg Arg Asp Pro Leu Gly Asp Pro Thr Met
 20 25 30
 Phe Phe Tyr Leu Ser Lys Lys Ile Ser Ile Pro Asn Asn Val Lys Leu
 35 40 45
 Gln Cys Val Ser Trp Asn Lys Glu Gln Gly Phe Ile Ala Cys Gly Gly
 50 55 60
 Glu Asp Gly Leu Leu Lys Val Leu Lys Leu Glu Thr Gln Thr Asp Asp
 65 70 75 80
 Ala Lys Leu Arg Gly Leu Ala Ala Pro Ser Asn Leu Ser Met Asn Gln
 85 90 95
 Thr Leu Glu Gly His Ser Gly Ser Val Gln Val Val Thr Trp Asn Glu
 100 105 110
 Gln Tyr Gln Lys Leu Thr Thr Ser Asp Glu Asn Gly Leu Ile Ile Val
 115 120 125
 Trp Met Leu Tyr Lys Gly Ser Trp Ile Glu Glu Met Ile Asn Asn Arg
 130 135 140
 Asn Lys Ser Val Val Arg Ser Met Ser Trp Asn Ala Asp Gly Gln Lys
 145 150 155 160
 Ile Cys Ile Val Tyr Glu Asp Gly Ala Val Ile Val Gly Ser Val Asp
 165 170 175
 Gly Asn Arg Ile Trp
 180

<210> 4735
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 4735
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 60
 gatgcacgag aacccggagt gggagaaggc ccgtcaggcc ctggccagca tcagcaagtc
 120
 aggagctgcc ggccggctctg ccaagtccag cagcaatggg cctgtggcca gtgcacagta
 180
 cgtgtcccg gcaaaagcct cagctttgca gcagcagcag tactaccagt ggtaccagca
 240
 ggacaactat gcctaccct acagctacta ctatcccatg cccccaggcc ccggcatgga
 300

<210> 4736
 <211> 93
 <212> PRT
 <213> Homo sapiens

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<400> 4736
Met Val Ala Gly Ala Gly Arg Glu Asn Gly Met Glu Thr Pro Met His
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Glu Asn Pro Glu Trp Glu Lys Ala Arg Gln Ala Leu Ala Ser Ile Ser
  20             25             30
Lys Ser Gly Ala Ala Gly Gly Ser Ala Lys Ser Ser Ser Asn Gly Pro
  35             40             45
Val Ala Ser Ala Gln Tyr Val Ser Gln Ala Lys Ala Ser Ala Leu Gln
  50             55             60
Gln Gln Gln Tyr Tyr Gln Trp Tyr Gln Gln Asp Asn Tyr Ala Tyr Pro
  65             70             75             80
Tyr Ser Tyr Tyr Tyr Pro Met Pro Pro Gly Pro Gly Met
  85             90

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<210> 4737
<211> 2602
<212> DNA
<213> Homo sapiens

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  120
caagctcggc ccctttcaac tctgccaaga atggctccca cctggctctc agacattccc
  180
ctgggtccaa cccagggcca tcaagatgtc tcagagaggg ggctagacac ccagagacct
  240
caagtgacca tgtgggaacg ggaatgttcc agtgacaggg agggagccagg cgggagaggg
  300
aggtcctggg ggctggaggg gtcacaggcc ctgagccagc aggctgaggt gatcggtcgg
  360
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<210> 4738

<211> 756

<212> PRT

<213> Homo sapiens

<400> 4738

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Thr Met Trp Glu Arg Asp Val Ser Ser Asp Arg Gln Glu Pro Gly Arg
 35              40              45
Arg Gly Arg Ser Trp Gly Leu Glu Gly Ser Gln Ala Leu Ser Gln Gln
 50              55              60
Ala Glu Val Ile Val Arg Gln Leu Gln Glu Leu Arg Arg Leu Glu Glu
 65              70              75              80
Glu Val Arg Leu Leu Arg Glu Thr Ser Leu Gln Gln Lys Met Arg Leu
 85              90              95
Glu Ala Gln Ala Met Glu Leu Glu Ala Leu Ala Arg Ala Glu Lys Ala
100              105              110
Gly Arg Ala Glu Ala Glu Gly Leu Arg Ala Ala Leu Ala Gly Ala Glu
115              120              125
Val Val Arg Lys Asn Leu Glu Glu Gly Arg Gln Arg Glu Leu Glu Glu
130              135              140
Val Gln Arg Leu His Gln Glu Gln Leu Ser Ser Leu Thr Gln Ala His
145              150              155              160
Glu Glu Ala Leu Ser Ser Leu Thr Ser Lys Ala Glu Gly Leu Glu Lys
165              170              175
Ser Leu Ser Ser Leu Glu Thr Arg Arg Ala Gly Glu Ala Lys Glu Leu
180              185              190
Ala Glu Ala Gln Arg Glu Ala Glu Leu Leu Arg Lys Gln Leu Ser Lys
195              200              205
Thr Gln Glu Asp Leu Glu Ala Gln Val Thr Leu Val Glu Asn Leu Arg
210              215              220
Lys Tyr Val Gly Glu Gln Val Pro Ser Glu Val His Ser Gln Thr Trp
225              230              235              240
Glu Leu Glu Arg Gln Lys Leu Leu Glu Thr Met Gln Leu Leu Gln Glu
245              250              255
Asp Arg Asp Ser Leu His Ala Thr Ala Glu Leu Leu Gln Val Arg Val
260              265              270
Gln Ser Leu Thr His Ile Leu Ala Leu Gln Glu Glu Glu Leu Thr Arg
275              280              285
Lys Val Gln Pro Ser Asp Ser Leu Glu Pro Glu Phe Thr Arg Lys Cys
290              295              300
Gln Ser Leu Leu Asn Arg Trp Arg Glu Lys Val Phe Ala Leu Met Val
305              310              315              320
Gln Leu Lys Ala Gln Glu Leu Glu His Ser Asp Ser Val Lys Gln Leu
325              330              335
Lys Gly Gln Val Ala Ser Leu Gln Glu Lys Val Thr Ser Gln Ser Gln
340              345              350
Glu Gln Ala Ile Leu Gln Arg Ser Leu Gln Asp Lys Ala Ala Glu Val
355              360              365
Glu Val Glu Arg Met Gly Ala Lys Gly Leu Gln Leu Glu Leu Ser Arg

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370
 Ala Gln Glu Ala Arg Arg Trp Trp Gln Gln Gln Thr Ala Ser Ala Glu
 385 390 395 400
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 405 410 415
 Leu Glu Thr Thr Met Ala Lys Val Glu Gly Ala Ala Ala Gln Leu Pro
 420 425 430
 Ser Leu Asn Asn Arg Leu Ser Tyr Ala Val Arg Lys Val His Thr Ile
 435 440 445
 Arg Gly Leu Ile Ala Arg Lys Leu Ala Leu Ala Gln Leu Arg Gln Glu
 450 455 460
 Ser Cys Pro Leu Pro Pro Pro Val Thr Asp Val Ser Leu Glu Leu Gln
 465 470 475 480
 Gln Leu Arg Glu Glu Arg Asn Arg Leu Asp Ala Glu Leu Gln Leu Ser
 485 490 495
 Ala Arg Leu Ile Gln Gln Glu Val Gly Arg Ala Arg Glu Gln Gly Glu
 500 505 510
 Ala Glu Arg Gln Gln Leu Ser Lys Val Ala Gln Gln Leu Glu Gln Glu
 515 520 525
 Leu Gln Gln Thr Gln Glu Ser Leu Ala Ser Leu Gly Leu Gln Leu Glu
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 Val Ala Arg Gln Gly Gln Gln Glu Ser Thr Glu Glu Ala Ala Ser Leu
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 Arg Gln Glu Leu Thr Gln Gln Gln Glu Tyr Gly Gln Ala Leu Gln
 565 570 575
 Glu Lys Val Ala Glu Val Glu Thr Arg Leu Arg Glu Gln Leu Ser Asp
 580 585 590
 Thr Glu Arg Arg Leu Asn Glu Ala Arg Arg Glu His Ala Lys Ala Val
 595 600 605
 Val Ser Leu Arg Gln Ile Gln Arg Arg Ala Ala Gln Glu Lys Glu Arg
 610 615 620
 Ser Gln Glu Leu Arg Arg Leu Gln Glu Glu Ala Arg Lys Glu Glu Gly
 625 630 635 640
 Gln Arg Leu Ala Arg Arg Leu Gln Glu Leu Glu Arg Asp Lys Asn Leu
 645 650 655
 Met Leu Ala Thr Leu Gln Gln Glu Gly Leu Leu Ser Arg Tyr Lys Gln
 660 665 670
 Gln Arg Leu Leu Thr Val Leu Pro Ser Leu Leu Asp Lys Lys Ser
 675 680 685
 Val Val Ser Ser Pro Arg Pro Pro Glu Cys Ser Ala Ser Ala Pro Val
 690 695 700
 Ala Ala Ala Val Pro Arg Glu Ser Ile Lys Gly Ser Leu Ser Val
 705 710 715 720
 Leu Leu Asp Asp Leu Gln Asp Leu Ser Glu Ala Ile Ser Lys Glu Glu
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 Ala Val Cys Gln Gly Asp Asn Leu Asp Arg Cys Ser Ser Ser Asn Pro
 740 745 750
 Gln Met Ser Ser
 755

<210> 4739

<211> 684

<212> DNA

<213> Homo sapiens

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 240
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 300
 gctcagctcg caccttgag cctgccagag cctccacag caggtgctct caggcaaggc
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 480
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 540
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 684

<210> 4740
 <211> 119
 <212> PRT
 <213> Homo sapiens

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 Pro Ala Val Thr Gln Leu Ser His Leu Arg Gly Ser Leu Asp Ala Ala
 20 25 30
 Trp Leu Ser Asp Lys Asp Lys Glu Lys Ile Gln Met Ser Thr Arg Ala
 35 40 45
 Val His Ile Leu Trp Val Ser Trp Glu Gln Gly Trp Ala Val Pro Glu
 50 55 60
 Ala Pro Ser Gln Pro Ala Pro Gln Ala Ala Asn Gly Ser Leu Leu Leu
 65 70 75 80
 Gly Gln Gly Ile Cys Gly Gln Glu Ser Thr Leu Val Arg Arg Arg Leu
 85 90 95
 Ala Ser Asn Thr Gln Pro Cys Leu Arg Ala Pro Ala Val Glu Gly Ser
 100 105 110
 Gly Arg Val Gln Gly Ala Asp
 115

<210> 4741
 <211> 411
 <212> DNA
 <213> Homo sapiens

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<400> 4741
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120
ttccgaaaaa aagaggggaa ttttttaaaa aaccgaaag gggggaagg ggggggtata
180
aaagataaaa ttgtgttttt tgggggggaa aatttgaca cccacccctc gggttttttt
240
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300
ataaaaaaaa aatgggggttc caaatcatt gaaaaatag ggggactcca aaaccttgaa
360
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411

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<210> 4742
<211> 109
<212> PRT
<213> Homo sapiens

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<400> 4742
Met Ile Leu Glu Pro His Phe Phe Phe Ile Trp Lys Leu Lys Lys Lys
1 5 10 15
Phe Phe Leu Gly Pro Pro Phe Lys Ile Phe Trp Gly Gly Lys Lys
20 25 30
Pro Glu Gly Gly Val Ser Lys Phe Ser Pro Pro Lys Asn Gln Ile Leu
35 40 45
Ser Phe Ile Pro Pro Pro Phe Pro Phe Gly Phe Phe Lys Lys Phe
50 55 60
Pro Ser Phe Phe Arg Lys Gly Lys Gly Glu Arg Gly Gly Gln Arg
65 70 75 80
Lys Thr Pro Phe Phe Phe Leu Arg Lys Lys Arg Glu Lys Lys Lys Lys
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Lys Glu Arg Lys Thr Pro Val Asp Leu Arg Glu Val Asn
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<210> 4743
<211> 473
<212> DNA
<213> Homo sapiens

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180
gagatgggtc acagaccga ggggaagatgt ctgaagggtg aaggaaatcc agcctgctcc
240
agaaaagcaa agcagatagc agtgggggtc gaaaggggtg cctgcagtc acgttgctgg
300

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aagggcatgg cacagctcca cctgacctgg atctctctgc tattaatgac aaaagcatcg
 360
 tcaaaaagac gccacagtta gcaaaaacaa tatcaagaa acctgagtcac acatcatttt
 420
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 473

<210> 4744
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 4744
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 1 5 10 15
 Thr Asn Ser Ser Ser Ala Lys Lys Lys Asp Lys Arg Val Gln Gly Gly
 20 25 30
 Arg Val Ile Glu Ser Arg Tyr Leu Gln Tyr Glu Lys Lys Thr Thr Gln
 35 40 45
 Lys Ala Pro Ala Gly Asp Gly Ser Gln Thr Arg Gly Lys Met Ser Glu
 50 55 60
 Gly Gly Arg Lys Ser Ser Leu Leu Gln Lys Ser Lys Ala Asp Ser Ser
 65 70 75 80
 Gly Val Gly Lys Gly Asp Leu Gln Ser Thr Leu Leu Glu Gly His Gly
 85 90 95
 Thr Ala Pro Pro Asp Leu Asp Leu Ser Ala Ile Asn Asp Lys Ser Ile
 100 105 110
 Val Lys Lys Thr Pro Gln Leu Ala Lys Thr Ile Ser Lys Lys Pro Glu
 115 120 125
 Ser Thr Ser Phe Ser Ala Pro Arg Lys Lys Ser Pro Asp Leu Ser Glu
 130 135 140
 Ala Asn Gly Met Met Glu
 145 150

<210> 4745
 <211> 666
 <212> DNA
 <213> Homo sapiens

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 120
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 180
 caaagaggta ctacagaaat aggtatgata ggatcaaagc ctttctcaac agttaagtc
 240
 aaaaatgagg gtccagatta tagactctac aagagtgaac cacaggttaac aacagtggca
 300
 gaagttgatg aatctaattg agaagaaaaa tcagaacctg ttccagagat agaaaattca
 360
 gttgttaaag gtccaccatt tcctgttgga gtagtccctc caagagcaaa atcaccaaca
 420


```

cccgaatctt cgacaatagc ttcctatgta accttgagga aaactaagaa gatgatggat
480
ctaagaacgg aaagaccaag aagtgcagtg gaacagctct gtttgctga aagtactcga
540
ccaaggatga ctgtggaaga gcaaatggaa agaataagaa gatatacaaa agcgtgcctg
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660
ccttaa
666

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<210> 4746
<211> 221
<212> PRT
<213> Homo sapiens

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<400> 4746
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20     25     30
Ser Ala Gly Ile Gln Arg Ala Gln Ile Gln Lys Glu Leu Trp Arg Ile
35     40     45
Gln Asp Val Met Glu Gly Leu Ser Lys His Lys Gln Gln Arg Gly Thr
50     55     60
Thr Glu Ile Gly Met Ile Gly Ser Lys Pro Phe Ser Thr Val Lys Tyr
65     70     75     80
Lys Asn Glu Gly Pro Asp Tyr Arg Leu Tyr Lys Ser Glu Pro Glu Leu
85     90     95
Thr Thr Val Ala Glu Val Asp Glu Ser Asn Gly Glu Glu Lys Ser Glu
100    105    110
Pro Val Ser Glu Ile Glu Thr Ser Val Val Lys Gly Ser His Phe Pro
115    120    125
Val Gly Val Val Pro Pro Arg Ala Lys Ser Pro Thr Pro Glu Ser Ser
130    135    140
Thr Ile Ala Ser Tyr Val Thr Leu Arg Lys Thr Lys Lys Met Met Asp
145    150    155    160
Leu Arg Thr Glu Arg Pro Arg Ser Ala Val Glu Gln Leu Cys Leu Ala
165    170    175
Glu Ser Thr Arg Pro Arg Met Thr Val Glu Glu Gln Met Glu Arg Ile
180    185    190
Arg Arg Tyr Gln Gln Ala Cys Leu Arg Glu Lys Lys Gly Leu Asn
195    200    205
Val Ile Gly Ala Ser Asp Gln Ser Pro Leu Gln Ser Pro
210    215    220

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<210> 4747
<211> 1091
<212> DNA
<213> Homo sapiens

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<400> 4747
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 720
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 1091

<210> 4748

<211> 273

<212> PRT

<213> Homo sapiens

<400> 4748

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 20 25 30
 Thr Gly Ser Ser Pro Arg Gly Pro Gly Cys Ser Leu Arg His Phe Ala
 35 40 45
 Cys Glu Gln Asn Leu Leu Ser Arg Pro Asp Gly Ser Ala Ser Phe Leu
 50 55 60
 Gln Gly Asp Thr Ser Val Leu Ala Gly Val Tyr Gly Pro Ala Glu Val
 65 70 75 80
 Lys Val Ser Lys Glu Ile Phe Asn Lys Ala Thr Leu Glu Val Ile Leu

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2196

<210> 4750

<211> 276
 <212> PRT
 <213> Homo sapiens

<400> 4750
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 20 25 30
 Gln Glu Leu Gln Gln Thr Asp Pro Thr Leu Leu Ser Val Val Val Ala
 35 40 45
 Val Leu Ala Val Leu Leu Thr Leu Val Phe Trp Lys Leu Ile Arg Ser
 50 55 60
 Arg Arg Ser Ser Gln Arg Ala Val Leu Leu Val Gly Leu Cys Asp Ser
 65 70 75 80
 Gly Lys Thr Leu Leu Phe Val Arg Leu Leu Thr Gly Leu Tyr Arg Asp
 85 90 95
 Thr Gln Thr Ser Ile Thr Asp Ser Cys Ala Val Tyr Arg Val Asn Asn
 100 105 110
 Asn Arg Gly Asn Ser Leu Thr Leu Ile Asp Leu Pro Gly His Glu Ser
 115 120 125
 Leu Arg Leu Gln Phe Leu Glu Arg Phe Lys Ser Ser Ala Arg Ala Ile
 130 135 140
 Val Phe Val Val Asp Ser Ala Ala Phe Gln Arg Glu Val Lys Asp Val
 145 150 155 160
 Ala Glu Phe Leu Tyr Gln Val Leu Ile Asp Ser Met Gly Leu Lys Asn
 165 170 175
 Thr Pro Ser Phe Leu Ile Ala Cys Asn Lys Gln Asp Ile Ala Met Ala
 180 185 190
 Lys Ser Ala Lys Leu Ile Gln Gln Gln Leu Glu Lys Glu Leu Asn Thr
 195 200 205
 Leu Arg Val Thr Arg Ser Ala Ala Pro Ser Thr Leu Asp Ser Ser Ser
 210 215 220
 Thr Ala Pro Ala Gln Leu Gly Lys Lys Gly Lys Glu Phe Glu Phe Ser
 225 230 235 240
 Gln Leu Pro Leu Lys Val Glu Phe Leu Glu Cys Ser Ala Lys Gly Gly
 245 250 255
 Arg Gly Asp Val Gly Ser Ala Asp Ile Gln Asp Leu Glu Lys Trp Leu
 260 265 270
 Ala Lys Ile Ala
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<210> 4751
 <211> 2777
 <212> DNA
 <213> Homo sapiens

<400> 4751
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<210> 4756

<211> 188

<212> PRT

<213> Homo sapiens

<400> 4756

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			20				25					30			
Ser	Glu	Asp	Gly	Thr	Leu	Arg	Ser	Leu	Glu	Pro	Glu	Pro	Gln	Gln	Ser
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Leu	Glu	Asp	Gly	Ser	Pro	Ala	Lys	Gly	Glu	Pro	Ser	Gln	Ala	Trp	Arg
	50					55				60					
Glu	Gln	Arg	Arg	Pro	Ser	Thr	Ser	Ser	Ala	Ser	Gly	Gln	Trp	Ser	Pro
65					70					75				80	
Thr	Pro	Glu	Trp	Val	Leu	Ser	Trp	Lys	Ser	Lys	Leu	Pro	Leu	Gln	Thr
			85					90					95		
Ile	Met	Arg	Leu	Leu	Gln	Val	Leu	Val	Pro	Gln	Val	Glu	Lys	Ile	Cys
			100					105					110		
Ile	Asp	Lys	Gly	Leu	Thr	Asp	Glu	Ser	Glu	Ile	Leu	Arg	Phe	Leu	Gln
			115				120					125			
His	Gly	Thr	Leu	Val	Gly	Leu	Leu	Pro	Val	Pro	His	Pro	Ile	Leu	Ile
	130					135					140				
Arg	Lys	Tyr	Gln	Ala	Asn	Ser	Gly	Thr	Ala	Met	Trp	Phe	Arg	Thr	Tyr
145					150					155				160	
Met	Trp	Gly	Val	Ile	Tyr	Leu	Arg	Asn	Val	Asp	Pro	Pro	Val	Trp	Tyr
			165						170					175	
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<210> 4757

<211> 272

<212> DNA

<213> Homo sapiens

<400> 4757

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 120
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<210> 4758
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 4758
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 20 25 30
 Leu Ala Ala Gly Asp Val Asp Gly Asp Val Phe Val Phe Ser Tyr Ser
 35 40 45
 Cys Gln Glu Gly Glu Thr Lys Glu Leu Val Ile Arg Ser His Leu Lys
 50 55 60
 Ala Cys Arg Ala Val Ala Phe Ser Glu Asp Gly Gln Lys Leu Ile Thr
 65 70 75 80
 Val Ser Lys Asp Lys Ala Ile His Val Leu
 85 90

<210> 4759
 <211> 1087
 <212> DNA
 <213> Homo sapiens

<400> 4759
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 180
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 240
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 480
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<210> 4760

<211> 78

<212> PRT

<213> Homo sapiens

<400> 4760

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Thr	Thr	Ala	Ala	Thr	Val	Ser	Val	Pro	Gln	Asp	Gly	Cys	Arg	Leu	Arg
		20						25				30			
Lys	Gly	Gln	Thr	Lys	Thr	Leu	Phe	Glu	Phe	Ser	Ser	Ser	Arg	Ala	Gly
		35				40						45			
Phe	Leu	Pro	Leu	Trp	Asp	Val	Ala	Ala	Thr	Asp	Phe	Gly	Gln	Thr	Asn
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Gln	Lys	Phe	Gly	Phe	Glu	Leu	Gly	Pro	Val	Cys	Phe	Ser	Ser		
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<210> 4761

<211> 3973

<212> DNA

<213> Homo sapiens

<400> 4761

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<210> 4762

<211> 251

<212> PRT

<213> Homo sapiens

<400> 4762

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			20					25					30		
Lys	Gly	Trp	Pro	Pro	Lys	Tyr	Ser	Thr	Trp	Glu	Pro	Glu	Glu	His	Ile
		35					40					45			
Leu	Asp	Pro	Arg	Leu	Val	Met	Ala	Tyr	Glu	Glu	Lys	Glu	Glu	Arg	Asp
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Arg	Ala	Ser	Gly	Tyr	Arg	Lys	Arg	Gly	Pro	Lys	Pro	Lys	Arg	Leu	Leu
65					70					75				80	
Leu	Gln	Arg	Leu	Tyr	Ser	Met	Asp	Leu	Arg	Ser	Ser	His	Lys	Ala	Lys
			85						90					95	
Gly	Lys	Glu	Lys	Leu	Cys	Phe	Ser	Leu	Thr	Cys	Pro	Leu	Gly	Ser	Gly
			100					105					110		
Ser	Pro	Glu	Gly	Val	Val	Lys	Ala	Gly	Ala	Pro	Glu	Leu	Val	Asp	Lys
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Gly	Pro	Leu	Val	Pro	Thr	Leu	Pro	Phe	Pro	Leu	Arg	Lys	Pro	Arg	Lys
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Ala	His	Lys	Tyr	Leu	Arg	Leu	Ser	Arg	Lys	Lys	Phe	Pro	Pro	Arg	Gly
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				165					170					175	
Pro	Pro	Ala	Pro	Asp	Val	Leu	Gln	Ala	Ala	Gly	Glu	Trp	Glu	Pro	Ala
		180					185						190		
Ala	Gln	Pro	Pro	Glu	Glu	Glu	Ala	Asp	Ala	Asp	Leu	Ala	Glu	Gly	Pro
		195					200					205			
Pro	Pro	Trp	Thr	Pro	Ala	Leu	Pro	Ser	Ser	Glu	Val	Thr	Val	Thr	Asp
	210					215					220				
Ile	Thr	Ala	Asn	Ser	Ile	Thr	Val	Thr	Phe	Arg	Glu	Ala	Gln	Ala	Ala
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<210> 4763

<211> 2158

<212> DNA

<213> Homo sapiens

<400> 4763

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180
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<210> 4764

<211> 719

<212> PRT

<213> Homo sapiens

<400> 4764

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 35 40 45
 Lys Gly Pro Leu Cys Lys Ser Val Thr Pro Thr Lys Glu Phe Leu Lys
 50 55 60
 Asp Glu Ile Lys Gln Glu Glu Thr Cys Lys Arg Ile Ser Thr Ile
 65 70 75 80
 Thr Ala Leu Gly His Glu Gly Lys Gln Leu Val Asn Gly Glu Val Ser
 85 90 95
 Asp Glu Arg Val Ala Pro Asn Phe Lys Thr Glu Pro Ile Glu Thr Lys
 100 105 110
 Phe Tyr Glu Thr Lys Glu Glu Ser Tyr Ser Pro Ser Lys Asp Arg Asn
 115 120 125
 Ile Ile Thr Glu Gly Asn Gly Thr Glu Ser Leu Asn Ser Val Ile Thr
 130 135 140
 Ser Met Lys Thr Gly Glu Leu Glu Lys Glu Thr Ala Pro Leu Arg Lys
 145 150 155 160
 Asp Ala Asp Ser Ser Ile Ser Val Leu Glu Ile His Ser Gln Lys Ala
 165 170 175
 Gln Ile Glu Glu Pro Asp Pro Pro Glu Met Glu Thr Ser Leu Asp Ser

180										185					190						
Ser	Glu	Met	Ala	Lys	Asp	Leu	Ser	Ser	Lys	Thr	Ala	Leu	Ser	Ser	Thr						
		195						200					205								
Glu	Ser	Cys	Thr	Met	Lys	Gly	Glu	Glu	Lys	Ser	Pro	Lys	Thr	Lys	Lys						
		210				215					220										
Asp	Lys	Arg	Pro	Pro	Ile	Leu	Glu	Cys	Leu	Glu	Lys	Leu	Glu	Lys	Ser						
225					230					235					240						
Lys	Lys	Thr	Phe	Leu	Asp	Lys	Asp	Ala	Gln	Arg	Leu	Ser	Pro	Ile	Pro						
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Glu	Ala	Ala	Glu	Thr	Ser	Pro	Pro	Ser	Asn	Ile	Ile	Asp	His	Cys	Glu						
		275					280					285									
Lys	Leu	Ala	Ser	Glu	Lys	Glu	Val	Val	Glu	Cys	Gln	Ser	Thr	Ser	Thr						
		290				295					300										
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		340						345					350								
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		435				440						445									
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Leu	Cys	Glu	Lys	Leu	Glu	Glu	Gln	Leu	Gln	Asp	Leu	Asp	Val	Ala	Leu						
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Lys	Lys	Lys	Glu	Arg	Ala	Glu	Arg	Arg	Lys	Glu	Arg	Leu	Val	Tyr	Val						

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Gly Ile Ser Ile Glu Asn Ile Ile Pro Pro Gln Glu Pro Asp Phe Ser					
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Glu Asp Gln Glu Glu Lys Lys Lys Asp Ser Lys Lys Ser Lys Ala Asn					
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Leu Leu Glu Arg Arg Ser Thr Arg Thr Arg Lys Cys Ile Ser Tyr Arg					
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Phe Asp Glu Phe Asp Glu Ala Ile Asp Glu Ala Ile Glu Asp Asp Ile					
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Lys Glu Ala Asp Gly Gly Gly Val Gly Arg Gly Lys Asp Ile Ser Thr					
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<210> 4765

<211> 1707

<212> DNA

<213> Homo sapiens

<400> 4765

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<210> 4766

<211> 280

<212> PRT

<213> Homo sapiens

<400> 4766

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 Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
 85 90 95
 Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
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 Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
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 Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
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 Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
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 Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
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Phe	Tyr	Ser	Tyr	Trp	Thr	Gly	Leu	Leu	Arg	Pro	Asp	Ser	Gly	Lys	Ala				
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Cys	Glu	Arg	Arg	Ala	Gly	Met	Val	Lys	Pro	Glu	Ser	Leu	His	Val	Pro				
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<211> 1380
<212> DNA
<213> Homo sapiens
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720		a	gtggcccag			
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<210> 4768

<211> 460

<212> PRT

<213> Homo sapiens

<400> 4768

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Leu Gln Ile Lys	His Ala Val Thr	Glu Ala Glu Ile	Gln Gln Leu	Lys
	325	330		335
Arg Lys Leu Gln	Ser Leu Glu Gln	Glu Lys Gly Arg	Trp Arg Val	Glu
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Lys Ala Gln Leu	Glu Gln Ser Val	Glu Glu Asn Lys	Glu Arg Met	Glu
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Lys Leu Glu Gly	Tyr Trp Gly Glu	Ala Gln Ser Leu	Cys Gln Ala	Val
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Asp Glu His Leu	Arg Glu Thr Gln	Ala Gln Tyr Gln	Ala Leu Glu	Arg
385	390	395		400
Lys Tyr Ser Lys	Ala Lys Arg Leu	Ile Lys Asp Tyr	Gln Gln Lys	Glu
	405	410		415
Ile Glu Phe Leu	Lys Lys Glu Thr	Ala Gln Arg Arg	Val Leu Glu	Glu
	420	425		430
Ser Glu Leu Ala	Arg Lys Glu Glu	Met Asp Lys Leu	Leu Asp Lys	Ile
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<210> 4769

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 4769

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<211> 237

<212> PRT

<213> Homo sapiens

<400> 4770

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<212> DNA

<213> Homo sapiens

<400> 4771

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 <213> Homo sapiens

<400> 4772
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 Lys Pro Asp Val Val Gln Asp Lys Glu Thr Glu Arg Asn Leu Gln Arg
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 Gln Lys Asn Val Asp Glu Lys Val Lys Glu Ala Gly Ser Ser Met Arg
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 Lys Arg Ala Lys Leu Ile Ser Thr Val Ser Lys Lys Asp Phe Ile Ser
 100 105 110
 Val Leu Arg Gly Met Asp Gly Ser Thr Asn Glu Thr Ala Ser Ser Arg
 115 120 125
 Lys Lys Pro Lys Ala Lys Gln Thr Glu Val Lys Ser Glu Glu Gly Pro
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 Gly Trp Thr Ile Leu Arg Asp Asp Phe Met Met Gly Ala Ser Met Lys
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 Asp Trp Asp Lys Glu Ser Asp Gly Pro Asp Asp Ser Arg Pro Glu Ser
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 Ala Ser Asp Ser Asp Thr
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 <211> 319
 <212> DNA
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<210> 4774
 <211> 91
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<213> Homo sapiens

<400> 4774

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Ala Thr Glu Gly Asp Lys Ile Pro Lys Cys Cys Arg Pro Gln Pro Arg
      20              25              30
Pro Asn Pro Ser Ser Leu Phe Pro Pro Ser Pro Gln Ala Arg Ala Ala
 35              40              45
Met Gly Trp Arg Val Leu Ala Trp Thr Gln His Pro Ile Ser Ser Ala
 50              55              60
Leu Ser Leu Asp Pro Ala Ser His Leu Leu Ser Ser Gln Gly Gly Gly
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Ser Trp Glu Pro His Pro Gln Pro Leu His Ala
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<210> 4775

<211> 433

<212> DNA

<213> Homo sapiens

<400> 4775

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<211> 97

<212> PRT

<213> Homo sapiens

<400> 4776

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      20              25              30
Leu Trp Leu His Cys Pro Pro Cys Tyr Phe Phe Glu Arg Ala Asn His
 35              40              45
Thr Ala Thr Ser Leu Pro Leu His Leu Leu Ser Leu Leu Leu Leu Thr
 50              55              60
Ile His Ala Ala His Pro Val Thr Ser Phe Gln Phe Leu Leu Thr Phe

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65		70		75		80
Leu	Lys	Arg	Pro	Ser	Leu	Thr
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				Asn	Ile	Pro
				Pro	Pro	Arg
						Leu
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<212> DNA

<213> Homo sapiens

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<211> 144

<212> PRT

<213> Homo sapiens

<400> 4778

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 35 40 45
 Glu Ser Arg Tyr Leu Arg Ala Val Leu Ala Asn Glu Thr Gly Leu Ala
 50 55 60
 Arg Leu Leu Ser Arg Leu Ser Gly Val Gly Leu Arg Leu Thr Thr Ser
 65 70 75 80
 Leu Phe Arg Asp Ser Pro Ala Gly Asp His Asp Tyr Ala Leu Pro Val
 85 90 95
 Gly Lys Gln Lys Gln Asp Leu Leu Glu Glu Asp Asp Ser Ala Gly Gly
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 Val Cys Leu His Val Asp Lys Asp Lys Val Ser Val Glu Phe Cys Ser

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<210> 4779
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 <212> DNA
 <213> Homo sapiens

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<210> 4780

<211> 1241
 <212> PRT
 <213> Homo sapiens

<400> 4780

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20          25          30
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35          40          45
Gln Gln Gln Gln Gln Gln Gln Gln Pro Gln Gln Pro Gln Val Leu
50          55          60
Ser Ser Glu Gly Gly Gln Leu Arg His Asn Pro Leu Asp Ile Gln Met
65          70          75          80
Leu Ser Arg Gly Leu His Glu Gln Ile Phe Gly Gln Gly Gly Glu Met
85          90          95
Pro Gly Glu Ala Ala Val Arg Arg Ser Val Glu His Leu Gln Lys His
100         105         110
Gly Leu Trp Gly Gln Pro Ala Val Pro Leu Pro Asp Val Glu Leu Arg
115         120         125
Leu Pro Pro Leu Tyr Gly Asp Asn Leu Asp Gln His Phe Arg Leu Leu
130         135         140
Ala Gln Lys Gln Ser Leu Pro Tyr Leu Glu Ala Ala Asn Leu Leu Leu
145         150         155         160
Gln Ala Gln Leu Pro Pro Lys Pro Pro Ala Trp Ala Trp Ala Glu Gly
165         170         175
Trp Thr Arg Tyr Gly Pro Glu Gly Glu Ala Val Pro Val Ala Ile Pro
180         185         190
Glu Glu Arg Ala Leu Val Phe Asp Val Glu Val Cys Leu Ala Glu Gly
195         200         205
Thr Cys Pro Thr Leu Ala Val Ala Ile Ser Pro Ser Ala Trp Tyr Ser
210         215         220
Trp Cys Ser Gln Arg Leu Val Glu Glu Arg Tyr Ser Trp Thr Ser Gln
225         230         235         240
Leu Ser Pro Ala Asp Leu Ile Pro Leu Glu Val Pro Thr Gly Ala Ser
245         250         255
Ser Pro Thr Gln Arg Asp Trp Gln Glu Leu Val Val Gly His Asn
260         265         270
Val Ser Phe Asp Arg Ala His Ile Arg Glu Gln Tyr Leu Ile Gln Gly
275         280         285
Ser Arg Met Arg Phe Leu Asp Thr Met Ser Met His Met Ala Ile Ser
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325         330         335
Lys Ala Arg Arg Gly Pro Ala Ile Ser Ser Trp Asp Trp Leu Asp Ile
340         345         350
Ser Ser Val Asn Ser Leu Ala Glu Val His Arg Leu Tyr Val Gly Gly
355         360         365
Pro Pro Leu Glu Lys Glu Pro Arg Glu Leu Phe Val Lys Gly Thr Met
370         375         380
Lys Asp Ile Arg Glu Asn Phe Gln Asp Leu Met Gln Tyr Cys Ala Gln

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 Tyr Lys Glu Asp Pro Trp Leu Trp Asp Leu Glu Trp Asp Leu Gln Glu
 485 490 495
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 675 680 685
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 690 695 700
 Ala Lys Met Glu Asn Leu Arg Ala Ala Val Pro Gly Gln Pro Leu Ala
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 Leu Thr Ala Arg Gly Gly Pro Lys Asp Thr Gln Pro Ser Tyr His His
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 Lys Leu Pro His Lys Asp Gly Asn Ser Cys Asn Val Gly Ser Pro Phe
 755 760 765
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 Pro Gly Gly Ala Ser Gly Pro Arg Ala Leu Glu Ile Asn Lys Met Ile
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 Ser Phe Trp Arg Asn Ala His Lys Arg Ile Ser Ser Gln Met Val Val
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 Trp Leu Pro Arg Ser Ala Leu Pro Arg Ala Val Ile Arg His Pro Asp

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885										890										895																											
Glu	Leu	Trp	Ile	Ala	Ala	Val	Leu	Gly	Asp	Ala	His	Phe	Ala	Gly	Met	Glu	Leu	Trp	Ile	Ala	Ala	Val	Leu	Gly	Asp	Ala	His	Phe	Ala	Gly	Met	Glu	Leu	Trp	Ile	Ala	Ala	Val	Leu	Gly	Asp	Ala	His	Phe	Ala	Gly	Met
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915										920										925																											
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930										935										940																											
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945										950										955																											
Gln	Pro	Phe	Ala	Glu	Arg	Leu	Leu	Met	Gln	Phe	Asn	His	Arg	Leu	Thr	Gln	Pro	Phe	Ala	Glu	Arg	Leu	Leu	Met	Gln	Phe	Asn	His	Arg	Leu	Thr	Gln	Pro	Phe	Ala	Glu	Arg	Leu	Leu	Met	Gln	Phe	Asn	His	Arg	Leu	Thr
965										970										975																											
Gln	Gln	Glu	Ala	Ala	Glu	Lys	Ala	Gln	Gln	Met	Tyr	Ala	Ala	Thr	Lys	Gln	Gln	Glu	Ala	Ala	Glu	Lys	Ala	Gln	Gln	Met	Tyr	Ala	Ala	Thr	Lys	Gln	Gln	Glu	Ala	Ala	Glu	Lys	Ala	Gln	Gln	Met	Tyr	Ala	Ala	Thr	Lys
980										985										990																											
Gly	Leu	Arg	Trp	Tyr	Arg	Leu	Ser	Asp	Glu	Gly	Glu	Trp	Leu	Val	Arg	Gly	Leu	Arg	Trp	Tyr	Arg	Leu	Ser	Asp	Glu	Gly	Glu	Trp	Leu	Val	Arg	Gly	Leu	Arg	Trp	Tyr	Arg	Leu	Ser	Asp	Glu	Gly	Glu	Trp	Leu	Val	Arg
995										1000										1005																											
Glu	Leu	Asn	Leu	Pro	Val	Asp	Arg	Thr	Glu	Gly	Gly	Trp	Ile	Ser	Leu	Glu	Leu	Asn	Leu	Pro	Val	Asp	Arg	Thr	Glu	Gly	G																				

<210> 4781
 <211> 344
 <212> DNA
 <213> Homo sapiens

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 180
 gcggcaacca cagccaagac gctcattccc aaaagtcagc acagaatgct ggctccca
 240
 ggagcagttt caacaaggac gagacagaaa ggagtgaacca cagcagtcac cccacctaag
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 344

<210> 4782
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 4782
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 35 40 45
 Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala Lys Thr Leu Ile
 50 55 60
 Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly Ala Val Ser Thr
 65 70 75 80
 Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile Pro Pro Lys Glu
 85 90 95
 Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe Gln
 100 105

<210> 4783
 <211> 1143
 <212> DNA
 <213> Homo sapiens

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 240

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 720
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 900
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<210> 4784

<211> 212

<212> PRT

<213> Homo sapiens

<400> 4784

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			20					25					30		
Ala	Leu	Asn	Leu	Ser	Leu	Cys	Lys	Gln	Ile	Thr	Asp	Ser	Ser	Leu	Gly
		35					40				45				
Arg	Ile	Ala	Gln	Tyr	Leu	Lys	Gly	Leu	Glu	Val	Leu	Glu	Leu	Gly	Gly
		50				55				60					
Cys	Ser	Asn	Ile	Thr	Asn	Thr	Gly	Leu	Leu	Leu	Ile	Ala	Trp	Gly	Leu
65				70					75					80	
Gln	Arg	Leu	Lys	Ser	Leu	Asn	Leu	Arg	Ser	Cys	Arg	His	Leu	Ser	Asp
			85					90					95		
Val	Gly	Ile	Gly	His	Leu	Ala	Gly	Met	Thr	Arg	Ser	Ala	Ala	Glu	Gly
			100					105					110		
Cys	Leu	Gly	Leu	Glu	Gln	Leu	Thr	Leu	Gln	Asp	Cys	Gln	Lys	Leu	Thr

115	120	125
Asp Leu Ser Leu Lys His Ile Ser Arg Gly Leu Thr Gly Leu Arg Leu		
130	135	140
Leu Asn Leu Ser Phe Cys Gly Gly Ile Ser Asp Ala Gly Leu Leu His		
145	150	155
Leu Ser His Met Gly Ser Leu Arg Ser Leu Asn Leu Arg Ser Cys Asp		160
	165	170
Asn Ile Ser Asp Thr Gly Ile Met His Leu Ala Met Gly Ser Leu Arg		175
	180	185
Leu Ser Gly Leu Asp Val Ser Phe Cys Asp Lys Val Gly Asp Gln Ser		190
195	200	205
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210		

<210> 4785
 <211> 3289
 <212> DNA
 <213> Homo sapiens

<400> 4785
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 120
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 180
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 240
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 300
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 360
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 420
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 480
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1080
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1140
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2160
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2580
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<210> 4786

<211> 322

<212> PRT

<213> Homo sapiens

<400> 4786

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 35 40 45
 Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met
 50 55 60
 Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Lys
 65 70 75 80
 Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu
 85 90 95
 Asp Leu Thr Glu Ile Arg Asp Met Leu Leu Ala Asn Lys Val Pro Ala
 100 105 110
 Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala
 115 120 125
 Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu
 130 135 140
 Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp
 145 150 155 160
 Val Gln Leu Ile Lys Thr Gly Asp Lys Val Gly Ala Ser Glu Ala Thr
 165 170 175
 Leu Leu Asn Met Met Asn Ile Ser Pro Phe Ser Phe Gly Leu Val Ile
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<210> 4787

<211> 1258

<212> DNA

<213> Homo sapiens

<400> 4787

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360					
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480					
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900					

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<210> 4788

<211> 197

<212> PRT

<213> Homo sapiens

<400> 4788

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Pro	Gly	Pro	Ser	Ser	Ser	Ile	Gly	Ser	Pro	Gln	Ala	Ser	Ser	Pro	Pro
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		50			55					60					
Val	Leu	Val	Asp	Glu	Glu	Ser	Gln	Arg	Glu	Pro	Gly	Ala	Ser	Gly	Ala
			70						75					80	
Pro	Gly	Gln	Lys	Lys	Cys	Tyr	Ser	Cys	Pro	Val	Cys	Ser	Arg	Val	Phe
			85						90					95	
Glu	Tyr	Met	Ser	Tyr	Leu	Gln	Arg	His	Ser	Ile	Thr	His	Ser	Glu	Val
			100					105					110		
Lys	Pro	Phe	Glu	Cys	Asp	Ile	Cys	Gly	Lys	Ala	Phe	Lys	Arg	Ala	Ser
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His	Leu	Ala	Arg	His	His	Ser	Ile	His	Leu	Ala	Gly	Gly	Gly	Arg	Pro
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Ala	Gln	His	Ser	Arg	Val	His	Ser	Gly	Glu	Arg	Pro	Phe	Gln	Cys	Pro
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<210> 4789

<211> 1515

<212> DNA

<213> Homo sapiens

<400> 4789

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<211> 241

<212> PRT

<213> Homo sapiens

<400> 4790

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 4792

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<211> 1242

<212> DNA

<213> Homo sapiens

<400> 4793

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<210> 4794

<211> 118

<212> PRT

<213> Homo sapiens

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Asp Thr Pro Glu Ala Lys Cys Ser Met Gln Gln Pro Gly Ile Gln Ala
 35          40          45
Thr Ser Ser Val Ala Gly Arg Gln Pro Gly Ala Phe Ser Glu Glu Lys
 50          55          60
Gly Pro Val Ile Ile Pro Gln Met Leu Leu Glu Leu Trp Ala Gln Gly
 65          70          75          80
Asn Arg Pro Ile Met Val Leu Pro Glu Gly Leu His Leu Leu Tyr Thr
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<211> 2117

<212> DNA

<213> Homo sapiens

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<211> 541

<212> PRT

<213> Homo sapiens

<400> 4796

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Gly Pro Pro Glu Val Ala Gln Ser Asn Ile Gln Thr Gln Pro Val Asn
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Arg Glu Met Asp Ala Ala Gly Phe Asp Phe Ser Leu Pro Cys Thr Gln
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Lys Leu Thr Gln Asn Gly Thr Arg Ser Gln Trp Gly Leu Ser Leu Pro
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Ala Leu Met Thr Glu Gly Ser Val Lys His Gly Leu Gly Asp Val Ser
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<211> 2848

<212> DNA

<213> Homo sapiens

<400> 4797

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2520

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<210> 4798

<211> 401

<212> PRT

<213> Homo sapiens

<400> 4798

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			20					25				30			
Phe	Glu	Ser	Phe	Leu	Asp	Asp	Glu	Glu	Asp	Leu	Asp	Val	Lys	Ala	Gly
		35					40				45				
Gly	Gly	Cys	Val	Met	Thr	Ile	Gly	Glu	Met	Leu	Arg	Ser	Phe	Leu	Thr
		50				55					60				
Lys	Leu	Glu	Trp	Phe	Ser	Thr	Leu	Phe	Pro	Arg	Ile	Pro	Val	Pro	Val
65					70				75					80	
Gln	Lys	Asn	Ile	Asp	Gln	Gln	Ile	Lys	Thr	Arg	Pro	Arg	Lys	Ile	Lys
			85						90				95		
Lys	Asp	Gly	Lys	Glu	Gly	Ala	Glu	Glu	Ile	Asp	Arg	His	Val	Glu	Arg
			100					105					110		
Arg	Arg	Ser	Arg	Ser	Pro	Arg	Arg	Ser	Leu	Ser	Pro	Arg	Arg	Ser	Pro
		115						120				125			
Arg	Arg	Ser	Arg	Ser	Arg	Ser	His	His	Arg	Glu	Gly	His	Gly	Ser	Ser
		130				135					140				
Ser	Phe	Asp	Arg	Glu	Leu	Glu	Arg	Glu	Lys	Glu	Arg	Gln	Arg	Leu	Glu
145					150				155					160	
Arg	Glu	Ala	Lys	Glu	Arg	Glu	Lys	Glu	Arg	Arg	Ser	Arg	Ser	Ile	
			165					170					175		
Asp	Arg	Gly	Leu	Glu	Arg	Arg	Arg	Ser	Arg	Ser	Arg	Glu	Arg	His	Arg
		180						185					190		
Ser	Arg	Ser	Arg	Ser	Arg	Asp	Arg	Lys	Gly	Asp	Arg	Arg	Asp	Arg	Asp
		195				200					205				
Arg	Glu	Arg	Glu	Lys	Glu	Asn	Glu	Arg	Gly	Arg	Arg	Arg	Asp	Arg	Asp
		210				215					220				
Tyr	Asp	Lys	Glu	Arg	Gly	Asn	Glu	Arg	Glu	Lys	Glu	Arg	Glu	Arg	Ser
225					230				235					240	
Arg	Glu	Arg	Ser	Lys	Glu	Gln	Arg	Ser	Arg	Gly	Glu	Val	Glu	Glu	Lys
			245					250						255	
Lys	His	Lys	Glu	Asp	Lys	Asp	Asp	Arg	Arg	His	Arg	Asp	Asp	Lys	Arg
		260						265					270		
Asp	Ser	Lys	Lys	Glu	Lys	Lys	His	Ser	Arg	Ser	Arg	Ser	Arg	Glu	Arg

```

      275              280              285
Lys His Arg Ser Arg Ser Arg Ser Arg Asn Ala Gly Lys Arg Ser Arg
 290              295              300
Ser Arg Ser Lys Glu Lys Ser Ser Lys His Lys Asn Glu Ser Lys Glu
 305              310              315              320
Lys Ser Asn Lys Arg Ser Arg Ser Gly Ser Gln Gly Arg Thr Asp Ser
      325              330              335
Val Glu Lys Ser Lys Lys Arg Glu His Ser Pro Ser Lys Glu Lys Ser
      340              345              350
Arg Lys Arg Ser Arg Ser Lys Glu Arg Ser His Lys Arg Asp His Ser
      355              360              365
Asp Ser Lys Asp Gln Ser Asp Lys His Asp Arg Arg Arg Ser Gln Ser
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Ile Glu Gln Glu Ser Gln Glu Lys Gln His Lys Asn Lys Asp Glu Thr
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Val

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<210> 4799

<211> 358

<212> DNA

<213> Homo sapiens

<400> 4799

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120
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180
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240
aggccctttt ggtgggtcca tgagtctggt tactacagcc aggctccagc ccagggtcac
300
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<210> 4800

<211> 119

<212> PRT

<213> Homo sapiens

<400> 4800

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Ser Gln Asp Pro Leu Ser Val Leu Leu Pro Arg Gly Leu Leu Arg Leu
      20              25              30
Pro Pro Cys Gly His Arg Gly Ala Leu Asp Gln Pro His His Arg Val
      35              40              45
Ala Gln Pro His Leu Gln Val Val Arg Gln Arg Ser Pro Pro Ala Ser
      50              55              60
Trp Ser Pro Pro Pro Arg Ala Leu Ser His Val Phe Leu Phe Gly Asp
      65              70              75              80
Arg Pro Phe Trp Trp Val His Glu Ser Gly Tyr Ser Gln Ala Pro

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	85		90		95
Ala	Gln	Val	His	Gln	Phe
Pro	Ser	Ser	Cys	Glu	Thr
Gly	Pro	Gly	Ser		
	100		105		110
Pro	Ser	Gly	His	Cys	Met
	115				Ile

<210> 4801

<211> 1447

<212> DNA

<213> Homo sapiens

<400> 4801

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120
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180
tttctggcgc atcccaagat cctctttctg ttctacttcc ccggggccta ctacgcctcc
240
cgccgtgtgg gcacgcgggt gctctggatc agcctcatca ccgagtggct caacctcatc
300
ttcaagtggg ttcttttttg agacaggccc ttttggggg tccatgagtc tggttactac
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600
cagggtctgg ctggcctaata aactggcgct gtcctgggct ggctgatgac tnnccccgag
660
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720
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780
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1020
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1080
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1200
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1260

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gcaccacctg gtcttagccc caaagatggg ccttctctct ccagataag ttggctctcc
 1320
 ctctgccttt cctctcaagc ccccaagag caaaggcaac agcaagacca gcgggttctt
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 1440
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 1447

<210> 4802

<211> 377

<212> PRT

<213> Homo sapiens

<400> 4802

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		20					25					30			
Ser	Thr	Leu	Gly	Ala	Gly	Ile	Val	Ile	Ala	Glu	Ala	Leu	Gln	Asn	Gln
		35				40					45				
Leu	Ala	Trp	Leu	Glu	Asn	Val	Trp	Leu	Trp	Ile	Thr	Phe	Leu	Gly	Asp
	50				55					60					
Pro	Lys	Ile	Leu	Phe	Leu	Phe	Tyr	Phe	Pro	Ala	Ala	Tyr	Tyr	Ala	Ser
65				70					75					80	
Arg	Arg	Val	Gly	Ile	Ala	Val	Leu	Trp	Ile	Ser	Leu	Ile	Thr	Glu	Trp
			85					90					95		
Leu	Asn	Leu	Ile	Phe	Lys	Trp	Phe	Leu	Phe	Gly	Asp	Arg	Pro	Phe	Trp
		100					105					110			
Trp	Val	His	Glu	Ser	Gly	Tyr	Tyr	Ser	Gln	Ala	Pro	Ala	Gln	Val	His
		115				120					125				
Gln	Phe	Pro	Ser	Ser	Cys	Glu	Thr	Gly	Pro	Gly	Ser	Pro	Ser	Gly	His
	130				135					140					
Cys	Met	Ile	Thr	Gly	Ala	Ala	Leu	Trp	Pro	Ile	Met	Thr	Ala	Leu	Ser
145				150					155					160	
Ser	Gln	Val	Ala	Thr	Arg	Ala	Arg	Ser	Arg	Trp	Val	Arg	Val	Met	Pro
			165				170					175			
Ser	Leu	Ala	Tyr	Cys	Thr	Phe	Leu	Leu	Ala	Val	Gly	Leu	Ser	Arg	Ile
	180						185					190			
Phe	Ile	Leu	Ala	His	Phe	Pro	His	Gln	Val	Leu	Ala	Gly	Leu	Ile	Thr
	195					200					205				
Gly	Ala	Val	Leu	Gly	Trp	Leu	Met	Thr	Xaa	Pro	Glu	Cys	Leu	Trp	Ser
	210				215					220					
Gly	Ser	Xaa	Ser	Phe	Tyr	Gly	Leu	Thr	Ala	Leu	Ala	Leu	Met	Leu	Gly
	225				230				235					240	
Thr	Ser	Leu	Ile	Tyr	Trp	Thr	Leu	Phe	Thr	Leu	Gly	Leu	Asp	Leu	Ser
			245					250					255		
Trp	Ser	Ile	Ser	Leu	Ala	Phe	Lys	Trp	Cys	Glu	Arg	Pro	Glu	Trp	Ile
		260				265						270			
His	Val	Asp	Ser	Arg	Pro	Phe	Ala	Ser	Leu	Ser	Arg	Asp	Ser	Gly	Ala
	275					280						285			
Ala	Leu	Gly	Leu	Gly	Ile	Ala	Leu	His	Ser	Pro	Cys	Tyr	Ala	Gln	Val
	290				295					300					
Arg	Arg	Ala	Gln	Leu	Gly	Asn	Gly	Gln	Lys	Ile	Ala	Cys	Leu	Val	Leu

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305          310          315          320
Ala Met Gly Leu Leu Gly Pro Leu Asp Trp Leu Gly His Pro Pro Gln
          325          330          335
Ile Ser Leu Phe Tyr Ile Phe Asn Phe Leu Lys Tyr Thr Leu Trp Pro
          340          345          350
Cys Leu Val Leu Ala Leu Val Pro Trp Ala Val His Met Phe Ser Ala
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Gln Glu Ala Pro Pro Ile His Ser Ser
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<210> 4803

<211> 564

<212> DNA

<213> Homo sapiens

<400> 4803

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120
ccaaaacctg ctaatgcctg atttccatta cgtgctactc ctcaaaggc agcggtctct
180
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<210> 4804

<211> 53

<212> PRT

<213> Homo sapiens

<400> 4804

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Gln Gly Ala Ile Glu Lys Val Lys Glu Ser Asp Lys Leu Val Ala Thr
          20          25          30
Ser Lys Ile Thr Leu Gln Asp Lys Gln Asn Met Val Lys Arg Val Ser
          35          40          45
Ile Met Ser Tyr Ala
          50

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<210> 4805

<211> 1619

<212> DNA

<213> Homo sapiens

<400> 4805

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120
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180
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420
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<210> 4806

<211> 438

<212> PRT

<213> Homo sapiens

<400> 4806

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Glu	Ile	Phe	Thr	Thr	Asn	Asn	Gly	Tyr	Lys	Ser	Met	Gln	Lys	Lys	Leu
			20					25					30		
Arg	Ser	Asn	Trp	Lys	Ile	Gln	Ser	Leu	Lys	Asp	Glu	Ile	Thr	Ser	Glu
		35				40					45				
Lys	Leu	Asn	Gly	Val	Lys	Leu	Trp	Ile	Thr	Ala	Gly	Pro	Arg	Glu	Lys
		50				55					60				
Phe	Thr	Ala	Ala	Glu	Phe	Glu	Ile	Leu	Lys	Lys	Tyr	Leu	Asp	Thr	Gly
65				70						75				80	
Gly	Asp	Val	Leu	Val	Met	Leu	Gly	Glu	Gly	Gly	Glu	Ser	Arg	Phe	Asp
			85					90						95	
Thr	Asn	Ile	Asn	Phe	Leu	Leu	Glu	Glu	Tyr	Gly	Ile	Met	Val	Asn	Asn
			100					105					110		
Asp	Ala	Val	Val	Arg	Asn	Val	Tyr	His	Lys	Tyr	Phe	His	Pro	Lys	Glu
		115				120						125			
Ala	Leu	Val	Ser	Ser	Gly	Val	Leu	Asn	Arg	Glu	Ile	Ser	Arg	Ala	Ala
		130				135					140				
Gly	Lys	Ala	Val	Leu	Ala	Ile	Ile	Asp	Glu	Glu	Ser	Ser	Gly	Asn	Asn
145				150					155					160	
Ala	Gln	Ala	Leu	Thr	Phe	Val	Tyr	Pro	Phe	Gly	Ala	Thr	Leu	Ser	Val
			165					170					175		
Met	Lys	Pro	Ala	Val	Ala	Val	Leu	Ser	Thr	Gly	Ser	Val	Cys	Phe	Pro
		180						185					190		
Leu	Asn	Arg	Pro	Ile	Leu	Ala	Phe	Tyr	His	Ser	Lys	Asn	Gln	Gly	Gly
		195				200					205				
Lys	Leu	Ala	Val	Leu	Gly	Ser	Cys	His	Met	Phe	Ser	Asp	Gln	Tyr	Leu
		210				215					220				
Asp	Lys	Glu	Glu	Asn	Ser	Lys	Ile	Met	Asp	Val	Val	Val	Phe	Gln	Trp
225				230					235					240	
Leu	Thr	Thr	Gly	Asp	Ile	His	Leu	Asn	Gln	Ile	Asp	Ala	Glu	Asp	Pro
			245					250					255		
Glu	Ile	Ser	Asp	Tyr	Met	Met	Leu	Pro	Tyr	Thr	Ala	Thr	Leu	Ser	Lys
			260				265						270		
Arg	Asn	Arg	Glu	Cys	Leu	Gln	Glu	Ser	Asp	Glu	Ile	Pro	Arg	Asp	Phe
		275					280					285			
Thr	Thr	Leu	Phe	Asp	Leu	Ser	Ile	Phe	Gln	Leu	Asp	Thr	Thr	Ser	Phe
		290				295					300				
His	Ser	Val	Ile	Glu	Ala	His	Glu	Gln	Leu	Asn	Val	Lys	His	Glu	Pro
305					310					315				320	
Leu	Gln	Leu	Ile	Gln	Pro	Gln	Phe	Glu	Thr	Pro	Leu	Pro	Thr	Leu	Gln
			325					330					335		
Pro	Ala	Val	Phe	Pro	Pro	Ser	Phe	Arg	Glu	Leu	Pro	Pro	Pro	Pro	Leu

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<210> 4808

<211> 313

<212> PRT

<213> Homo sapiens

<400> 4808

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Arg	Gly	Ile	Gly	Arg	Gly	Ile	Ala	Leu	Gln	Leu	Cys	Lys	Ala	Gly	Ala
		20					25						30		
Thr	Val	Tyr	Ile	Thr	Gly	Arg	His	Leu	Asp	Thr	Leu	Arg	Val	Val	Ala
		35				40						45			
Gln	Glu	Ala	Gln	Ser	Leu	Gly	Gly	Gln	Cys	Val	Pro	Val	Val	Cys	Asp
	50				55					60					
Ser	Ser	Gln	Glu	Ser	Glu	Val	Arg	Ser	Leu	Phe	Glu	Gln	Val	Asp	Arg
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Glu	Gln	Gln	Gly	Arg	Leu	Asp	Val	Leu	Val	Asn	Asn	Ala	Tyr	Ala	Gly
			85					90						95	
Val	Gln	Thr	Ile	Leu	Asn	Thr	Arg	Asn	Lys	Ala	Phe	Trp	Glu	Thr	Pro
		100					105						110		
Ala	Ser	Met	Trp	Asp	Asp	Ile	Asn	Asn	Val	Gly	Leu	Arg	Gly	His	Tyr
		115				120						125			
Phe	Cys	Ser	Val	Tyr	Gly	Ala	Arg	Leu	Met	Val	Pro	Ala	Gly	Gln	Gly
	130					135					140				
Leu	Ile	Val	Val	Ile	Ser	Ser	Pro	Gly	Ser	Leu	Gln	Tyr	Met	Phe	Asn
145				150						155				160	
Val	Pro	Tyr	Gly	Val	Gly	Lys	Ala	Ala	Cys	Asp	Lys	Leu	Ala	Ala	Asp
			165						170					175	
Cys	Ala	His	Glu	Leu	Arg	Arg	His	Gly	Val	Ser	Cys	Val	Ser	Leu	Trp
		180						185					190		
Pro	Gly	Ile	Val	Gln	Thr	Glu	Leu	Leu	Lys	Glu	His	Met	Ala	Lys	Glu
	195					200						205			
Glu	Val	Leu	Gln	Asp	Pro	Val	Leu	Lys	Gln	Phe	Lys	Ser	Ala	Phe	Ser
	210					215					220				
Ser	Ala	Glu	Thr	Thr	Glu	Leu	Ser	Gly	Lys	Cys	Val	Val	Ala	Leu	Ala
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Thr	Asp	Pro	Asn	Ile	Leu	Ser	Leu	Ser	Gly	Lys	Val	Leu	Pro	Ser	Cys
			245						250					255	
Asp	Leu	Ala	Arg	Arg	Tyr	Gly	Leu	Arg	Asp	Val	Asp	Gly	Arg	Pro	Val
		260					265					270			
Gln	Asp	Tyr	Leu	Ser	Leu	Ser	Ser	Val	Leu	Ser	His	Val	Ser	Gly	Leu
	275					280						285			
Gly	Trp	Leu	Ala	Ser	Tyr	Leu	Pro	Ser	Phe	Leu	Arg	Val	Pro	Lys	Trp
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Ile	Ile	Ala	Leu	Tyr	Thr	Ser	Lys	Phe							
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<210> 4809
 <211> 999
 <212> DNA
 <213> Homo sapiens

<400> 4809
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 180
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 420
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 780
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<210> 4810
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 4810
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 Val Ser Lys Ser Cys Leu Asp Ser Asp Pro Ala Gly Pro Phe Gln Gly
 20 25 30
 Ser Gln Pro Gly Cys His Ser Gly Leu Leu Thr Asn Thr Pro Ala Ala
 35 40 45
 Leu Val Pro Ala His Ala Arg Gln Arg Ser Gln Pro Ser Leu Leu Leu

50		55		60	
Ser Ser Ser Pro Arg Lys Ser Arg Ser Trp Gln Gly Ser Gly Pro Met					
65		70		75	80
Trp Pro Gly Pro Gly Tyr Phe Pro Asp Leu Thr Ser Pro Thr Ala Gln					
	85		90		95
Pro Leu Gln Leu Leu Gly Ala Leu His Gly Cys Ser Phe Pro Pro Pro					
	100	105		110	
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<210> 4811

<211> 3207

<212> DNA

<213> Homo sapiens

<400> 4811

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1140

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2700
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<210> 4812

<211> 306

<212> PRT

<213> Homo sapiens

<400> 4812

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 Lys Val Thr Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu
 35 40 45
 Ser Ala Leu Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln
 50 55 60
 Lys Thr Gly Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly
 65 70 75 80
 Ser Trp Val Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly
 85 90 95
 Ser Val Gly Gly Val Arg Tyr Phe Ile Cys Pro Pro Lys Gln Gly Leu
 100 105 110
 Phe Ala Ser Val Ser Lys Ile Ser Lys Ala Val Asp Ala Pro Pro Ser
 115 120 125
 Ser Val Thr Ser Thr Pro Gly Pro Pro Arg Met Asp Phe Ser Arg Val
 130 135 140
 Thr Gly Lys Gly Arg Arg Glu His Lys Gly Lys Lys Thr Pro Ser
 145 150 155 160
 Ser Pro Ser Leu Gly Ser Leu Gln Gln Arg Asp Gly Ala Lys Ala Glu
 165 170 175
 Val Gly Asp Gln Val Leu Val Ala Gly Gln Lys Gln Gly Ile Val Arg
 180 185 190
 Phe Tyr Gly Lys Thr Asp Phe Ala Pro Gly Tyr Trp Tyr Gly Ile Glu
 195 200 205
 Leu Asp Gln Pro Thr Gly Lys His Asp Gly Ser Val Phe Gly Val Arg
 210 215 220
 Tyr Phe Thr Cys Pro Pro Arg His Gly Val Phe Ala Pro Ala Ser Arg
 225 230 235 240
 Ile Gln Arg Ile Gly Gly Ser Thr Asp Ser Pro Gly Asp Ser Val Gly

<210> 4815
 <211> 528
 <212> DNA
 <213> Homo sapiens

<400> 4815
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 240
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 360
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 420
 tagtttggag taatattcat acggcatgga cttttaccaag atggcgattt taagtttaca
 480
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<210> 4816
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 4816
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 Glu Gly Glu Glu Lys Thr Leu Thr Gly Asp Val Lys Thr Ser Pro Pro
 20 25 30
 Arg Thr Ala Pro Lys Lys Gln Leu Pro Ser Ile Pro Lys Asn Ala Leu
 35 40 45
 Pro Ile Thr Lys Pro Thr Ser Pro Ala Pro Ala Ala Gln Ser Thr Asn
 50 55 60
 Gly Thr His Ala Ser Tyr Gly Pro Phe Tyr Leu Glu Tyr Ser Leu Leu
 65 70 75 80
 Ala Glu Phe Thr Leu Val Val Lys Gln Lys Leu Pro Gly Val Tyr Val
 85 90 95
 Gln Pro Ser Tyr Arg Ser Ala Leu Met
 100 105

<210> 4817
 <211> 1106
 <212> DNA
 <213> Homo sapiens

<400> 4817
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 180
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 300
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 480
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<210> 4818

<211> 135

<212> PRT

<213> Homo sapiens

<400> 4818

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			20					25					30		
Ser	Gln	Ala	Gly	Leu	Asn	Gln	Lys	Leu	Asn	Phe	Ile	Val	Thr	Gly	Leu
			35				40				45				
Gln	Asp	Ile	Asp	Lys	Cys	Arg	Gln	Gln	Leu	His	Asp	Ile	Thr	Val	Pro
	50				55						60				
Leu	Glu	Val	Phe	Glu	Tyr	Ile	Asp	Gln	Gly	Arg	Asn	Pro	Gln	Leu	Tyr
	65				70				75				80		
Thr	Lys	Glu	Cys	Leu	Glu	Arg	Ala	Leu	Ala	Lys	Asn	Glu	Gln	Val	Lys

	85		90		95										
Gly	Lys	Ile	Asp	Thr	Met	Lys	Lys	Phe	Lys	Ser	Leu	Leu	Ile	Gln	Glu
		100						105					110		
Leu	Ser	Lys	Val	Phe	Pro	Glu	Asp	Met	Ala	Lys	Tyr	Arg	Ser	Ile	Arg
		115					120						125		
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<210> 4819

<211> 1655

<212> DNA

<213> Homo sapiens

<400> 4819

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<210> 4820

<211> 551

<212> PRT

<213> Homo sapiens

<400> 4820

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 35 40 45
 Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu
 50 55 60
 Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro
 65 70 75 80
 Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu
 85 90 95
 Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile
 100 105 110
 Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val
 115 120 125
 Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
 130 135 140
 Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln
 145 150 155 160
 Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys
 165 170 175
 Leu Gly Glu Val Ala Leu Leu Ala Ser Ile Asp Gln His Cys Ser Thr
 180 185 190
 Thr Arg Leu Cys Asn Leu Val Phe Thr Pro Ala Trp Phe Ser Pro Ile
 195 200 205
 Met Tyr Lys Thr Thr Ser Gly His Val Gln Phe Asp Asn Cys Asn Phe
 210 215 220
 Glu Asn Gly His Ile Gln Val His Gly Pro Gly Thr Cys Gln Val Lys
 225 230 235 240
 Phe Cys Thr Phe Lys Asn Thr His Ile Phe Leu His Asn Val Pro Leu

245 250 255
 Cys Val Leu Glu Asn Cys Glu Phe Val Gly Ser Glu Asn Asn Ser Val
 260 265 270
 Thr Val Glu Gly His Pro Ser Ala Asp Lys Asn Trp Ala Tyr Lys Tyr
 275 280 285
 Leu Leu Gly Leu Ile Lys Ser Ser Pro Thr Phe Leu Pro Thr Glu Asp
 290 295 300
 Ser Asp Phe Leu Met Ser Leu Asp Leu Glu Ser Arg Asp Gln Ala Trp
 305 310 315 320
 Ser Pro Lys Thr Cys Asp Ile Val Ile Glu Gly Ser Gln Ser Pro Thr
 325 330 335
 Ser Pro Ala Ser Ser Ser Pro Lys Pro Gly Ser Lys Ala Gly Ser Gln
 340 345 350
 Glu Ala Glu Val Gly Ser Asp Gly Glu Arg Val Ala Gln Thr Pro Asp
 355 360 365
 Ser Ser Asp Gly Gly Leu Ser Pro Ser Gly Glu Asp Glu Asp Glu Asp
 370 375 380
 Gln Leu Met Tyr Arg Leu Ser Tyr Gln Val Gln Gly Pro Arg Pro Val
 385 390 395 400
 Leu Gly Gly Ser Phe Leu Gly Pro Pro Leu Pro Gly Ala Ser Ile Gln
 405 410 415
 Leu Pro Ser Cys Leu Val Leu Asn Ser Leu Gln Gln Glu Leu Gln Lys
 420 425 430
 Asp Lys Glu Ala Met Ala Leu Ala Asn Ser Val Gln Gly Cys Leu Ile
 435 440 445
 Arg Lys Cys Leu Phe Arg Asp Gly Lys Gly Gly Val Phe Val Cys Ser
 450 455 460
 His Gly Arg Ala Lys Met Glu Gly Asn Ile Phe Arg Asn Leu Thr Tyr
 465 470 475 480
 Ala Val Arg Cys Ile His Asn Ser Lys Ile Met Leu Arg Asn Asp
 485 490 495
 Ile Tyr Arg Cys Arg Ala Ser Gly Ile Phe Leu Arg Leu Glu Gly Gly
 500 505 510
 Gly Leu Ile Ala Gly Asn Asn Ile Tyr His Asn Ala Glu Ala Gly Val
 515 520 525
 Asp Ile Arg Lys Lys Ser Asn Pro Leu Gln Ile Gly Asn Pro Arg Ala
 530 535 540
 Glu Phe Leu Ala Ser Arg Ala
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<210> 4821

<211> 585

<212> DNA

<213> Homo sapiens

<400> 4821

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<211> 195

<212> PRT

<213> Homo sapiens

<400> 4822

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Lys	Pro	Val	Val	Lys	Leu	Leu	His	Asn	Arg	Ser	Asn	Asn	Lys	Tyr	Ser
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<210> 4823

<211> 1984

<212> DNA

<213> Homo sapiens

<400> 4823

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<211> 547

<212> PRT

<213> Homo sapiens

<400> 4824

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<212> DNA

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<400> 4825

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<212> PRT

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<210> 4828

<211> 1322

<212> PRT

<213> Homo sapiens

<400> 4828

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Glu	Lys	Glu	Glu	Lys	Lys	Lys	Lys	Lys	Ile	Lys	Thr	Ile	Lys	Ser	Glu				
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 595 600 605
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 Glu Leu Leu Lys Asp Ser Gln Phe Leu Ala Pro Asp Val Thr Ser Thr
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 Gln Val Asn Thr Val Val Ser Gly Ala Leu Asp Arg Leu His Tyr Glu
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 Lys Asp Pro Cys Val Lys Tyr Asp Ile Gly Arg Lys Leu Trp Ile Tyr
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 Leu His Arg Asp Arg Ser Glu Glu Glu Phe Glu Arg Ile His Gln Ala
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 Gln Ala Ala Ala Ala Lys Ala Arg Lys Ala Leu Gln Gln Lys Pro Lys
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 770 775 780
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Gln Val Arg Ile Gln Thr Val Pro Ala Ser Xaa Leu Gln Gln Gly Thr
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<210> 4829

<211> 1605

<212> DNA

<213> Homo sapiens

<400> 4829

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 <211> 512
 <212> PRT
 <213> Homo sapiens

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 Gly Lys Thr Glu Ala Ser Lys Leu Val Met Ser Tyr Val Ala Ala Val
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 Lys Gly Asp Pro Leu Gly Gly Val Ile Ser Asn Tyr Leu Leu Glu Lys
 180 185 190
 Ser Arg Val Val Lys Gln Pro Arg Gly Glu Arg Asn Phe His Val Phe
 195 200 205
 Tyr Gln Leu Leu Ser Gly Ala Ser Glu Glu Leu Leu Asn Lys Leu Lys
 210 215 220
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 225 230 235 240
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 245 250 255
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      420              425              430
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Ile Glu Asn Asn Thr Asn Gly Ile Leu Ala Met Leu Asp Glu Glu Cys
      450              455              460
Leu Arg Pro Gly Thr Val Thr Asp Glu Thr Phe Leu Glu Lys Leu Asn
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<211> 578

<212> DNA

<213> Homo sapiens

<400> 4831

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<211> 105

<212> PRT

<213> Homo sapiens

<400> 4832

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<400> 4834

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Lys Thr Arg Leu Gln Asn Gln His Gly Lys Ala Met Tyr Lys Gly Met
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Ile Asp Cys Leu Met Lys Thr Ala Arg Ala Glu Gly Phe Phe Gly Met
      50           55           60
Tyr Arg Gly Ala Ala Val Asn Leu Thr Leu Val Thr Pro Glu Lys Ala
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Ile Lys Leu Ala Ala Asn Asp Phe Phe Arg Arg Leu Leu Met Glu Asp
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Gly Met Gln Arg Asn Leu Lys Met Glu Met Leu Ala Gly Cys Gly Ala
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Gly Met Cys Gln Val Val Val Thr Cys Pro Met Glu Met Leu Lys Ile
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<210> 4835

<211> 1846

<212> DNA

<213> Homo sapiens

<400> 4835

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780

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<210> 4836

<211> 349

<212> PRT

<213> Homo sapiens

<400> 4836

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 35 40 45
 His Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile
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 Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp
 65 70 75 80
 Tyr Phe Thr Glu Gln His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg

	85		90		95										
Cys	Pro	Leu	Arg	Gly	Ala	Asp	Arg	Ala	Asp	Val	Ala	Asp	Val	Leu	Gly
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Thr	Ala	Leu	Glu	Glu	Leu	Asn	Arg	Arg	Tyr	His	Pro	Ala	Leu	Arg	Leu
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Gln	Lys	Gln	Gln	Leu	Val	Asn	Gly	Tyr	Arg	Arg	Phe	Asp	Pro	Ala	Arg
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Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Gln	Leu	Glu	Ala	Leu	Thr	Pro	Gln
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Gly	Gly	Arg	Arg	Pro	Leu	Thr	Arg	Arg	Val	Gln	Leu	Leu	Arg	Pro	Leu
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Ser	Arg	Val	Glu	Ile	Leu	Pro	Val	Pro	Tyr	Val	Thr	Glu	Ala	Ser	Arg
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Leu	Thr	Val	Leu	Leu	Pro	Leu	Ala	Ala	Glu	Arg	Asp	Leu	Ala	Pro	
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Glu	Leu	Glu	Arg	Arg	Phe	Pro	Gly	Ala	Arg	Val	Pro	Trp	Leu	Ser	Val
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Gln	Thr	Ala	Ala	Pro	Ser	Pro	Leu	Arg	Leu	Met	Asp	Leu	Leu	Ser	Lys
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Lys	His	Pro	Leu	Asp	Thr	Leu	Phe	Leu	Leu	Ala	Gly	Pro	Asp	Thr	Val
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Leu	Thr	Pro	Asp	Phe	Leu	Asn	Arg	Cys	Arg	Met	His	Ala	Ile	Ser	Gly
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<211> 906

<212> DNA

<213> Homo sapiens

<400> 4837

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<212> PRT

<213> Homo sapiens

<400> 4838

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 50 55 60
 Asn Leu Thr Asn Gly Ser Asn Gly Arg Asn Thr Glu Ser Pro Ala Ala
 65 70 75 80
 Ile His Pro Cys Gly Asn Pro Thr Val Ile Glu Asp Ala Leu Asp Lys
 85 90 95
 Ile Lys Ser Asn Asp Pro Asp Thr Thr Glu Val Asn Leu Asn Asn Ile
 100 105 110
 Glu Asn Ile Thr Thr Gln Thr Leu Thr Arg Phe Ala Glu Ala Leu Lys
 115 120 125
 Asp Asn Thr Val Val Lys Thr Phe Ser Leu Ala Asn Thr His Ala Asp
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 Asp Ser Ala Ala Met Ala Ile Ala Glu Met Leu Lys Val Asn Glu His
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 165 170 175
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 195 200 205
 Ile Val Lys Leu Leu Lys Glu Asn Thr Thr Leu Leu Arg Leu Gly Tyr
 210 215 220
 His Phe Glu Leu Pro Gly Pro Arg Met Ser Met Thr Ser Ile Leu Thr

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				245					250					255
Gln	Glu	Gly	Tyr	Asp	Gly	Gly	Pro	Asn	Leu	Arg	Thr	Lys	Val	Trp
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Arg	Gly	Thr	Pro	Ser	Pro	Ser	Pro	Tyr	Val	Ser	Pro	Arg	His	Ser
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<212> DNA

<213> Homo sapiens

<400> 4839

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<211> 66

<212> PRT

<213> Homo sapiens

<400> 4840

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<210> 4841

<211> 558

<212> DNA

<213> Homo sapiens

<400> 4841

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<213> Homo sapiens

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Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp Leu Phe Cys
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His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu Glu Gln Thr
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Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Asp Ala Cys Ile Gly
65              70              75              80
His Ile His Val Leu Arg Ala Tyr Ile Lys Thr Gln Val Asn Lys Glu
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<212> DNA

<213> Homo sapiens

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<211> 1675

<212> PRT

<213> Homo sapiens

<400> 4844

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Lys Asn Leu Glu Asp Thr Lys Met Asn Gly His Leu Arg Leu Leu Asn
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<210> 4845

<211> 3286

<212> DNA

<213> Homo sapiens

<400> 4845

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<210> 4846

<211> 626

<212> PRT

<213> Homo sapiens

<400> 4846

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Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val
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Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro
65          70          75          80
Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn
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Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser

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<212> DNA

<213> Homo sapiens

<400> 4847

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2160
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2280
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2340
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2400
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2640

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<210> 4848

<211> 242

<212> PRT

<213> Homo sapiens

<400> 4848

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			20				25					30			
Ile	Leu	Gln	Asp	Met	Tyr	Lys	Thr	Lys	Lys	Lys	Lys	Thr	Arg	Val	Ile
	35					40					45				
Leu	Arg	Met	Leu	Pro	Ile	Ser	Gly	Thr	Cys	Lys	Ala	Phe	Leu	Glu	Asp
	50				55				60						
Met	Lys	Lys	Tyr	Ala	Glu	Thr	Phe	Leu	Glu	Pro	Trp	Phe	Lys	Ala	Pro
65				70				75						80	
Asn	Lys	Gly	Thr	Phe	Gln	Ile	Val	Tyr	Lys	Ser	Arg	Asn	Asn	Ser	His
			85					90					95		
Val	Asn	Arg	Glu	Glu	Val	Ile	Arg	Glu	Leu	Ala	Gly	Ile	Val	Cys	Thr
		100					105					110			
Leu	Asn	Ser	Glu	Asn	Lys	Val	Asp	Leu	Thr	Asn	Pro	Gln	Tyr	Thr	Val
		115				120					125				
Val	Val	Glu	Ile	Ile	Lys	Ala	Val	Cys	Cys	Leu	Ser	Val	Val	Lys	Asp
	130				135						140				
Tyr	Met	Leu	Phe	Arg	Lys	Tyr	Asn	Leu	Gln	Glu	Val	Val	Lys	Ser	Pro
145				150				155						160	
Lys	Asp	Pro	Ser	Gln	Leu	Asn	Ser	Lys	Gln	Gly	Asn	Gly	Lys	Glu	Ala
			165					170					175		
Lys	Leu	Glu	Ser	Ala	Asp	Lys	Ser	Asp	Gln	Asn	Asn	Thr	Ala	Glu	Gly
		180				185					190				
Lys	Asn	Asn	Gln	Gln	Val	Pro	Glu	Asn	Thr	Glu	Glu	Leu	Gly	Gln	Thr
	195					200					205				
Lys	Pro	Thr	Ser	Asn	Pro	Gln	Val	Val	Asn	Glu	Gly	Gly	Ala	Lys	Pro
	210				215					220					
Glu	Leu	Ala	Ser	Gln	Ala	Thr	Glu	Gly	Ser	Lys	Ser	Asn	Glu	Asn	Asp
225				230						235					240
Phe	Ser														

<210> 4849

<211> 321

<212> DNA

<213> Homo sapiens

<400> 4849

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 120
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 180
 aagtgatcc ccaagaaggc cctccggggc aaggaggccc tggtgagaa cgagatcgca
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<210> 4850

<211> 90

<212> PRT

<213> Homo sapiens

<400> 4850

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			20					25					30		
Gln	Glu	Arg	Gly	Ser	Ala	His	Leu	Val	Ala	Leu	Lys	Cys	Ile	Pro	Lys
			35				40					45			
Lys	Ala	Leu	Arg	Gly	Lys	Glu	Ala	Leu	Val	Glu	Asn	Glu	Ile	Ala	Val
			50			55					60				
Leu	Arg	Arg	Ile	Ser	His	Pro	Asn	Ile	Val	Ala	Leu	Glu	Asp	Val	His
65					70				75					80	
Glu	Ser	Pro	Ser	His	Leu	Tyr	Leu	Ala	Met						
				85					90						

<210> 4851

<211> 820

<212> DNA

<213> Homo sapiens

<400> 4851

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 120
 cagcatgcgg ccgcccagtc gctgggtgat cagtcggcgg cgctgcaccg gcgggtagca
 180
 gctatgcggg aggcggggac agcgcttccg gaccagtatc aagaggatgc atccgatatg
 240
 aaggacatgt ccaaatataa acctcacatt ctgctgtccc aagagaacac acagattaga
 300
 gacttgcaac agggaaaacag agagctatgg atttccttgg aggaacacca ggatgctttg
 360
 gaacttatca tgagcaaata tcggaaaacag atgttacagt taatggttgc taaaaaagcg
 420
 gtggatgctg aaccagtcct gaaagctcac cagtctcact ctgcagaaat tgagagtcag
 480
 attgacagaa tctgtgaaat gggagaagtg atgaggaaag cagttcaggt ggatgatgac
 540

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600
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660
gcttcccaag ccatcaaata actgaactct gaatgatggc tggagattgt ctatcaagga
720
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<210> 4852

<211> 207

<212> PRT

<213> Homo sapiens

<400> 4852

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20 25 30
Ser Ala Ala Leu His Arg Arg Val Ala Ala Met Arg Glu Ala Gly Thr
35 40 45
Ala Leu Pro Asp Gln Tyr Gln Glu Asp Ala Ser Asp Met Lys Asp Met
50 55 60
Ser Lys Tyr Lys Pro His Ile Leu Leu Ser Gln Glu Asn Thr Gln Ile
65 70 75 80
Arg Asp Leu Gln Gln Glu Asn Arg Glu Leu Trp Ile Ser Leu Glu Glu
85 90 95
His Gln Asp Ala Leu Glu Leu Ile Met Ser Lys Tyr Arg Lys Gln Met
100 105 110
Leu Gln Leu Met Val Ala Lys Lys Ala Val Asp Ala Glu Pro Val Leu
115 120 125
Lys Ala His Gln Ser His Ser Ala Glu Ile Glu Ser Gln Ile Asp Arg
130 135 140
Ile Cys Glu Met Gly Glu Val Met Arg Lys Ala Val Gln Val Asp Asp
145 150 155 160
Asp Gln Phe Cys Lys Ile Gln Glu Lys Leu Ala Gln Leu Glu Leu Glu
165 170 175
Asn Lys Glu Leu Arg Glu Leu Leu Ser Ile Ser Ser Glu Ser Leu Gln
180 185 190
Ala Arg Lys Glu Asn Ser Met Asp Thr Ala Ser Gln Ala Ile Lys
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<210> 4853

<211> 1467

<212> DNA

<213> Homo sapiens

<400> 4853

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120

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 360
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 720
 ggccccacaa gttactacta catgctgccc atgaagggtg gggcgctggg tctcaaagtg
 780
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 1020
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 1320
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<210> 4854

<211> 311

<212> PRT

<213> Homo sapiens

<400> 4854

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Gly Ser Gln	Gly Leu Ser Ser	Leu Ala Glu Glu	Ala Ala Arg Ala Thr
	20	25	30
Glu Asn Pro	Glu Gln Val Ala Ser	Glu Leu Pro Glu	Pro Val Leu
	35	40	45
Arg Lys Val	Glu Leu Pro Val	Pro Thr His Arg	Arg Pro Val Gln Ala
	50	55	60
Trp Val Glu	Ser Leu Arg Gly	Phe Glu Gln Glu	Arg Val Gly Leu Ala
	65	70	75
Asp Leu His	Pro Asp Val Phe	Ala Thr Ala Pro	Arg Leu Asp Ile Leu
	85	90	95
His Gln Val	Ala Met Trp Gln	Lys Asn Phe Lys	Arg Ile Ser Tyr Ala
	100	105	110
Lys Thr Lys	Thr Arg Ala Glu	Val Arg Gly Gly	Gly Arg Lys Pro Xaa
	115	120	125
Ala Ala Glu	Arg His Trp Ala	Gly Pro Ala Trp	Gln His Pro Leu Ser
	130	135	140
Ala Leu Ala	Arg Arg Arg Cys	Cys Pro Trp Pro	Pro Gly Pro Thr Ser
	145	150	155
Tyr Tyr Tyr	Met Leu Pro Met	Lys Val Arg Ala	Leu Gly Leu Lys Val
	165	170	175
Ala Leu Thr	Val Lys Leu Ala	Gln Asp Asp Leu	His Ile Met Asp Ser
	180	185	190
Leu Glu Leu	Pro Thr Gly Asp	Pro Gln Tyr Leu	Thr Glu Leu Ala His
	195	200	205
Tyr Arg Arg	Trp Gly Asp Ser	Val Leu Leu Val	Asp Leu Thr His Glu
	210	215	220
Glu Met Pro	Gln Ser Ile Val	Glu Ala Thr Ser	Arg Leu Lys Thr Phe
	225	230	235
Asn Leu Ile	Pro Ala Val Gly	Leu Asn Val His	Ser Met Leu Lys His
	245	250	255
Gln Thr Leu	Val Leu Thr Leu	Pro Thr Val Ala	Phe Leu Glu Asp Lys
	260	265	270
Leu Leu Trp	Gln Asp Ser Arg	Tyr Arg Pro Leu	Tyr Pro Phe Ser Leu
	275	280	285
Pro Tyr Ser	Asp Phe Pro Arg	Pro Leu Pro His	Ala Thr Gln Gly Pro
	290	295	300
Ala Ala Thr	Pro Tyr His Cys		
	305	310	

<210> 4855

<211> 750

<212> DNA

<213> Homo sapiens

<400> 4855

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120

tttgggacaa catctacaac tgcagggtct gcattcagct tttctgcccc aactaacaca
180

ggcactactg gactcttttg tggactcag aacaaaggtt ttggatttgg tactggtttt
240

ggcaacaac cggaactag tactggttta ggtactgggt tggaactgg actgggattt
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 360
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 420
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 540
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 720
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<210> 4856

<211> 237

<212> PRT

<213> Homo sapiens

<400> 4856

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Ala	Thr	Ala	Ala	Pro	Ala	Gly	Gly	Phe	Gly	Gly	Phe	Gly	Thr	Thr	Ser
		20					25						30		
Thr	Thr	Ala	Gly	Ser	Ala	Phe	Ser	Phe	Ser	Ala	Pro	Thr	Asn	Thr	Gly
		35					40					45			
Thr	Thr	Gly	Leu	Phe	Gly	Gly	Thr	Gln	Asn	Lys	Gly	Phe	Gly	Phe	Gly
		50				55					60				
Thr	Gly	Phe	Gly	Thr	Thr	Gly	Thr	Ser	Thr	Gly	Leu	Gly	Thr	Gly	
65				70					75				80		
Leu	Gly	Thr	Gly	Leu	Gly	Phe	Gly	Gly	Phe	Asn	Thr	Gln	Gln	Gln	Gln
			85						90				95		
Gln	Gln	Thr	Thr	Leu	Gly	Gly	Leu	Phe	Ser	Gln	Pro	Thr	Gln	Ala	Pro
			100				105						110		
Thr	Gln	Ser	Asn	Gln	Leu	Ile	Asn	Thr	Ala	Ser	Ala	Leu	Ser	Ala	Pro
			115				120						125		
Thr	Leu	Leu	Gly	Asp	Glu	Arg	Asp	Ala	Ile	Leu	Ala	Lys	Trp	Asn	Gln
		130				135					140				
Leu	Gln	Ala	Phe	Trp	Gly	Thr	Gly	Lys	Gly	Tyr	Phe	Asn	Asn	Asn	Ile
145				150						155				160	
Pro	Pro	Val	Glu	Phe	Thr	Gln	Glu	Asn	Pro	Phe	Cys	Arg	Phe	Lys	Ala
				165					170					175	
Val	Gly	Tyr	Ser	Cys	Met	Pro	Ser	Asn	Lys	Asp	Glu	Asp	Gly	Leu	Val
			180					185					190		
Val	Leu	Val	Phe	Asn	Lys	Lys	Glu	Thr	Glu	Ile	Arg	Ser	Gln	Gln	Gln
			195					200				205			
Gln	Leu	Val	Glu	Ser	Leu	His	Lys	Val	Leu	Gly	Gly	Asn	Gln	Thr	Leu
		210				215						220			
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225

230

235

<210> 4857

<211> 2887

<212> DNA

<213> Homo sapiens

<400> 4857

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180
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240
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1380

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<210> 4858

<211> 269

<212> PRT

<213> Homo sapiens

<400> 4858

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 35 40 45
 Gln Ala Lys Glu Lys Glu Ile Glu Glu Leu Lys Ser Glu Arg Asp Thr
 50 55 60
 Leu Leu Ala Arg Ile Glu Arg Met Glu Arg Arg Met Gln Leu Val Lys
 65 70 75 80
 Lys Asp Asn Glu Lys Glu Arg His Lys Leu Phe Gln Gly Tyr Glu Thr
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 Glu Glu Arg Glu Glu Thr Glu Leu Ser Glu Lys Ile Lys Leu Glu Cys
 100 105 110
 Gln Pro Glu Leu Ser Glu Thr Ser Gln Thr Leu Pro Pro Lys Pro Phe
 115 120 125
 Ser Cys Gly Arg Ser Gly Lys Gly His Lys Arg Lys Ser Pro Phe Gly
 130 135 140
 Ser Thr Glu Arg Lys Thr Pro Val Lys Lys Leu Ala Pro Glu Phe Ser
 145 150 155 160
 Lys Val Lys Thr Lys Thr Pro Lys His Ser Pro Ile Lys Glu Glu Pro
 165 170 175
 Cys Gly Ser Leu Ser Glu Thr Val Cys Lys Arg Glu Leu Arg Ser Gln
 180 185 190
 Glu Thr Pro Glu Lys Pro Arg Ser Ser Val Asp Thr Pro Pro Arg Leu
 195 200 205
 Ser Thr Pro Gln Lys Gly Pro Ser Thr His Pro Lys Glu Lys Ala Phe
 210 215 220
 Ser Ser Glu Ile Glu Asp Leu Pro Tyr Leu Ser Thr Thr Glu Met Tyr
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 Leu Cys Arg Trp His Gln Pro Pro Pro Ser Pro Leu Pro Leu Arg Glu
 245 250 255
 Ser Ser Pro Lys Lys Glu Glu Thr Val Ala Ser Lys Ala
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<210> 4859

<211> 689

<212> DNA

<213> Homo sapiens

<400> 4859

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 120
 ggccctccac ggtgcctgtg ctgggtggcg gtgggtgtgc caagaggaat ggaatgtcct
 180
 gggctccttc aggagctctc tacccagggg caaggagagc ccagagagaa gcgccctggt
 240

ctcttgagct tcttgatctg ctctgtgcc ccgtctcct ccactccctt gcctttccct
 300
 aggttggtccc ctccctgggc ttttggtgt tttgggagat gtcacctaac caggacattg
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 420
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 480
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 540
 tggatgacag tagaggaaat ggacaaggtc agtttgaata tcccagaaca cagtgtctctg
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 689

<210> 4860

<211> 173

<212> PRT

<213> Homo sapiens

<400> 4860

Met Arg Thr Arg Leu Phe Ala Val Pro Gly Arg Val Ala Lys Glu Asp
 1 5 10 15
 Trp Thr Leu Asp Leu Glu Pro Arg Gly Pro Val His Ile His Pro Thr
 20 25 30
 Arg Val Ser Gly Gly Leu Pro Arg Cys Leu Cys Trp Val Ala Val Val
 35 40 45
 Val Pro Arg Gly Met Glu Cys Pro Gly Leu Leu Gln Glu Leu Ser Thr
 50 55 60
 Gln Gly Gln Gly Glu Pro Arg Glu Lys Arg Pro Gly Leu Leu Ser Phe
 65 70 75 80
 Leu Ile Cys Ser Cys Pro Pro Leu Ser Ser Thr Pro Leu Pro Phe Pro
 85 90 95
 Arg Leu Ser Pro Pro Trp Ala Phe Val Cys Phe Gly Arg Cys His Leu
 100 105 110
 Thr Arg Thr Leu Ile Phe Asn Pro Ile Pro Leu Pro Pro Thr Leu Pro
 115 120 125
 His Phe Asp Leu Ile Leu Trp Leu Trp Ala Glu Ala Ser Gln Gly Ser
 130 135 140
 Trp Val Gly Trp Val Leu Arg Pro Pro Gln Thr Ser Thr Glu Thr Cys
 145 150 155 160
 Pro Cys Ala Val Cys Thr Leu His Ser Leu Pro Cys Leu
 165 170

<210> 4861

<211> 1622

<212> DNA

<213> Homo sapiens

<400> 4861

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120
cggacaggcg ctgagcacct gtggctgacc cgacatctca gggacccatt tgtgaaggct
180
gcgaagggtg agagttaccg gtgtcgaagc gccttcaagc tcctggagggt gaacgagagg
240
caccagattc tgcggcccg ccttcgggtg ttagactgtg gggcagctcc tggggcctgg
300
agtcagggtg cgggtgcagaa ggtcaacgcc gcaggcacag atcccagctc tcctgttggc
360
ttcgtgcttg gggtagatct tcttcacata tccccctgg aaggagcaac ttttctgtgc
420
cctgctgacg tgactgaccc gagaacctca cagagaatcc tcgagggtgc tcctggcagg
480
agagcagatg tgattctgag cgacatggcg cccaatgcca cagggttccg ggacctcgat
540
catgacaggc tcatcagcct gtgcctgacc cttctcagcg tgaccccaga catcctgcaa
600
cctgggggga cattccttg taaaacctgg gctggaagtc aaagccgtcg gttacagagg
660
agactgacag aggaattcca gaatgtaagg atcatcaaac ctgaaggcag caggaaagag
720
tcatcagaag tgtacttctt ggccacacag taccacggaa ggaagggcac tgtgaagcag
780
tgaggatttc ttgtgccatt ttcataatgg tcattagctc cttttaagct agaaacgtag
840
cctgagctcc tgaagagttc ctgggagatt tgagctgatt ttggagatgg agcaggacaa
900
gtggggagtc tctctctctc tttctctctc tctcttttta accaaaaaga gatgacaaaa
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gttatcaaga gaaagagggt aggatggaag gatggagaaa aacagactgt ggggaaggatc
1080
agaaggaatc cgccgaggca gggatgggtg tgcccatgtg tgccttgacg ggacttcac
1140
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1260
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1320
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1380
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1440
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1500
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1620
aa
1622

<210> 4862
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 4862
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 Gly Tyr Leu Lys Leu Val Cys Val Ser Phe Gln Arg Gln Gly Phe His
 20 25 30
 Thr Val Gly Ser Arg Cys Lys Asn Arg Thr Gly Ala Glu His Leu Trp
 35 40 45
 Leu Thr Arg His Leu Arg Asp Pro Phe Val Lys Ala Ala Lys Val Glu
 50 55 60
 Ser Tyr Arg Cys Arg Ser Ala Phe Lys Leu Leu Glu Val Asn Glu Arg
 65 70 75 80
 His Gln Ile Leu Arg Pro Gly Leu Arg Val Leu Asp Cys Gly Ala Ala
 85 90 95
 Pro Gly Ala Trp Ser Gln Val Ala Val Gln Lys Val Asn Ala Ala Gly
 100 105 110
 Thr Asp Pro Ser Ser Pro Val Gly Phe Val Leu Gly Val Asp Leu Leu
 115 120 125
 His Ile Phe Pro Leu Glu Gly Ala Thr Phe Leu Cys Pro Ala Asp Val
 130 135 140
 Thr Asp Pro Arg Thr Ser Gln Arg Ile Leu Glu Val Leu Pro Gly Arg
 145 150 155 160
 Arg Ala Asp Val Ile Leu Ser Asp Met Ala Pro Asn Ala Thr Gly Phe
 165 170 175
 Arg Asp Leu Asp His Asp Arg Leu Ile Ser Leu Cys Leu Thr Leu Leu
 180 185 190
 Ser Val Thr Pro Asp Ile Leu Gln Pro Gly Gly Thr Phe Leu Cys Lys
 195 200 205
 Thr Trp Ala Gly Ser Gln Ser Arg Arg Leu Gln Arg Arg Leu Thr Glu
 210 215 220
 Glu Phe Gln Asn Val Arg Ile Ile Lys Pro Glu Ala Ser Arg Lys Glu
 225 230 235 240
 Ser Ser Glu Val Tyr Phe Leu Ala Thr Gln Tyr His Gly Arg Lys Gly
 245 250 255
 Thr Val Lys Gln
 260

<210> 4863
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 4863
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 gccccaata tcacagccaa cctcacctcg tcctgctga gcgtctgtgg gtggagccag
 120
 accatcaacc ctgaggacga cacggatcct ggccatgctg acctggtcct ctatatcact
 180

aggtttgacc tggagttgcc tgaaggtaac ncggcagtc ggggcgtcac ccagctgggc
 240
 ggggcctgct ccccaacctg gagctgctc attaccgagg aactggctt cgacctggga
 300
 gtcaccattg cccatgagat tgggcacagc ttcggcctgg agcacgacgg cgcgc
 355

<210> 4864
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 4864
 Leu Gly Ala His Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr
 1 5 10 15
 Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser Leu
 20 25 30
 Leu Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp Asp Thr
 35 40 45
 Asp Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg Phe Asp Leu
 50 55 60
 Glu Leu Pro Asp Gly Asn Xaa Ala Val Arg Gly Val Thr Gln Leu Gly
 65 70 75 80
 Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu Ile Thr Glu Asp Thr Gly
 85 90 95
 Phe Asp Leu Gly Val Thr Ile Ala His Glu Ile Gly His Ser Phe Gly
 100 105 110
 Leu Glu His Asp Gly Ala
 115

<210> 4865
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 4865
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 ctcacaaac accagcgac ccacactggc gagcgccctt acaaatgtcc ccgttgcggc
 120
 aaggccttcg ccgacagctc ttacctgctt cgccaccagc gactcactc tggccagaag
 180
 ccctacaagt gccacattg tggcaaggcc ttcggcgaca gctcctacct cctgcgacac
 240
 cagcgcaacc acagccacga gcggccctac agctgcaccg agtgcggcaa gtgctatagc
 300
 cagaactcgt ccctgcgcag ccatcagagg gtgcacaccg gtcagaggcc cttcagctgt
 360
 ggcactctgc gcaagagctt ctcccagcgg tcggccctta tccccatgc ccgcagccac
 420
 gcccgaggaga agcccttcac gcgt
 444

<210> 4866

<211> 148

<212> PRT

<213> Homo sapiens

<400> 4866

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Thr Gly Glu Lys Pro Tyr Lys Cys Glu Val Cys Ser Lys Ala Phe Ser
  1              5              10              15
Gln Ser Ser Asp Leu Ile Lys His Gln Arg Thr His Thr Gly Glu Arg
      20              25              30
Pro Tyr Lys Cys Pro Arg Cys Gly Lys Ala Phe Ala Asp Ser Ser Tyr
  35              40              45
Leu Leu Arg His Gln Arg Thr His Ser Gly Gln Lys Pro Tyr Lys Cys
  50              55              60
Pro His Cys Gly Lys Ala Phe Gly Asp Ser Ser Tyr Leu Leu Arg His
  65              70              75              80
Gln Arg Thr His Ser His Glu Arg Pro Tyr Ser Cys Thr Glu Cys Gly
      85              90              95
Lys Cys Tyr Ser Gln Asn Ser Ser Leu Arg Ser His Gln Arg Val His
      100              105              110
Thr Gly Gln Arg Pro Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser
      115              120              125
Gln Arg Ser Ala Leu Ile Pro His Ala Arg Ser His Ala Arg Glu Lys
      130              135              140
Pro Phe Thr Arg
145

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<210> 4867

<211> 391

<212> DNA

<213> Homo sapiens

<400> 4867

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ggatcccaga gggagtctta tctggacttg ccccaagcag gttgctaggc agtagcctca
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tatccttggg gggaggatga gaaggacaaa aagaggcaac cagcctaggg acatcggcct
 120
ccttctccac atccccattc tggtaggaaa agtcacccat gccaggatat cccagccca
 180
gagacagccc cagggggtgc tgcttgagga cagccgggat agcttcagtc tctgacctt
 240
gacacgggct gcaccaccag acaatgggca ttttcaggcc agactctggc acaagagaa
 300
ggggcagggc caaggctatg gccacaagc tcctcagcag ctgagatggg tgcaggaggt
 360
agcgctctac tcccatagct cccactgta t
391

```

<210> 4868

<211> 125

<212> PRT

<213> Homo sapiens

<400> 4868

```

Met Gly Val Glu Arg Tyr Leu Leu His Pro Ser Gln Leu Leu Arg Ser

```

```

      1             5             10             15
Leu Trp Ala Ile Ala Leu Ala Leu Pro Leu Leu Phe Val Pro Glu Ser
      20             25             30
Gly Leu Lys Met Pro Ile Val Trp Trp Cys Ser Pro Cys Gln Gly Gln
      35             40             45
Glu Thr Glu Ala Ile Pro Ala Val Ser Arg Gln His Pro Leu Gly Leu
      50             55             60
Ser Leu Gly Trp Gly Tyr Pro Gly Met Gly Asp Phe Ser Tyr Gln Asn
      65             70             75             80
Gly Asp Val Glu Lys Glu Ala Asp Val Pro Arg Leu Val Ala Ser Phe
      85             90             95
Cys Pro Ser His Pro Pro Thr Lys Asp Met Arg Leu Leu Pro Ser Asn
      100            105            110
Leu Leu Gly Ala Ser Pro Asp Arg Thr Pro Ser Gly Ile
      115            120            125

```

<210> 4869

<211> 418

<212> DNA

<213> Homo sapiens

<400> 4869

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cccggaaga gggctgcccc ccataaatgc ggaacagtt aaatggcgat gggaatagga
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tggaactca atggtgttgc tacctttgga tggactcgga ggcagcccag ctctctggga
120
caggactgca cggactgcct ggggaggggt ctttggcccc ccggttcctg cagggggggt
180
cggggagggc ctgtgagcag ttggtcacag gtgggtccca ttcgatgcga tctgtttcct
240
ccccaacagc cctggagaag ggggacgttg cctgctgttg ctgcggctgt tttcctggcc
300
tgtgagaggg ggggccagag tggccgttgg gaatctgggt gttgcaaggt gaccacaaac
360
agctctctgg gggaggagga ggaaaatgca attgattttc aggagccttc tgaggtcg
418

```

<210> 4870

<211> 125

<212> PRT

<213> Homo sapiens

<400> 4870

```

Met Ala Met Gly Ile Gly Trp Glu Leu Asn Gly Val Ala Thr Phe Gly
1             5             10             15
Trp Thr Arg Arg Gln Pro Ser Phe Leu Gly Gln Asp Cys Thr Asp Cys
      20             25             30
Leu Gly Arg Gly Leu Trp Pro Pro Gly Ser Cys Arg Gly Ala Arg Gly
      35             40             45
Gly Pro Val Ser Ser Trp Ser Gln Val Gly Pro Ile Arg Cys Asp Pro
      50             55             60
Val Pro Pro Gln Gln Pro Trp Arg Arg Gly Thr Leu Pro Ala Val Ala
      65             70             75             80
Ala Ala Val Phe Leu Ala Cys Glu Arg Arg Gly Gln Ser Gly Arg Trp

```

	85		90		95
Glu Ser Gly Cys Cys Lys Val Thr Thr Asn Ser Ser Leu Gly Glu Glu					
	100		105		110
Glu Glu Asn Ala Ile Asp Phe Gln Glu Pro Ser Glu Val					
	115		120		125

<210> 4871

<211> 1354

<212> DNA

<213> Homo sapiens

<400> 4871

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ggtagggatct gagggaggaa gaggctgcag tcttgctggg cagccccctcg gtcagtcacg
120
cagccccctca ggccatgctg ctgctcagct gcatggcaaa gtcctgcaca tgcctcctca
180
gagtcctggcg ggcatctgcc tgtgcccgcg tctcccgtgc ccgctcctgc tgcagcttgg
240
tcagtcctcaa ccgagccgcg tgcctccgcg gcttgccaggc ctgcagctgg cgctgggcct
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360
gtagctgtgt tcattctgga tgtaggctcc ggccgggtgg ggccaggcag catatacgct
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600
tcttccacag gaaagcagg gacatcagca ggtggagggt gagaaaaatg agttgtgggc
660
cctcgccctc cggagcagcg cttcctgcat cgtctaagcc ggctgacttc aggggggcca
720
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780
atggtagggga ctgccccctc ctttagcctg tgatatccac tgattccac cagctcaaa
840
cagtcctcct caaagtgttt ggagcagaag tagatgtact cggatgccgg gtcacacagg
900
ccctggccgc tgggggtccag ccgctggcag ttggccagcc acaagcctcg cctcggttgg
960
tccttcttgg gaagtctgtg gagccacaaa ccgctgagca ccaggctgtc cacagccctg
1020
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1080
acctccctgc gaccccgccg ggtaagcacc accgccggg ccagacgag gcaacggagg
1140
cctcgagaag aaaagcagtt tcctcagcgt catctggcag gtaacagagt ggggggggtc
1200
caagccggct agacttcccg tcctccctt ccgactgca ttcagtcgg ccgggaccgt
1260

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tccgcttcac ctcccaccca caggttcaag cctcctcagt atctgagaaa ggcgcgaagc
 1320
 ctctacgcag ttgcgacccg aggcgagcaa caac
 1354

<210> 4872

<211> 90

<212> PRT

<213> Homo sapiens

<400> 4872

Gly	Arg	Lys	Arg	Leu	Gln	Ser	Cys	Trp	Ala	Ala	Pro	Arg	Ser	Val	Gln
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Gln	Pro	Leu	Arg	Pro	Cys	Cys	Cys	Ser	Ala	Ala	Trp	Gln	Ser	Pro	Ala
			20					25					30		
His	Ala	Pro	Ser	Glu	Ser	Gly	Gly	His	Leu	Pro	Val	Pro	Ala	Ser	Pro
			35				40						45		
Val	Pro	Ala	Pro	Ala	Ala	Ala	Trp	Ser	Val	Ser	Thr	Ala	Ala	Ala	Ala
			50			55					60				
Pro	Ala	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Ala	Gly	Pro	Cys	Gln	Gly	His
65				70						75				80	
Gln	Gly	Leu	Pro	Gly	Ser	Pro	Leu	Pro	Glu						
				85					90						

<210> 4873

<211> 948

<212> DNA

<213> Homo sapiens

<400> 4873

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 120
 ccaactgtgag ttgaactctt tcgtgttgac cggccactct cegtgtctgt gatgatgtcg
 180
 gaacacgacc tggccgatgt ggttcaaatt gcagtggaag acctgagccc tgaccaccca
 240
 ggtacagagc tgtgggacag tgttgttttg gagaatcatg tagtgacaga tgaagacgaa
 300
 cctgtcttga aacgccagcg actagaaaac aattgccagg atccatctat aaagtcatct
 360
 ctgtattcca tcaaccagac aatctgcttg cggttgata gcattgaagc caaattgcaa
 420
 gccctggagg ctacttgtaa atccttagaa gaaaagctgg atctggctac gaacaagcag
 480
 cacagcccca tccaggttcc catggtggcc ggctcccctc tcaggacaac ccagatgtgc
 540
 aacaaagtgc gatgtaaga acagaccagg gtgccggggc cttcagggtca cttgggggaa
 600
 agcgcgtcac ctctcgtccc atgcccgcag cttagtggct cagtttgctg gagatgcgca
 660
 gtgtctgctt cagcagctctc agcagtttct aactaaagct gacttttagtt agaccgaaac
 720

cgaacacatg gcacccctgcc aggatgacct gaagtcaccc tcacctttcc ttccacata
 780
 aagccggccc atacaccttt tctttggaac taaccaccca gatcttagaa gatgtacag
 840
 tgcttctttc ctttttccca cctacacctgg ctagtcttta gatatgtttt tcttcgtatg
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 948

<210> 4874

<211> 128

<212> PRT

<213> Homo sapiens

<400> 4874

Met	Met	Ser	Glu	His	Asp	Leu	Ala	Asp	Val	Val	Gln	Ile	Ala	Val	Glu
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Asp	Leu	Ser	Pro	Asp	His	Pro	Gly	Thr	Glu	Leu	Trp	Asp	Ser	Val	Val
			20					25					30		
Leu	Glu	Asn	His	Val	Val	Thr	Asp	Glu	Asp	Glu	Pro	Ala	Leu	Lys	Arg
		35					40				45				
Gln	Arg	Leu	Glu	Ile	Asn	Cys	Gln	Asp	Pro	Ser	Ile	Lys	Ser	Phe	Leu
	50					55				60					
Tyr	Ser	Ile	Asn	Gln	Thr	Ile	Cys	Leu	Arg	Leu	Asp	Ser	Ile	Glu	Ala
	65				70				75					80	
Lys	Leu	Gln	Ala	Leu	Glu	Ala	Thr	Cys	Lys	Ser	Leu	Glu	Glu	Lys	Leu
			85					90						95	
Asp	Leu	Val	Thr	Asn	Lys	Gln	His	Ser	Pro	Ile	Gln	Val	Pro	Met	Val
			100					105					110		
Ala	Gly	Ser	Pro	Leu	Arg	Thr	Thr	Gln	Met	Cys	Asn	Lys	Val	Arg	Trp
	115						120						125		

<210> 4875

<211> 1255

<212> DNA

<213> Homo sapiens

<400> 4875

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 120
 tggacgcagt tttagaaaga gcgttttcgc tacgtaaaag acattcgata aaggatatgg
 180
 aaaatacttt gcagctgggtg agaaatatca tacctctctc gtcttcacaa aagcacaaa
 240
 ggcaagatgg aagaataggc gtagttggag gctgtcagga gtacactgga gccccatatt
 300
 ttgcagcaat ctcagctctc aaagtgggag cagacttgct ccacgtgttc tgtgccagtg
 360
 cggccgcacc tgtgattaag gcctacagcc cggagctgat cgtccacca gttcttgaca
 420
 gcccacatgc tgttcattgag gtggagaagt ggctgccccg gctgcatgct cttgtcgtag
 480

gacctggcctt gggtagagat gatcgtccac ccagttcttg acagcccca tgctgttcat
 540
 gaggtggaga agtggctgcc ccggctgcat gctcttgctg taggaactgg cttgggtaga
 600
 gatgatgcgc ttctcagaaa tgtccagggc attttggaag tgtcaaaggc cagggacatc
 660
 cctgttgta tgcacgcgga tggcctgtgg ctggtcgctc agcagccggc cctcatccat
 720
 ggctaccgga aggtgtgtct cactcccaac cacgtggagt tcagcagact gtatgacgct
 780
 gtgctcagag gccctatgga cagcgatgac agccatggat ctgtgctaag actcagccaa
 840
 gccctgggca acgtgacggt ggtccagaaa ggagagcgcg acatcctctc caacggccag
 900
 caggtgcttg tgtgcagcca ggaaggcagc agccgcaggt gtggagggca aggggacctc
 960
 ctgtcgggct cctcgggct cctgggtacac tgggcgctcc ttgctggacc acagaaaaca
 1020
 aatgggtcca gccctctcct ggtggcgcg tttggcgct cctctctcac caggcagtgc
 1080
 aaccaccaag ccttcagaa gcacggtgc tccaccacca cctccgacat gatcgccgag
 1140
 gtggggggcc ccttcagcaa gctctttgaa acctgagccc gcgcagacca gaagtaaaaa
 1200
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 1255

<210> 4876

<211> 230

<212> PRT

<213> Homo sapiens

<400> 4876

Leu Ala Trp Val Glu Met Ile Val His Pro Val Leu Asp Ser Pro Asn
 1 5 10 15
 Ala Val His Glu Val Glu Lys Trp Leu Pro Arg Leu His Ala Leu Val
 20 25 30
 Val Gly Thr Gly Leu Gly Arg Asp Asp Ala Leu Leu Arg Asn Val Gln
 35 40 45
 Gly Ile Leu Glu Val Ser Lys Ala Arg Asp Ile Pro Val Val Ile Asp
 50 55 60
 Ala Asp Gly Leu Trp Leu Val Ala Gln Gln Pro Ala Leu Ile His Gly
 65 70 75 80
 Tyr Arg Lys Ala Val Leu Thr Pro Asn His Val Glu Phe Ser Arg Leu
 85 90 95
 Tyr Asp Ala Val Leu Arg Gly Pro Met Asp Ser Asp Asp Ser His Gly
 100 105 110
 Ser Val Leu Arg Leu Ser Gln Ala Leu Gly Asn Val Thr Val Val Gln
 115 120 125
 Lys Gly Glu Arg Asp Ile Leu Ser Asn Gly Gln Gln Val Leu Val Cys
 130 135 140
 Ser Gln Glu Gly Ser Ser Arg Arg Cys Gly Gly Gln Gly Asp Leu Leu
 145 150 155 160
 Ser Gly Ser Leu Gly Val Leu Val His Trp Ala Leu Leu Ala Gly Pro

	165		170		175										
Gln	Lys	Thr	Asn	Gly	Ser	Ser	Pro	Leu	Leu	Val	Ala	Ala	Phe	Gly	Ala
	180						185						190		
Cys	Ser	Leu	Thr	Arg	Gln	Cys	Asn	His	Gln	Ala	Phe	Gln	Lys	His	Gly
	195						200						205		
Arg	Ser	Thr	Thr	Thr	Ser	Asp	Met	Ile	Ala	Glu	Val	Gly	Ala	Ala	Phe
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<210> 4877

<211> 1182

<212> DNA

<213> Homo sapiens

<400> 4877

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<210> 4878

<211> 122

<212> PRT

<213> Homo sapiens

<400> 4878

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Leu Arg Asp Glu Ser Val Ala His Gly Arg Ile Asp Asn Val Asp Ala
 35           40          45
Phe Met Asn Ile Arg Leu Ala Lys Val Thr Tyr Thr Asp Arg Trp Gly
 50           55          60
His Gln Val Lys Leu Asp Asp Leu Phe Val Thr Gly Arg Asn Val Arg
 65           70          75          80
Tyr Val His Ile Pro Asp Asp Val Asn Ile Thr Ser Thr Ile Glu Gln
      85           90          95
Gln Leu Gln Ile Ile His Arg Val Arg Asn Phe Gly Gly Lys Gly Gln
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Gly Arg Trp Glu Phe Pro Pro Lys Lys Leu
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<210> 4879

<211> 1941

<212> DNA

<213> Homo sapiens

<400> 4879

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<210> 4880

<211> 202

<212> PRT

<213> Homo sapiens

<400> 4880

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Ser	Leu	Ala	Ala	Ser	Ala	Gly	His	Ala	Ala	Ser	Pro	Val	Leu	Pro	Ser			
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Ala	Thr	Ala	Ser	Gly	Pro	His	Val	Lys	Ser	His	Leu	Thr	Arg	Val	Val			
	50					55					60							
Thr	Thr	Val	Leu	Phe	Trp	Gly	Phe	Ser	Lys	Ala	Ser	Pro	Val	Val	Leu			
65					70					75					80			
Arg	Gly	His	Ser	Glu	Gln	Ala	Asn	Thr	Ala	Arg	Val	Thr	His	Tyr	Thr			
				85					90					95				
Gln	Arg	Lys	Asp	Asn	Glu	Gln	Met	Ala	Ile	Val	Glu	Asn	Ser	Val	Val			
			100					105					110					
Cys	Phe	Ser	Asn	Ala	Thr	Tyr	Phe	Ser	Arg	Gln	Val	Ile	Leu	Pro	Met			
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Met	Thr	Ser	Ala	Thr	Lys	Leu	Arg	Ala	Arg	Gly	Leu	Pro	Met	Arg	Leu			
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Val	Glu	Ser	Asn	His	Val	Cys	Ser	Glu	Ala	Ser	Gly	Pro	Ser	Arg	Pro			
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				165					170					175				
Glu	Ala	Gly	Val	Ser	Val	Gly	Gly	Gly	Glu	Glu	Gly	Thr	Ser	Ala	Phe			
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<210> 4881

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 4881

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600	ggaggccgtg	atccgggtgc	acagtaagtg	tggagatggg	acactcgctg
660	gaaggatctt	ggtggtaacc	tgccccaccg	tggccagatc	ctagggcttc
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<210> 4882

<211> 100

<212> PRT

<213> Homo sapiens

<400> 4882

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 Leu Pro Phe Leu Pro Ser Gln Pro Leu Gly Phe Gly Tyr Met Thr Gln
 35 40 45
 Gln Leu Met Asn Leu Ala Gly Gly Ala Val Val Leu Ala Leu Glu Gly
 50 55 60
 Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ala
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 Ala Leu Leu Gly Asn Arg Val Ser Arg Leu Pro Pro Pro Ser Met Leu
 85 90 95
 Leu Ser Gly Arg
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<210> 4883

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 4883

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<210> 4884<211> 410

<212> PRT

<213> Homo sapiens

<400> 4884

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			20					25					30		
Leu	Arg	Leu	Leu	Asn	Phe	Gln	His	Asn	Phe	Ile	Thr	Arg	Ile	Gln	Asn
			35					40					45		

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Ile Glu Glu Ile Ser Gly Leu Ser Thr Leu Arg Cys Leu Arg Val Leu
  65                      70                      75                      80
Leu Leu Gly Lys Asn Arg Ile Lys Lys Ile Ser Asn Leu Glu Asn Leu
                      85                      90                      95
Lys Ser Leu Asp Val Leu Asp Leu His Gly Asn Gln Ile Thr Lys Ile
                      100                      105                      110
Glu Asn Ile Asn His Leu Cys Glu Leu Arg Val Leu Asn Leu Ala Arg
                      115                      120                      125
Asn Phe Leu Ser His Val Asp Asn Leu Asn Gly Leu Asp Ser Leu Thr
                      130                      135                      140
Glu Leu Asn Leu Arg His Asn Gln Ile Thr Phe Val Arg Asp Val Asp
                      145                      150                      155                      160
Asn Leu Pro Cys Leu Gln His Leu Phe Leu Ser Phe Asn Asn Ile Ser
                      165                      170                      175
Ser Phe Asp Ser Val Ser Cys Leu Ala Asp Ser Ser Ser Leu Ser Asp
                      180                      185                      190
Ile Thr Phe Asp Gly Asn Pro Ile Ala Gln Glu Ser Trp Tyr Lys His
                      195                      200                      205
Thr Val Leu Gln Asn Met Met Gln Leu Arg Gln Leu Asp Met Lys Arg
                      210                      215                      220
Ile Thr Glu Glu Glu Arg Arg Met Ala Ser Val Leu Ala Lys Lys Glu
                      225                      230                      235                      240
Glu Glu Lys Lys Arg Glu Ser His Lys Gln Ser Leu Leu Lys Glu Lys
                      245                      250                      255
Lys Arg Leu Thr Ile Asn Asn Val Ala Arg Gln Trp Asp Leu Gln Gln
                      260                      265                      270
Arg Val Ala Asn Ile Ala Thr Asn Glu Asp Arg Lys Asp Ser Asp Ser
                      275                      280                      285
Pro Gln Asp Pro Cys Gln Ile Asp Gly Ser Thr Leu Ser Ala Phe Pro
                      290                      295                      300
Glu Glu Thr Gly Pro Leu Asp Ser Gly Leu Asn Asn Ala Leu Gln Gly
                      305                      310                      315                      320
Leu Ser Val Ile Asp Thr Tyr Leu Val Glu Val Asp Gly Asp Thr Leu
                      325                      330                      335
Ser Leu Tyr Gly Ser Gly Ala Leu Glu Ser Leu Asp Arg Asn Trp Ser
                      340                      345                      350
Val Gln Thr Ala Gly Met Ile Thr Thr Val Ser Phe Thr Phe Ile Glu
                      355                      360                      365
Phe Asp Glu Ile Val Gln Val Leu Pro Lys Leu Lys Ile Lys Phe Pro
                      370                      375                      380
Asn Ser Leu His Leu Lys Phe Lys Glu Thr Asn Leu Val Met Gln Gln
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Phe Asn Ala Leu Ala Gln Leu Arg Arg Tyr
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<210> 4885

<211> 489

<212> DNA

<213> Homo sapiens

<400> 4885

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<210> 4886

<211> 77

<212> PRT

<213> Homo sapiens

<400> 4886

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			20				25						30		
Val	Asn	Phe	Thr	Arg	Xaa	Glu	Trp	Arg	Glu	Leu	Asp	Leu	Ala	Gln	Arg
			35				40					45			
Val	Leu	Tyr	Arg	Asp	Val	Met	Leu	Glu	Asn	Tyr	Arg	Asn	Leu	Val	Ser
			50				55					60			
Leu	Val	Gly	Phe	Pro	Phe	Ser	Lys	Pro	Gly	Ile	Ile	Ser			
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<210> 4887

<211> 2271

<212> DNA

<213> Homo sapiens

<400> 4887

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 2271

<210> 4888

<211> 429

<212> PRT

<213> Homo sapiens

<400> 4888

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 Ser His Asn Asn Thr Ser Val Ile Lys Ser Asn Ser Ser His Ser Val
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 Cys Asp Glu Gly Ala Ile Gly Tyr Cys Thr Asp His Glu Ser Ser Ser
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 His His Asp Leu Glu Gly Ala Val Gly Gly Tyr Tyr Pro Glu Pro Ser
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 Lys Leu Cys His Leu Asp Gln Ser Asp Ser Asp Phe His Gly Asp Leu
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 Thr Phe Gln His Val Phe His Asn His Thr Tyr His Leu Gln Pro Thr
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 Asp Asp Gln Arg Ala Lys Ala Leu His Ile Pro Phe Ser Val Asp Glu
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Gly Lys Asn Lys Val Ala Ala Gln Asn Cys Arg Lys Arg Lys Leu Asp				
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Ile Ile Leu Asn Leu Glu Asp Asp Val Cys Asn Leu Gln Ala Lys Lys				
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Glu Thr Leu Lys Arg Glu Gln Ala Gln Cys Asn Lys Ala Ile Asn Ile				
	355		360	365
Met Lys Gln Lys Leu His Asp Leu Tyr His Asp Ile Phe Ser Arg Leu				
	370		375	380
Arg Asp Asp Gln Gly Arg Pro Val Asn Pro Asn His Tyr Ala Leu Gln				
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Cys Thr His Asp Gly Ser Ile Leu Ile Val Pro Lys Glu Leu Val Ala				
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<210> 4889

<211> 619

<212> DNA

<213> Homo sapiens

<400> 4889

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<210> 4890

<211> 90

<212> PRT

<213> Homo sapiens

<400> 4890

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Pro Ser Pro Thr Leu Phe Pro Asp Ser Gln Gln Thr Asp Val Gly Ser	50	55	60
Arg Thr Asp Pro Phe Thr His Thr His Ser His Ser Phe Ala	65	70	75
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<210> 4891

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 4891

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<210> 4892

<211> 216

<212> PRT

<213> Homo sapiens

<400> 4892

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		35				40						45			
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Ser	Asp	Arg	Ala	Ala	Ala	Gly	Met	Val	Trp	Lys	Pro	Lys	Ser	Cys	Glu
65				70					75				80		
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Ser	Thr	Thr	Phe	Val	Leu	Gly	Ser	Arg	Ala	Asn	Lys	Ala	Leu	Gly	Met
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165	170	175
Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu		
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<210> 4893

<211> 5212

<212> DNA

<213> Homo sapiens

<400> 4893

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<210> 4894

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<212> PRT

<213> Homo sapiens

<400> 4894

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Lys	Ile	Ser	Glu	Trp	Glu	Gly	Lys	Lys	Glu	Val	Pro	Thr	Pro	Ala	Pro
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Ser	Arg	Arg	Ala	Asp	Gly	Gln	Glu	Asp	Tyr	Leu	Pro	Ser	Ser	Thr	Val
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    310              315              320
Phe  Glu  Asp  Leu  Leu  Gln  Ser  Ser  Ser  Glu  Ser  Ser  Arg  Val  Asp  Trp
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Tyr  Ala  Gln  Thr  Lys  Leu  Gly  Leu  Thr  Arg  Thr  Leu  Ser  Glu  Glu  Asn
    340              345              350
Val  Tyr  Glu  Asp  Ile  Leu  Asp  Pro  Pro  Met  Lys  Glu  Asn  Pro  Tyr  Glu
    355              360              365
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<210> 4895

<211> 1087

<212> DNA

<213> Homo sapiens

<400> 4895

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360

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<210> 4896

<211> 109

<212> PRT

<213> Homo sapiens

<400> 4896

Met	Glu	Ala	Glu	Val	Asp	Lys	Leu	Glu	Leu	Met	Phe	Gln	Lys	Ala	Glu
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Ser	Asp	Leu	Asp	Tyr	Ile	Gln	Tyr	Arg	Leu	Glu	Tyr	Glu	Ile	Lys	Thr
			20					25					30		
Asn	His	Pro	Asp	Ser	Ala	Ser	Glu	Lys	Asn	Pro	Val	Thr	Leu	Leu	Lys
		35					40				45				
Glu	Leu	Ser	Val	Ile	Lys	Ser	Arg	Tyr	Gln	Thr	Leu	Tyr	Ala	Arg	Phe
		50				55				60					
Lys	Pro	Val	Ala	Val	Glu	Gln	Lys	Glu	Ser	Lys	Ser	Arg	Ile	Cys	Ala
65					70				75					80	
Thr	Val	Lys	Lys	Thr	Met	Asn	Met	Ile	Gln	Lys	Leu	Gln	Lys	Gln	Thr
			85					90						95	
Asp	Leu	Glu	Val	Met	Leu	Ser	Val	Asp	Ser	Cys	His	His			
			100					105							

<210> 4897

<211> 1733

<212> DNA

<213> Homo sapiens

<400> 4897

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480
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600
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720
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780
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 1733

<210> 4898
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 4898
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 Gln Pro Leu Pro Leu Arg Phe Lys Gln Phe Ser Cys Phe Ser Leu Pro
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 Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Cys Pro Ala Asn Phe Cys
 35 40 45
 Ile Phe Ser Lys Asp Arg Val Ser Pro Cys Trp Leu Gly Trp Ser Gln
 50 55 60
 Thr Pro Asp Xaa Thr Arg Leu Gly Leu Pro Lys Cys Trp Asp Tyr Arg
 65 70 75 80
 Arg Glu Pro Pro Arg Pro Gly Asp Leu Trp Asn Phe
 85 90

<210> 4899
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 4899
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 120
 gtggcggtc tggaggcagc aacggggtcc tttgggtgg gtgggagttc tgctggatcc
 180
 aggtggaggt gaacatctgc cgttccca cccctgcgtg ccccccaaa tgctgtggtc
 240
 ccacagaatc agccagtgc acggcccccac cacagccagg cttggccctg tcagcggcca
 300
 gcatcccgag ggccagggtc cgagtgtcct caccaaggag gctcttggtg tcgctgtgcc
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 420
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 444

<210> 4900
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 4900
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Ser Lys Pro Gln Gln Leu Trp Arg Arg Val Arg Glu Trp Arg Leu Trp	20	25	30
Arg Gln Gln Arg Gly Pro Leu Gly Trp Val Gly Val Leu Leu Asp Ser	35	40	45
Gly Gly Gly Glu His Leu Pro Phe Pro Gln Pro Cys Val His Pro Gln	50	55	60
Met Leu Leu Ala His Arg Ile Ser Gln Cys His Gly Pro Thr Thr Ala	65	70	75
Arg Leu Gly Pro Val Ser Gly Gln His Pro Glu Gly Gln Gly Pro Ser	85	90	95
Val Leu Thr Lys Glu Ala Leu Gly Val Ala Val Pro Ala Pro Met Gly	100	105	110
Leu Leu Leu Gly Arg Gly			
115			

<210> 4901

<211> 1520

<212> DNA

<213> Homo sapiens

<400> 4901

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180
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240
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300
ttggcgccgt ttggggtcg ggtctgaggg ttgggcgctg cctggggcca gcggagatcg
360
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420
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660
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720
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840
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960

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<210> 4902

<211> 184

<212> PRT

<213> Homo sapiens

<400> 4902

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 Leu Val Gly Pro Tyr Gln Asn Thr Ile Gly Ala Ala Phe Val Ala Lys
 35 40 45
 Val Met Ser Val Gly Asp Arg Thr Val Thr Leu Gly Ile Trp Asp Thr
 50 55 60
 Ala Gly Ser Glu Arg Tyr Glu Ala Met Ser Arg Ile Tyr Tyr Arg Gly
 65 70 75 80
 Ala Lys Ala Ala Ile Val Cys Tyr Asp Leu Thr Asp Ser Ser Ser Phe
 85 90 95
 Glu Arg Ala Lys Phe Trp Val Lys Glu Leu Arg Ser Leu Glu Gly Gly
 100 105 110
 Cys Gln Ile Tyr Leu Cys Gly Thr Lys Ser Asp Leu Leu Glu Glu Asp
 115 120 125
 Arg Arg Arg Arg Arg Val Asp Phe His Asp Val Gln Asp Tyr Ala Asp
 130 135 140
 Ser Ser Cys Ser Ser Ala Leu Trp Gly Val Gly Val Cys Gly Cys Leu
 145 150 155 160
 Gly Gly Ser Lys Lys Ile Gly Thr Ala Leu Ala Ala Arg Ala Arg Cys
 165 170 175
 Ser Arg Arg Ser Ser Trp Pro Pro
 180

<210> 4903

<211> 1064

<212> DNA

<213> Homo sapiens

<400> 4903

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 180
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 300
 gctcagctgt acaaggagga aggggaaccg cgctaccggg aagggaagta ccgagatgct
 360
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 420
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 480
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 540
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 900
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 960
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 1064

<210> 4904

<211> 106

<212> PRT

<213> Homo sapiens

<400> 4904

Cys Trp Ala Ser Leu Phe Pro His Pro Phe Pro Tyr Tyr Leu Pro Ala
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 20 25 30
 Asn Lys Gln Thr Ala Val Pro Val Gly Gly Leu Ser Arg Lys Lys Val
 35 40 45
 Pro Gln Glu Pro Trp Ala Thr Val Met Glu Lys Arg Leu Gln Glu Ala

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      50              55              60
Gln Leu Tyr Lys Glu Gly Asn Gln Arg Tyr Arg Glu Gly Lys Tyr
65              70              75              80
Arg Asp Ala Val Ser Arg Tyr His Arg Ala Leu Leu Gln Leu Arg Gly
      85              90              95
Leu Asp Pro Xaa Ser Ala Leu Ser Val Thr
      100              105

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<210> 4905
 <211> 615
 <212> DNA
 <213> Homo sapiens

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<400> 4905
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180
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<210> 4906
 <211> 144
 <212> PRT
 <213> Homo sapiens

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<400> 4906
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Cys Ala Glu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu Glu
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Gln Leu Pro Trp Glu Ala Leu Gly Arg Leu Gly Asn Val Asn Thr Leu
35     40     45
Gly Leu Asp His Asn Leu Leu Ala Ser Val Pro Ala Gly Ala Phe Ser
50     55     60
Arg Leu His Lys Leu Ala Arg Leu Asp Met Thr Ser Asn Arg Leu Thr
65     70     75     80
Thr Ile Pro Pro Asp Pro Leu Phe Ser Arg Leu Pro Leu Leu Ala Arg

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	85						90						95		
Pro	Arg	Gly	Ser	Pro	Ala	Ser	Ala	Leu	Val	Leu	Ala	Phe	Gly	Gly	Asn
			100						105				110		
Pro	Leu	His	Cys	Asn	Cys	Glu	Leu	Val	Trp	Leu	Arg	Arg	Leu	Ala	Arg
		115					120					125			
Glu	Asp	Asp	Leu	Glu	Ala	Cys	Ala	Ser	Pro	Pro	Ala	Leu	Gly	Gly	Arg
	130					135					140				

<210> 4907

<211> 1748

<212> DNA

<213> Homo sapiens

<400> 4907

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120
gtggccagca gctgggtccg tctctcttcg cccaacagct gtatccacag gttgtgaggc
180
gggaacgact gttctgtaac ccctacaacg gagcctggca ggaaggaaat cacctaaaaa
240
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1200

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<210> 4908

<211> 55

<212> PRT

<213> Homo sapiens

<400> 4908

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Pro	Tyr	Pro	Cys	Pro	His	Gly	Asp	Arg	Leu	Leu	Pro	Pro	Ser	Arg	Pro
			20					25					30		
Leu	Pro	Ala	Gly	Pro	Ala	Ser	Ala	Phe	Pro	Pro	Ala	Glu	Arg	Ser	Arg
		35					40					45			
Gly	His	Arg	Arg	Ala	Ser	Leu									
	50					55									

<210> 4909

<211> 1960

<212> DNA

<213> Homo sapiens

<400> 4909

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 360

ctgatggaga agggaggagga ggggatgctg tcgcccatcc tggcccacgg ggggggtccgt
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960
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1380
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1440
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<210> 4910
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 4910

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 20           25           30
Phe Met Pro Ile Leu Met Glu Lys Glu Glu Glu Gly Met Leu Ser Pro
 35           40           45
Ile Leu Ala His Gly Gly Val Arg Phe Met Trp Ile Lys His Asn Asn
 50           55           60
Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu Val
 65           70           75           80
Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe Lys
 85           90           95
Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr Glu
100           105           110
Leu Leu Asp Glu Leu Met Asp Phe Gly Phe Pro Gln Thr Thr Asp Ser
115           120           125
Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln Ser Asn Lys Leu Glu Thr
130           135           140
Gly Lys Ser Arg Val Pro Thr Val Thr Asn Ala Val Ser Trp Arg
145           150           155           160
Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu Val Phe Ile Asp Val Ile
165           170           175
Glu Ser Val Asn Leu Leu Val Asn Ala Asn Gly Ser Val Leu Leu Ser
180           185           190
Glu Ile Val Gly Thr Ile Lys Met Arg Val Phe Leu Ser Gly Met Pro
195           200           205
Glu Leu Arg Leu Gly Leu Asn Asp Lys Val Leu Phe Asp Asn Thr Gly
210           215           220
Arg Gly Lys Ser Lys Ser Val Glu Leu Glu Asp Val Lys Phe His Gln
225           230           235           240
Cys Val Arg Leu Ser Arg Phe Glu Asn Asp Arg Thr Ile Ser Phe Ile
245           250           255
Pro Pro Asp Gly Glu Phe Glu Leu Met Ser Tyr Arg Leu Asn Thr His
260           265           270
Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys Phe Ser His
275           280           285
Ser Arg Ile Glu Tyr Met Val Lys Ala Lys Gly Gln Phe Lys Lys Gln
290           295           300
Ser Val Ala Asn Gly Val Glu Ile Ser Val Pro Val Pro Ser Asp Ala
305           310           315           320
Asp Ser Pro Arg Phe Lys Thr Ser Val Gly Ser Ala Lys Tyr Val Pro
325           330           335
Glu Arg Asn Val Val Ile Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys
340           345           350
Glu Tyr Leu Met Arg Ala His Phe Gly Leu Pro Ser Val Glu Lys Glu
355           360           365
Glu Val Glu Gly Arg Pro Pro Ile Gly Val Lys Phe Glu Ile Pro Tyr

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      370              375              380
Phe Thr Val Ser Gly Ile Gln Val Arg Tyr Met Lys Ile Ile Glu Lys
385              390              395              400
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<210> 4911

<211> 1862

<212> DNA

<213> Homo sapiens

<400> 4911

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180
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240
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300
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420
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480
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1200

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 1740
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 1860
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 1862

<210> 4912

<211> 453

<212> PRT

<213> Homo sapiens

<400> 4912

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			20					25					30		
Leu	Lys	Ala	Ile	Leu	Ile	Gln	Arg	Gln	Ile	Asp	Val	Asp	Thr	Val	Phe
			35			40					45				
Glu	Val	Glu	Asp	Glu	Asn	Met	Val	Leu	Ala	Ser	Tyr	Lys	Gln	Gly	Tyr
	50				55						60				
Trp	Leu	Pro	Ser	Tyr	Lys	Leu	Lys	Ser	Ser	Trp	Ala	Thr	Gly	Leu	His
				70					75					80	
Leu	Ser	Val	Leu	Phe	Gly	His	Val	Glu	Cys	Leu	Leu	Val	Leu	Leu	Asp
			85						90					95	
His	Asn	Ala	Thr	Ile	Asn	Cys	Arg	Pro	Asn	Gly	Lys	Thr	Pro	Leu	His
			100						105				110		
Val	Ala	Cys	Glu	Met	Ala	Asn	Val	Asp	Cys	Val	Lys	Ile	Leu	Cys	Asp
			115			120						125			
Arg	Gly	Ala	Lys	Leu	Asn	Cys	Tyr	Ser	Leu	Ser	Gly	His	Thr	Ala	Leu
			130			135					140				
His	Phe	Cys	Thr	Thr	Pro	Ser	Ser	Ile	Leu	Cys	Ala	Lys	Gln	Leu	Val
				145		150				155				160	
Trp	Arg	Val	Thr	Gln	Val	Asn	His	Met	Leu	Gly	Asn	Ser	Leu	Val	Asn
				165				170						175	
Glu	Val	Glu	His	Val	Thr	Gln	Val	Asn	His	Met	Leu	Gly	Asn	Ser	Leu

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195      200      205
Gln Asp Glu Glu Thr Pro Leu His Thr Ala Ala His Phe Gly Leu Ser
210      215      220
Glu Leu Val Ala Phe Tyr Val Glu His Gly Ala Ile Val Asp Ser Val
225      230      235      240
Asn Ala His Met Glu Thr Pro Leu Ala Ile Ala Ala Tyr Trp Ala Leu
245      250      255
Arg Phe Lys Glu Gln Glu Tyr Ser Thr Glu His His Leu Val Cys Arg
260      265      270
Met Leu Leu Asp Tyr Lys Ala Glu Val Asn Ala Arg Asp Asp Asp Phe
275      280      285
Lys Ser Pro Leu His Lys Ala Ala Trp Asn Cys Asp His Val Leu Met
290      295      300
His Met Met Leu Glu Ala Gly Ala Glu Ala Asn Leu Met Asp Ile Asn
305      310      315      320
Gly Cys Ala Ala Ile Gln Tyr Val Leu Lys Val Thr Ser Val Arg Pro
325      330      335
Ala Ala Gln Pro Glu Ile Cys Tyr Gln Leu Leu Leu Asn His Gly Ala
340      345      350
Ala Arg Ile Tyr Pro Pro Gln Phe His Lys Val Ile Gln Ala Cys His
355      360      365
Ser Cys Pro Lys Ala Ile Glu Val Val Val Asn Ala Tyr Glu His Ile
370      375      380
Arg Trp Asn Thr Lys Trp Arg Arg Ala Ile Pro Asp Asp Asp Leu Glu
385      390      395
Val Asn Asn Arg Phe Pro Ser Asn Ser Phe His Tyr Gln Val Leu Pro
405      410      415
Asp Cys Ser Arg Ser Thr Glu Asn Cys Asn Lys Lys Val Gly Phe Glu
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Cys Arg Phe Glu Ser
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<210> 4913

<211> 2090

<212> DNA

<213> Homo sapiens

<400> 4913

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360

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<210> 4914

<211> 529

<212> PRT

<213> Homo sapiens

<400> 4914

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			20					25					30		
Asn	Pro	Asn	Pro	Leu	Ile	Asn	Val	Arg	Asp	Arg	Leu	Phe	His	Ala	Leu
			35				40					45			
Phe	Phe	Lys	Met	Ala	Val	Thr	Tyr	Ser	Arg	Leu	Phe	Pro	Pro	Ala	Phe
			50				55				60				
Arg	Arg	Leu	Phe	Glu	Phe	Phe	Val	Leu	Leu	Lys	Ala	Leu	Phe	Val	Leu
			65			70				75				80	
Phe	Val	Leu	Ala	Tyr	Ile	His	Ile	Val	Phe	Ser	Arg	Ser	Pro	Ile	Asn
				85					90				95		
Cys	Leu	Glu	His	Val	Arg	Asp	Lys	Trp	Pro	Arg	Glu	Gly	Ile	Leu	Arg
			100					105					110		
Val	Glu	Val	Arg	His	Asn	Ser	Ser	Arg	Ala	Pro	Val	Phe	Leu	Gln	Phe
			115				120					125			
Cys	Asp	Ser	Gly	Gly	Arg	Gly	Ser	Phe	Pro	Gly	Leu	Ala	Val	Glu	Pro
			130				135				140				
Gly	Ser	Asn	Leu	Asp	Met	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Leu	Thr	Met
				145		150				155				160	
Glu	Met	Phe	Gly	Asn	Ser	Ser	Ile	Lys	Phe	Glu	Leu	Asp	Ile	Glu	Pro
				165					170				175		
Lys	Val	Phe	Lys	Pro	Pro	Ser	Ser	Thr	Glu	Ala	Leu	Asn	Asp	Ser	Gln
			180					185					190		
Glu	Phe	Pro	Phe	Pro	Glu	Thr	Pro	Thr	Lys	Val	Trp	Pro	Gln	Asp	Glu
			195				200					205			
Tyr	Ile	Val	Glu	Tyr	Ser	Leu	Glu	Tyr	Gly	Phe	Leu	Arg	Leu	Ser	Gln
			210			215				220					
Ala	Thr	Arg	Gln	Arg	Leu	Ser	Ile	Pro	Val	Met	Val	Val	Thr	Leu	Asp
			225			230				235				240	
Pro	Thr	Arg	Asp	Gln	Cys	Phe	Gly	Asp	Arg	Phe	Ser	Arg	Leu	Leu	Leu
			245					250					255		
Asp	Glu	Phe	Leu	Gly	Tyr	Asp	Asp	Ile	Leu	Met	Ser	Ser	Val	Lys	Gly
			260			265							270		
Leu	Ala	Glu	Asn	Glu	Glu	Asn	Lys	Gly	Phe	Leu	Arg	Asn	Val	Val	Ser
			275			280						285			
Gly	Glu	His	Tyr	Arg	Phe	Val	Ser	Met	Trp	Met	Ala	Arg	Thr	Ser	Tyr
			290			295					300				
Leu	Ala	Ala	Phe	Ala	Ile	Met	Val	Ile	Phe	Thr	Leu	Ser	Val	Ser	Met
			305			310				315				320	
Leu	Leu	Arg	Tyr	Ser	His	His	Gln	Ile	Phe	Val	Phe	Ile	Val	Asp	Leu
				325				330				335			
Leu	Gln	Met	Leu	Glu	Met	Asn	Met	Ala	Ile	Ala	Phe	Pro	Ala	Ala	Pro


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Leu Leu Thr Val Ile Leu Ala Leu Val Gly Met Glu Ala Ile Met Ser
      355          360          365
Glu Phe Phe Asn Asp Thr Thr Thr Ala Phe Tyr Ile Ile Leu Ile Val
      370          375          380
Trp Leu Ala Asp Gln Tyr Asp Ala Ile Cys Cys His Thr Ser Thr Ser
      385          390          395          400
Lys Arg His Trp Leu Arg Phe Phe Tyr Leu Tyr His Phe Ala Phe Tyr
      405          410          415
Ala Tyr His Tyr Arg Phe Asn Gly Gln Tyr Ser Ser Leu Ala Leu Val
      420          425          430
Thr Ser Trp Leu Phe Ile Gln His Ser Met Ile Tyr Phe Phe His His
      435          440          445
Tyr Glu Leu Pro Ala Ile Leu Gln Gln Val Arg Ile Gln Glu Met Leu
      450          455          460
Leu Gln Ala Pro Pro Leu Gly Pro Gly Thr Pro Thr Ala Leu Pro Asp
      465          470          475          480
Asp Met Asn Asn Asn Ser Gly Ala Pro Ala Thr Ala Pro Asp Ser Ala
      485          490          495
Gly Gln Pro Pro Ala Leu Gly Pro Val Phe Glu Leu Val Ser Lys Glu
      500          505          510
Arg Gly Trp Gly Ser Ala Glu Gly Ser Gly Gly Val Leu Val Gly Leu
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Gln

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<210> 4915

<211> 1157

<212> DNA

<213> Homo sapiens

<400> 4915

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660

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<210> 4916

<211> 59

<212> PRT

<213> Homo sapiens

<400> 4916

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Ala	Gly	Ala	Ser	Arg	Lys	Arg	Lys	Glu	Val	Pro	Ser	Arg	Leu	Arg	Thr
			20					25					30		
Trp	Gly	Pro	Gly	Gly	Asp	Ala	Pro	Arg	Gly	Ser	Gly	Leu	Lys	Arg	Pro
			35					40				45			
Arg	Gly	Pro	Arg	Gly	Pro	Ser	Ala	Ala	Pro	Arg					
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<210> 4917

<211> 1544

<212> DNA

<213> Homo sapiens

<400> 4917

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 1260
 ggtgctgaga cctgtgcggt gtgcctggac tacttctgca acaaacaggc tagtgcctcc
 1320
 gtggctccgg gtgctgcct gtaagcacga gtttcaccga gactgtgtgg acccctggct
 1380
 gatgctccag cagacctgcc cactgtgcaa attcaacgtc ctgggtgagc accaggggtg
 1440
 gggtcctcgt gcctactctg cctgctcctc acctgatgcc tctctcctg ttcttcttcc
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 1544

<210> 4918

<211> 347

<212> PRT

<213> Homo sapiens

<400> 4918

Met Gly Pro Ala Ala Arg Pro Ala Leu Arg Ser Pro Pro Pro Pro Pro
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 Pro Pro Pro Pro Ser Pro Leu Leu Leu Leu Leu Pro Leu Leu Pro Leu
 20 25 30
 Trp Leu Gly Leu Ala Gly Pro Gly Ala Ala Ala Asp Gly Ser Glu Pro
 35 40 45
 Ala Ala Gly Ala Gly Arg Gly Gly Ala Arg Ala Val Arg Val Asp Val
 50 55 60
 Arg Leu Pro Arg Gln Asp Ala Leu Val Leu Glu Gly Val Arg Ile Gly

65	70										75					80				
Ser	Glu	Ala	Asp	Pro	Ala	Pro	Leu	Leu	Gly	Gly	Arg	Leu	Leu	Leu	Met					
				85					90						95					
Asp	Val	Val	Asp	Ala	Glu	Gln	Glu	Ala	Pro	Ala	Asp	Gly	Trp	Ile	Ala					
			100					105						110						
Val	Ala	Tyr	Val	Gly	Lys	Glu	Gln	Ala	Ala	Gln	Phe	His	Gln	Glu	Asn					
		115				120						125								
Lys	Gly	Ser	Gly	Pro	Gln	Ala	Tyr	Pro	Lys	Ala	Leu	Val	Gln	Gln	Met					
	130				135						140									
Arg	Arg	Ala	Leu	Phe	Leu	Gly	Ala	Ser	Ala	Leu	Leu	Leu	Leu	Ile	Leu					
	145				150					155					160					
Asn	His	Asn	Val	Val	Arg	Glu	Leu	Asp	Ile	Ser	Gln	Leu	Leu	Leu	Arg					
				165					170					175						
Pro	Val	Ile	Val	Leu	His	Tyr	Ser	Ser	Asn	Val	Thr	Lys	Leu	Leu	Asp					
			180					185						190						
Ala	Leu	Leu	Gln	Arg	Thr	Gln	Ala	Thr	Ala	Glu	Ile	Thr	Ser	Gly	Glu					
	195					200						205								
Ser	Leu	Ser	Ala	Asn	Ile	Glu	Trp	Lys	Leu	Thr	Leu	Trp	Thr	Thr	Cys					
	210				215						220									
Gly	Leu	Ser	Lys	Asp	Gly	Tyr	Gly	Gly	Trp	Gln	Asp	Leu	Val	Cys	Leu					
	225			230						235					240					
Gly	Gly	Ser	Arg	Ala	Gln	Glu	Gln	Lys	Pro	Leu	Gln	Gln	Leu	Trp	Asn					
			245						250					255						
Ala	Ile	Leu	Leu	Val	Ala	Met	Leu	Leu	Cys	Thr	Gly	Leu	Val	Val	Gln					
		260					265						270							
Ala	Gln	Arg	Gln	Ala	Ser	Arg	Gln	Ser	Gln	Arg	Glu	Leu	Gly	Gly	Gln					
	275					280						285								
Val	Asp	Leu	Phe	Lys	Arg	Arg	Val	Val	Arg	Arg	Leu	Ala	Ser	Leu	Lys					
	290				295					300										
Thr	Arg	Arg	Cys	Arg	Leu	Ser	Arg	Ala	Ala	Gln	Gly	Leu	Pro	Asp	Pro					
	305			310						315					320					
Gly	Ala	Glu	Thr	Cys	Ala	Val	Cys	Leu	Asp	Tyr	Phe	Cys	Asn	Lys	Gln					
			325						330					335						
Ala	Ser	Ala	Pro	Val	Ala	Pro	Gly	Ala	Ala	Leu										
		340					345													

<210> 4919

<211> 1362

<212> DNA

<213> Homo sapiens

<400> 4919

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120
gggcttcctc tcatgggggt aggcatagac ctgaccaagg tgcacgctat tcaacagaaa
180
agacgggtgg cttttctaaa ccaatttgtg gtgcacactg tacagttcct caaccgcttt
240
tctacagttt gtgaggagaa actggcgagac ctttcacttc gtatccaaca aattgaacaa
300
actctcaata ttttagatgc aaagtgtgtc tctatccag gcctagatga tgtcacagtt
360

gaagtatctc ctttaaatgt caccagtgtc acaaatggag cacatcctga agccacttca
 420
 gagcaaccac agcagaacag tacacaagac tctggactac aggaaagtga agtatcagca
 480
 gaaaatatct taactgtagc caaggatcca agatatgcca gatattctcaa aatggttcaa
 540
 gtgggtgtac cagtgtatggc aataagaac aaaatgatat cagaaggact agaccagat
 600
 cttcttgaga ggccagatgc tccagtgcct gatggcgaaa gtgagaaaaa tgtagaagaa
 660
 agttcagata gcgaatcttc ttttagtgat taagcttaat tttgataaga attacatatg
 720
 catgcatagg ggtacattta cattctgtaa gagattgagc ctgaactctc ttagtcataa
 780
 aaacatcaaa tggccacatg tccactacca agcttcttct atgttaaaaa aataataata
 840
 aagcagtttt aacctgcccc gtatgtcttg ttgctaaaat aanggccctc aaattgaaaa
 900
 ttnggatacc ctataataag taccaattag tgctccaaat actaagatag aatattttag
 960
 agatgcaatg agcaattaca gtcaggcacg ggttgtcacg cctgtaatcc cagcactttg
 1020
 ggaggccgag gcgagtggat aacctgaggt caggagttca agaccagcct ggccaacatg
 1080
 gtgaaaacct catctctact aaaaatacaa aaagtagctg ggcgtgtgta caaaaattag
 1140
 ctgggctgtag tggcaggtgc ctgtaatccc agctactcgg gaagctgagg caggagaatc
 1200
 acctgaaccc agaaggtaaa ggtttcagtg agctgagatt gcgtcattgc actccagcca
 1260
 tggcgacaag agtgaaaactc tgtcttaaaa ataaaaagag atgcaatgag caatttttaa
 1320
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 1362

<210> 4920

<211> 194

<212> PRT

<213> Homo sapiens

<400> 4920

Met	Asp	Glu	Asp	Gly	Leu	Pro	Leu	Met	Gly	Ser	Gly	Ile	Asp	Leu	Thr
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Lys	Val	Pro	Ala	Ile	Gln	Gln	Lys	Arg	Thr	Val	Ala	Phe	Leu	Asn	Gln
				20				25					30		
Phe	Val	Val	His	Thr	Val	Gln	Phe	Leu	Asn	Arg	Phe	Ser	Thr	Val	Cys
			35				40					45			
Glu	Glu	Lys	Leu	Ala	Asp	Leu	Ser	Leu	Arg	Ile	Gln	Gln	Ile	Glu	Thr
			50			55				60					
Thr	Leu	Asn	Ile	Leu	Asp	Ala	Lys	Leu	Ser	Ser	Ile	Pro	Gly	Leu	Asp
65					70					75				80	
Asp	Val	Thr	Val	Glu	Val	Ser	Pro	Leu	Asn	Val	Thr	Ser	Val	Thr	Asn
					85				90					95	
Gly	Ala	His	Pro	Glu	Ala	Thr	Ser	Glu	Gln	Pro	Gln	Gln	Asn	Ser	Thr

	100		105		110
Gln	Asp	Ser	Gly	Leu	Gln
	115		120		125
Thr	Val	Ala	Lys	Asp	Pro
	130		135		140
Val	Gly	Val	Pro	Val	Met
	145		150		155
Leu	Asp	Pro	Asp	Leu	Glu
	165		170		175
Glu	Ser	Glu	Lys	Thr	Val
	180		185		190
Ser	Asp				

<210> 4921

<211> 1272

<212> DNA

<213> Homo sapiens

<400> 4921

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120
tcttccccgt tgcccctttg gggcgggatg gctgcggaag aagaagacga ggtggagtgg
180
gtagtggaga gcatcgcggt gctcctgcga ggcccagact ggtecatccc catcttggac
240
tttgtggaac agaaatgtga agtttttgat gatgaagaag aaagcaaatt gacctatata
300
gagattcatc aggaatacaa agaactagtt gaaaagctgt tagaagggtta cctcaaagaa
360
atttgaatta atgaagatca atttcaagaa gcatgcactt ctctctctgc aaagacccat
420
acatcacagg ccattttgca acctgtgttg gcagcagaag attttactat ctttaaagca
480
atgatgtgtc agaaaaacat tgaatgcag ctgcaagcca ttcgaaataa tcaagagaga
540
aatggtgtat tacctgactg cttaaccgat ggctctgatg tggtcagtga ccttgaacac
600
gaagagatga aaactcctg ggaagttctt agaaaatcaa aagaggaata tgaccaggaa
660
gaagaaagga agaggaaaaa acagtattca gaggctaaaa cagaagagcc cacagtgcac
720
tcagtgtaag ctgcaataat gaataattcc caaggggatg gtgaacattt tgcacaccca
780
ccctcagaag ttaaaatgca ttttgctaag cagtcaatag aacctttggg aagaaaagtg
840
gaaagggtct aaacttctc cctcccaaaa aaaggcctga agattcctgg cttagagcat
900
gcgagcattg aaggaccaat agcaaaacta tcagtacttg gaacagaaga acttcggcaa
960
cgagaacact atctcaagca gaagagagat aagttgatgt ccatgagaaa ggatatgagg
1020

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actaaacaga tacaaaatat ggagcagaaa ggaaaaccca ctggggaggt agaggaaatg
 1080
 acagagaaac cagaaatgac agcagaggag aagcaaacat tactaaagag gagattgctt
 1140
 gcagagaaac tcaagaaga agttattaat aagtaataat taagaacaat ttaacaaaaat
 1200
 ggaagtcca attgtcttaa aaataaatta tttagtcttt acactgaaaa aaaaaaaaaa
 1260
 aaaaaataaa aa
 1272

<210> 4922

<211> 342

<212> PRT

<213> Homo sapiens

<400> 4922

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Ala	Gly	Leu	Leu	Arg	Gly	Pro	Asp	Trp	Ser	Ile	Pro	Ile	Leu	Asp
		20					25					30		Phe
Val	Glu	Gln	Lys	Cys	Glu	Val	Phe	Asp	Asp	Glu	Glu	Glu	Ser	Lys
		35				40					45			Leu
Thr	Tyr	Thr	Glu	Ile	His	Gln	Glu	Tyr	Lys	Glu	Leu	Val	Glu	Lys
		50			55					60				Leu
Leu	Glu	Gly	Tyr	Leu	Lys	Glu	Ile	Gly	Ile	Asn	Glu	Asp	Gln	Phe
65				70				75						80
Glu	Ala	Cys	Thr	Ser	Pro	Leu	Ala	Lys	Thr	His	Thr	Ser	Gln	Ala
			85					90					95	Ile
Leu	Gln	Pro	Val	Leu	Ala	Ala	Glu	Asp	Phe	Thr	Ile	Phe	Lys	Ala
		100					105						110	Met
Met	Val	Gln	Lys	Asn	Ile	Glu	Met	Gln	Leu	Gln	Ala	Ile	Arg	Ile
		115				120					125			Ile
Gln	Glu	Arg	Asn	Gly	Val	Leu	Pro	Asp	Cys	Leu	Thr	Asp	Gly	Ser
		130			135						140			Asp
Val	Val	Ser	Asp	Leu	Glu	His	Glu	Glu	Met	Lys	Ile	Leu	Arg	Glu
145				150						155				Val
Leu	Arg	Lys	Ser	Lys	Glu	Glu	Tyr	Asp	Gln	Glu	Glu	Glu	Arg	Lys
			165					170					175	Arg
Lys	Lys	Gln	Leu	Ser	Glu	Ala	Lys	Thr	Glu	Glu	Pro	Thr	Val	His
		180					185					190		Ser
Ser	Glu	Ala	Ala	Ile	Met	Asn	Asn	Ser	Gln	Gly	Asp	Gly	Glu	His
		195				200					205			Phe
Ala	His	Pro	Pro	Ser	Glu	Val	Lys	Met	His	Phe	Ala	Asn	Gln	Ser
		210			215						220			Ile
Glu	Pro	Leu	Gly	Arg	Lys	Val	Glu	Arg	Ser	Glu	Thr	Ser	Ser	Leu
225				230						235				Pro
Gln	Lys	Gly	Leu	Lys	Ile	Pro	Gly	Leu	Glu	His	Ala	Ser	Ile	Glu
			245						250				255	Gly
Pro	Ile	Ala	Asn	Leu	Ser	Val	Leu	Gly	Thr	Glu	Glu	Leu	Arg	Gln
		260					265						270	Arg
Glu	His	Tyr	Leu	Lys	Gln	Lys	Arg	Asp	Lys	Leu	Met	Ser	Met	Arg
		275				280						285		Lys
Asp	Met	Arg	Thr	Lys	Gln	Ile	Gln	Asn	Met	Glu	Gln	Lys	Gly	Lys
														Pro

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      290              295              300
Thr Gly Glu Val Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu
305              310              315              320
Glu Lys Gln Thr Leu Leu Lys Arg Arg Leu Leu Ala Glu Lys Leu Lys
      325              330              335
Glu Glu Val Ile Asn Lys
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<210> 4923
 <211> 765
 <212> DNA
 <213> Homo sapiens

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<400> 4923
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aagccttctg ctctnctcc aaggacctca tttagctccg ccaggaggtc atcatcagcc
120
tccaaagtcgt cctcatccgt cccctcctcc tcctcctcat cgggtctctc catgcacagg
180
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240
gctgggggct gggcccgac caaagccaag aactcagcct ccagttcttc atcgtaggcc
300
ccgtctctag ggatcatcag gccatctggg gagaggtcaa ccaggagcc cagctggcgg
360
gcggccgcgg cgcctctgcc cgggggtccc gggggtcctt cctcttgtag atcttcaagg
420
ctggatgccc ggaccacctg cccccaagcc cggccttgcc ctgcccttc ccggggctct
480
gtcgccgcgc actcgccctt cctgagtcct gcaactcctc tcgggcgcct gcggccggtc
540
gatcccgagc cctcgcttcc ctgcttgccc gtcccacttc cgcctcgggc ctggggcgcc
600
gccgcacctn ggagcgcgcc cagctgggct cgccgaggtc tgcgagcg aaactacaac
660
tcccggcaga tttctcaagg ggaagataaa atgactaaga ggaagaagct gcggacctca
720
gctccccga tgaggaaaca ggatctccct gccggtctc cgcgt
765

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<210> 4924
 <211> 255
 <212> PRT
 <213> Homo sapiens

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<400> 4924
Ser Pro Ala Pro Asp Glu Gly Pro Gln Ala Ser Ala Gly Pro Gln Glu
1      5      10      15
Val Gly Ser Leu Lys Pro Ser Ala Pro Xaa Pro Arg Thr Ser Phe Ser
      20      25      30
Ser Ala Ser Arg Ser Ser Ser Ala Ser Lys Ser Ser Ser Val Pro
      35      40      45
Ser Ser Ser Ser Ser Ser Gly Ser Leu Met His Arg Leu Ala Ile Phe

```



```

      50              55              60
Ser Met Ala Ser Ile Gly Lys Gly Pro Leu Pro Leu Ser Phe Ser Arg
65              70              75              80
Ala Gly Gly Trp Pro Pro Thr Lys Ala Lys Asn Ser Ala Ser Ser Ser
      85              90              95
Ser Ser Leu Ala Pro Ser Ser Gly Ile Ile Arg Pro Ser Gly Glu Arg
      100              105              110
Ser Thr Ser Arg Pro Ser Trp Arg Ala Ala Ala Pro Leu Pro Gly
      115              120              125
Gly Pro Gly Gly Pro Ser Ser Cys Ala Ser Ser Arg Leu Asp Ala Arg
      130              135              140
Thr Thr Cys Pro Gln Ala Arg Pro Cys Pro Ala Pro Ser Pro Gly Ser
145              150              155              160
Val Ala Ala His Ser Pro Phe Leu Ser Pro Ala Leu Leu Val Gly Ala
      165              170              175
Leu Arg Pro Val Asp Pro Glu Pro Ser Leu Pro Cys Leu Ala Val Pro
      180              185              190
Leu Pro Pro Arg Ala Ser Gly Ala Ala Ala Pro Xaa Ser Ala Ala Ser
      195              200              205
Trp Ala Arg Arg Gly Leu Pro Ser Arg Asn Tyr Asn Ser Arg Gln Ile
      210              215              220
Ser Gln Gly Glu Asp Lys Met Thr Lys Arg Lys Lys Leu Arg Thr Ser
225              230              235              240
Ala Pro Leu Met Arg Lys Gln Asp Leu Pro Ala Gly Ser Ser Val
      245              250              255

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<210> 4925

<211> 374

<212> DNA

<213> Homo sapiens

<400> 4925

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ggatcgatgagg aaaatgaaat ggaagaacat gaactcaaag atgaggagga tggttaagac
120
agtgatgagg ccgaggacgc tgagctctat gatgaccttt actgcccagc atgtgacaaa
180
tcgttcaaga cagaaaaggc catgaagaat cacgagaagt caaagaagca tcgggaaatg
240
gtggccttgc taaaacaaca gctggaggag gaagaagaaa atttttcaag acctcaaat
300
gatgaaaatc cattagatga caattctgag gaagaaatgg aagatgcacc aaaacaaaag
360
ctttctaaaa aaaa
374

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<210> 4926

<211> 124

<212> PRT

<213> Homo sapiens

<400> 4926

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Ala Asn Leu Glu Lys Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys

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Glu Phe Gly Asp Gly Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu			
	20	25	30
Lys Asp Glu Glu Asp Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu			
	35	40	45
Leu Tyr Asp Asp Leu Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr			
	50	55	60
Glu Lys Ala Met Lys Asn His Glu Lys Ser Lys Lys His Arg Glu Met			
	65	70	75
Val Ala Leu Leu Lys Gln Gln Leu Glu Glu Glu Glu Asn Phe Ser			
	85	90	95
Arg Pro Gln Ile Asp Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu			
	100	105	110
Met Glu Asp Ala Pro Lys Gln Lys Leu Ser Lys Lys			
	115	120	

<210> 4927

<211> 1649

<212> DNA

<213> Homo sapiens

<400> 4927

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 120
 attcagttat ctggagcaga acaactagaa gctttgaaag cttttgtgga agcaatggta
 180
 aatgagaatg tcagctctgt gatctcgcgg cagttgtctga ctgatttttg cacacatctt
 240
 cctaacttgc ctgatagcac agccaaagaa atctatcact tcaccttgga aaagatccag
 300
 cctagagatc tttcatttga ggagcaggtt gcttcataa gacagcatct tgcatttata
 360
 tatgagaagc aagaagattg gagaagtga gcccaagtgt tgggtgggaat tcctttggaa
 420
 acaggacaaa aacagtacaa tgtagattat aaactggaga cttacttgaa gattgctagg
 480
 ctatatctgg aggatgatga tccagtccag gcagaggcct acataaatcg agcatcgttg
 540
 cttcagaatg aatcaaccaa tgaacaatta cagatacatt ataaggtatg ctatgcacgt
 600
 gttcttgatt atagaagaaa attcattgaa gctgcacaaa ggtacaatga gctctcttac
 660
 aagacaatag tccacgaaaag tgaagacta gaggccttaa aacatgcttt gcactgtacg
 720
 atcttagcat cagcaggaca gcagcgttct cggatgctgg ctaccctttt taaggatgaa
 780
 aggtgcaccg aacttgctgc ttatgggatc ctagagaaaa tgtatctaga caggatcatc
 840
 agaggggaac agcttcaaga atttgctgcc atgctgatgc ctcacacaaa agcaactaca
 900
 gctgatgggt ccagcatctt ggacagagct gttattgaac acaatttggt gctgcaagc
 960

aaattatata ataattattac ctctgaagaa ctgtggagctc ttttagagat cccgtcgagct
 1020
 aaggcggaagaa agatagcatc tcaaatgata accgaaggac gtatgaatgg atttattgac
 1080
 cagattgatg gaatagttca ttttgaaaca cgagaagccc tgccaacgtg ggataagcag
 1140
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 1200
 gaatggacag cacaagccat ggaagccag atggctcagt gaatccttgc agaactctg
 1260
 tgcacatgac atctttttcc atgttgtgca gatcagtttc actatctcca aagcatttgc
 1320
 atcatgacct tatacatttc aatccctttt atgctggatt ccgtttaaag aagacattat
 1380
 tagagcagga agtacaagca tttaaaatat gtagtccca tatatttcag ggtctctgtg
 1440
 tattaagcta actcagatgt tttgaaagct ttttctttaa acagagggtga aatatctgtg
 1500
 gctaaaaagt ttgagatttg tgataacttt gtagtcatgt aaaacttaag tgcttcatgc
 1560
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 1649

<210> 4928

<211> 405

<212> PRT

<213> Homo sapiens

<400> 4928

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Ser	His	Lys	Asp	Leu	Ala	Gly	Lys	Tyr	Arg	Gln	Ile	Leu	Glu	Lys	Ala
			20					25					30		
Ile	Gln	Leu	Ser	Gly	Ala	Glu	Gln	Leu	Glu	Ala	Leu	Lys	Ala	Phe	Val
		35				40					45				
Glu	Ala	Met	Val	Asn	Glu	Asn	Val	Ser	Leu	Val	Ile	Ser	Arg	Gln	Leu
		50				55				60					
Leu	Thr	Asp	Phe	Cys	Thr	His	Leu	Pro	Asn	Leu	Pro	Asp	Ser	Thr	Ala
					70				75					80	
Lys	Glu	Ile	Tyr	His	Phe	Thr	Leu	Glu	Lys	Ile	Gln	Pro	Arg	Val	Ile
				85					90					95	
Ser	Phe	Glu	Glu	Gln	Val	Ala	Ser	Ile	Arg	Gln	His	Leu	Ala	Ser	Ile
			100					105					110		
Tyr	Glu	Lys	Glu	Glu	Asp	Trp	Arg	Asn	Ala	Ala	Gln	Val	Leu	Val	Gly
		115				120					125				
Ile	Pro	Leu	Glu	Thr	Gly	Gln	Lys	Gln	Tyr	Asn	Val	Asp	Tyr	Lys	Leu
		130				135					140				
Glu	Thr	Tyr	Leu	Lys	Ile	Ala	Arg	Leu	Tyr	Leu	Glu	Asp	Asp	Asp	Pro
			145		150				155					160	
Val	Gln	Ala	Glu	Ala	Tyr	Ile	Asn	Arg	Ala	Ser	Leu	Leu	Gln	Asn	Glu
			165					170						175	
Ser	Thr	Asn	Glu	Gln	Leu	Gln	Ile	His	Tyr	Lys	Val	Cys	Tyr	Ala	Arg

180 185 190
 Val Leu Asp Tyr Arg Arg Lys Phe Ile Glu Ala Ala Gln Arg Tyr Asn
 195 200 205
 Glu Leu Ser Tyr Lys Thr Ile Val His Glu Ser Glu Arg Leu Glu Ala
 210 215 220
 Leu Lys His Ala Leu His Cys Thr Ile Leu Ala Ser Ala Gly Gln Gln
 225 230 235 240
 Arg Ser Arg Met Leu Ala Thr Leu Phe Lys Asp Glu Arg Cys Gln Gln
 245 250 255
 Leu Ala Ala Tyr Gly Ile Leu Glu Lys Met Tyr Leu Asp Arg Ile Ile
 260 265 270
 Arg Gly Asn Gln Leu Gln Glu Phe Ala Ala Met Leu Met Pro His Gln
 275 280 285
 Lys Ala Thr Thr Ala Asp Gly Ser Ser Ile Leu Asp Arg Ala Val Ile
 290 295 300
 Glu His Asn Leu Leu Ser Ala Ser Lys Leu Tyr Asn Asn Ile Thr Phe
 305 310 315 320
 Glu Glu Leu Gly Ala Leu Leu Glu Ile Pro Ala Ala Lys Ala Glu Lys
 325 330 335
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<212> DNA

<213> Homo sapiens

<400> 4929

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<211> 648

<212> PRT

<213> Homo sapiens

<400> 4930

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Val	Gln	Gln	Phe	Gly	Tyr	Gln	Arg	Arg	Ala	Ser	Asp	Asp	Gly	Lys	Leu
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Thr	Asp	Pro	Ser	Lys	Thr	Ser	Asn	Thr	Ile	Arg	Val	Phe	Leu	Pro	Asn
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Lys	Gln	Arg	Thr	Val	Val	Asn	Val	Arg	Asn	Gly	Met	Ser	Leu	His	Asp
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Cys	Leu	Met	Lys	Ala	Leu	Lys	Val	Arg	Gly	Leu	Gln	Pro	Glu	Cys	Cys
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Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
565          570          575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
580          585          590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
595          600          605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
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Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
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<211> 261

<212> DNA

<213> Homo sapiens

<400> 4931

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<211> 87

<212> PRT

<213> Homo sapiens

<400> 4932

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Thr	Gln	Gly	Thr	Arg	Lys	Ile	Leu	Tyr	Pro	Tyr	Ala	His	Leu	Ser	Ala
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Glu	Asp	Phe	Asn	Ile	Tyr	Gly	His	Gly	Gly	Arg	Gln	Phe	Trp	Leu	Val
	50					55					60				
Ser	Ser	Cys	Phe	Phe	Phe	Leu	Leu	Gly	Gly	Ala	Ser	Thr	Cys	Met	Arg
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<211> 181

<212> PRT

<213> Homo sapiens

<400> 4934

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<210> 4935

<211> 1668

<212> DNA

<213> Homo sapiens

<400> 4935

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<210> 4936

<211> 337

<212> PRT

<213> Homo sapiens

<400> 4936

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Asn	Phe	Asp	Ser	Val	Glu	Leu	His	Gly	Thr	Met	Lys	Ser	Tyr	Phe	Gly
		20						25					30		
Gly	Leu	Leu	Cys	Val	Cys	Trp	Ser	Pro	Asp	Gly	Lys	Tyr	Ile	Val	Thr
	35						40				45				
Gly	Gly	Glu	Asp	Asp	Leu	Val	Thr	Val	Trp	Ser	Phe	Val	Asp	Cys	Arg
	50				55					60					
Val	Ile	Ala	Arg	Gly	His	Gly	His	Lys	Ser	Trp	Val	Ser	Val	Val	Ala
65					70				75					80	
Phe	Asp	Pro	Tyr	Thr	Ser	Val	Glu	Glu	Gly	Asp	Pro	Met	Glu	Phe	
				85				90					95		
Ser	Gly	Ser	Asp	Glu	Asp	Phe	Gln	Asp	Leu	Leu	His	Phe	Gly	Glu	Ile
			100					105					110		
Glu	Gln	Ile	Val	His	Ser	Pro	Gly	Ser	Pro	Asn	Gly	Thr	Leu	Gln	Thr
		115					120					125			
Ala	Ala	Pro	Ser	Val	Thr	Tyr	Arg	Phe	Gly	Ser	Val	Gly	Gln	Asp	Thr
		130					135				140				
Gln	Leu	Cys	Leu	Trp	Asp	Leu	Thr	Glu	Asp	Ile	Leu	Phe	Pro	His	Gln
145				150					155					160	
Pro	Leu	Ser	Arg	Ala	Arg	Thr	His	Thr	Asn	Val	Met	Asn	Ala	Thr	Ser
				165					170					175	
Pro	Pro	Ala	Gly	Ser	Asn	Gly	Asn	Ser	Val	Thr	Thr	Pro	Gly	Asn	Ser
			180					185					190		
Val	Pro	Pro	Pro	Leu	Pro	Arg	Ser	Asn	Ser	Leu	Pro	His	Ser	Ala	Val
			195				200					205			
Ser	Asn	Ala	Gly	Ser	Lys	Ser	Ser	Val	Met	Asp	Gly	Ala	Ile	Ala	Ser
					215						220				
Gly	Val	Ser	Lys	Phe	Ala	Thr	Leu	Ser	Leu	His	Asp	Arg	Lys	Glu	Arg
225				230						235				240	
His	His	Glu	Lys	Asp	His	Lys	Arg	Asn	His	Ser	Met	Gly	His	Ile	Ser
				245					250					255	
Ser	Lys	Ser	Ser	Asp	Lys	Leu	Asn	Leu	Val	Thr	Lys	Thr	Lys	Thr	Asp
			260					265					270		
Pro	Ala	Lys	Thr	Leu	Gly	Thr	Pro	Leu	Cys	Pro	Arg	Met	Glu	Asp	Val
			275				280					285			
Pro	Leu	Leu	Glu	Pro	Leu	Ile	Cys	Lys	Lys	Ile	Ala	His	Glu	Arg	Leu
290						295					300				
Thr	Val	Leu	Ile	Phe	Leu	Glu	Asp	Cys	Ile	Val	Thr	Ala	Cys	Gln	Glu

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305              310              315              320
Gly Phe Ile Cys Thr Trp Gly Arg Pro Gly Lys Val Val Ser Phe Asn
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Pro

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<210> 4937
<211> 715
<212> DNA
<213> Homo sapiens

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<400> 4937
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120
aagcggggag tcccacactc tctgggtcca ggcacaaagc tatcctccgt tgttctgatc
180
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240
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gaagagacag accaacagga agtgttctct tcagggggtg ccagcccccac cctgaatctc
360
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420
cagagggagg caccogagct ggtgtgagca gctacgtggg tgggtggtcc agggaacaga
480
gggagggcac tggagccatt gcctgcctag ttcagtcctc aaatgggtcc aagccagctc
540
aggtctcgag cgccaggccc agggtaacct gcagcccagc cgatgggtacc attggctggt
600
gctcccactg aggtcttgag aaggtaatgg ggagagccac ttgcccttgc ctctgtcccc
660
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715

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<210> 4938
<211> 109
<212> PRT
<213> Homo sapiens

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<400> 4938
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Ser Val Val Leu Ile Cys Arg Ala Ser Ala Leu Ser Arg Tyr Leu Val
20          25          30
Val Ala Glu Pro Trp Pro Thr Arg Ser Gln Gly Gly Arg Gln Pro Gly
35          40          45
Cys Thr Leu Thr Leu Gly Val Cys Ala Asp Gly Arg Trp Glu Glu Thr
50          55          60
Asp Gln Gln Glu Val Phe Ser Ser Gly Val Ala Ser Pro Thr Leu Asn
65          70          75          80
Leu Arg Ala Ser Ser Ser Pro Ala Lys Ala Arg Ala Leu Ser Arg Pro

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85 90 95
 Trp Ala Leu Tyr Lys Gln Arg Glu Ala Pro Glu Leu Val
 100 105

<210> 4939

<211> 730

<212> DNA

<213> Homo sapiens

<400> 4939

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 120
 tcggcctcta cccgccctcc ccaaggtcct ccctccctgg actcaaaagc ctctacttgg
 180
 ctgcctctgc cagtcacctc ttctctgtct gagccctcca gaccaaattc ttgccacct
 240
 gcatgctctc ctgctgtgc ctcttctttt tctttcgagt ccagccttg ccaagcgcc
 300
 ccttccaaag cttcaccagc gccagcagcg ctgatgtgtg ggaccacatc acccccata
 360
 atcccagcag ccacagagcc agtctgtgca tcttcacggt cggggaggcc cacagccacc
 420
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 660
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 730

<210> 4940

<211> 158

<212> PRT

<213> Homo sapiens

<400> 4940

Ser Arg Ser Pro Pro Ala Ser Thr Met Ala Pro Ile Pro Ser Ala Leu
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 20 25 30
 Ala Asp Ser Ser Ala Ser Thr Arg Pro Pro Gln Gly Pro Pro Ser Leu
 35 40 45
 Asp Ser Lys Ala Ser Thr Trp Leu Pro Leu Pro Val Thr Ser Ser Ser
 50 55 60
 Ala Glu Pro Ser Arg Pro Asn Ser Cys Pro Pro Ala Cys Ser Pro Ala
 65 70 75 80
 Ala Ala Ser Ser Phe Ser Phe Glu Ser Gln Pro Cys Pro Ser Ala Pro

	85		90		95										
Ser	Lys	Ala	Ser	Pro	Ala	Pro	Ala	Ala	Leu	Met	Cys	Gly	Thr	Thr	Ser
		100						105					110		
Pro	Pro	Ile	Ile	Pro	Ala	Ala	Thr	Glu	Pro	Val	Cys	Ala	Ser	Ser	Arg
		115					120					125			
Ser	Gly	Arg	Pro	Thr	Ala	Thr	Ala	Cys	Ser	Leu	Gln	Pro	Leu	Leu	Asp
	130				135						140				
Val	Leu	Ser	Ala	Ser	Ala	Ser	Ser	Ser	Ser	Val	Ser	Leu	Ala		
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<210> 4941

<211> 1718

<212> DNA

<213> Homo sapiens

<400> 4941

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gatctgctcc tgggcagcct gaaggagaag cccgtcacca aggaggcccg ggcttcacac
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240
cgtgtgaggc gcactaccc tcagctgctc ctggcctcgc tcattcaggt ccattaccac
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360
ccctctccct tcgtacctgt gcgctgggtg gtgaaagtgg tgaaccct gctactgagg
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480
caggtggaga gccaccaccg cggagtggcc ttgctggcaa gggccatggt gcagtactcc
540
tgccaggagc tgtgccgcat cctctacctg ctcatcccg tctgggagcg aggcgacgag
600
aagcacagga tcacggccac cgcctctctc gtggagctcc tccagatgga gcaggtgcgc
660
cggatccccg aggaatactc tctggggcgg atggcagaag gcctgagcca ccacgacccc
720
atcatgaagg tgctgtccat tcgaggccctg gtcactcctg cccgcaggtc tgaagaagcc
780
gccaaagtga aggccctcct gccttccatg gtgaagggcc tgaagaacat ggaatgggatg
840
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900
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960
cgagaggtgc tgcgctctc ctgcatcaac ctgtatggga aggtgtgtcca gaagcttcgg
1020
gcaccacgca ctcaggccat ggaggagcag ctggtcagca ccttggtgcc cctactgctg
1080
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1140

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 1260
 ttcattatcc tcagccagag cctggagat gccagaact cacgggctc cctccggaag
 1320
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 1620
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<210> 4942

<211> 469

<212> PRT

<213> Homo sapiens

<400> 4942

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Ile	Gln	Val	His	Tyr	His	Ile	Gly	Leu	Asn	Leu	Pro	Gly	Cys	Val	Ala
			20					25					30		
Pro	Pro	Lys	Asp	Thr	Lys	Lys	Gly	Ala	Gln	Pro	Ser	Pro	Phe	Val	Pro
		35					40				45				
Val	Arg	Trp	Val	Val	Lys	Val	Val	Lys	Thr	Leu	Leu	Leu	Arg	Met	Gly
		50			55					60					
Cys	Ser	Tyr	Glu	Thr	Thr	Phe	Leu	Glu	Asp	Gln	Gly	Gly	Trp	Glu	Leu
65				70					75					80	
Met	Glu	Gln	Val	Glu	Ser	His	His	Arg	Gly	Val	Ala	Leu	Leu	Ala	Arg
			85						90					95	
Ala	Met	Val	Gln	Tyr	Ser	Cys	Gln	Glu	Leu	Cys	Arg	Ile	Leu	Tyr	Leu
			100					105					110		
Leu	Ile	Pro	Leu	Leu	Glu	Arg	Gly	Asp	Glu	Lys	His	Arg	Ile	Thr	Ala
		115					120					125			
Thr	Ala	Phe	Phe	Val	Glu	Leu	Leu	Gln	Met	Glu	Gln	Val	Arg	Arg	Ile
		130			135					140					
Pro	Glu	Glu	Tyr	Ser	Leu	Gly	Arg	Met	Ala	Glu	Gly	Leu	Ser	His	His
145				150					155					160	
Asp	Pro	Ile	Met	Lys	Val	Leu	Ser	Ile	Arg	Gly	Leu	Val	Ile	Leu	Ala
			165					170					175		
Arg	Arg	Ser	Glu	Lys	Thr	Ala	Lys	Val	Lys	Ala	Leu	Leu	Pro	Ser	Met
			180				185						190		
Val	Lys	Gly	Leu	Lys	Asn	Met	Asp	Gly	Met	Leu	Val	Val	Glu	Ala	Val
		195			200						205				
His	Asn	Leu	Lys	Ala	Val	Phe	Lys	Gly	Arg	Asp	Gln	Lys	Leu	Met	Asp

```

      210              215              220
Ser Ala Val Tyr Val Glu Met Leu Gln Ile Leu Leu Pro His Phe Ser
225              230              235              240
Asp Ala Arg Glu Val Val Arg Ser Ser Cys Ile Asn Leu Tyr Gly Lys
      245              250              255
Val Val Gln Lys Leu Arg Ala Pro Arg Thr Gln Ala Met Glu Glu Gln
      260              265              270
Leu Val Ser Thr Leu Val Pro Leu Leu Leu Thr Met Gln Glu Gly Asn
      275              280              285
Ser Lys Val Ser Gln Lys Cys Val Lys Thr Leu Leu Arg Cys Ser Tyr
      290              295              300
Phe Met Ala Trp Glu Leu Pro Lys Arg Ala Tyr Ser Arg Lys Pro Trp
305              310              315              320
Asp Asn Gln Gln Gln Thr Val Ala Lys Ile Cys Lys Cys Leu Val Asn
      325              330              335
Thr His Arg Asp Ser Ala Phe Ile Phe Leu Ser Gln Ser Leu Glu Tyr
      340              345              350
Ala Lys Asn Ser Arg Ala Ser Leu Arg Lys Cys Ser Val Met Phe Ile
      355              360              365
Gly Ser Leu Val Pro Cys Met Glu Ser Ile Met Thr Glu Asp Arg Leu
      370              375              380
Asn Glu Val Lys Ala Ala Leu Asp Asn Leu Arg His Asp Pro Glu Ala
385              390              395              400
Ser Val Cys Ile Tyr Ala Ala Gln Val Gln Asp His Ile Leu Ala Ser
      405              410              415
Cys Trp Gln Asn Ser Trp Leu Pro His Gly Asn Ser Trp Val Cys Tyr
      420              425              430
Ser Ala Thr Thr His Arg Trp Ser Pro Ser Cys Glu Asn Leu Pro Thr
      435              440              445
Ser His Gln Arg Arg Ser Trp Ile Met Gln Ala Leu Gly Ser Trp Lys
      450              455              460
Met Ser Leu Lys Lys
465

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<210> 4943

<211> 1020

<212> DNA

<213> Homo sapiens

<400> 4943

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180
cttggccttt ttctgcctca gttgggggat ttcttaaacy tagaataccc gcgtttccgc
240
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300
cagttttctc gctcatcaca cggccttcgg cactgtagct ttgggtgggt ggctgcagat
360
taattttgta accaccttaa gaaaaatacy gaactctaac tccttgccac tcaagaaatg
420

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 540
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 600
 atgcagacgc tccgatttct tggactctac agagatgagc atcaggattt tatggatgag
 660
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 780
 gagaagaaaag tgcatttatt gtctttccac atattggagg aatgtcatct tcctaaatga
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 900
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 960
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 1020

<210> 4944

<211> 106

<212> PRT

<213> Homo sapiens

<400> 4944

Met Ser Ser Leu Ser Glu Tyr Ala Phe Arg Met Ser Arg Leu Ser Ala
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 Arg Leu Phe Gly Glu Val Thr Arg Pro Thr Asn Ser Lys Ser Met Lys
 20 25 30
 Val Val Lys Leu Phe Ser Glu Leu Pro Leu Ala Lys Lys Lys Glu Thr
 35 40 45
 Tyr Asp Trp Tyr Pro Asn His His Thr Tyr Ala Glu Leu Met Gln Thr
 50 55 60
 Leu Arg Phe Leu Gly Leu Tyr Arg Asp Glu His Gln Asp Phe Met Asp
 65 70 75 80
 Glu Gln Lys Arg Leu Lys Lys Leu Arg Gly Lys Glu Lys Pro Lys Lys
 85 90 95
 Gly Glu Gly Lys Arg Ala Ala Lys Arg Lys
 100 105

<210> 4945

<211> 1792

<212> DNA

<213> Homo sapiens

<400> 4945

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 120
 tacaacacat atgatgtcca cttttatgct tcctttgccc tcatcatgct ctggcccaaa
 180

ctctgagctca gcctacagta tgacatggct ctggccactc tcagggaggga cctgacacgg
 240
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 300
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 360
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 420
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 480
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 660
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 720
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 780
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 1020
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 1200
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 1680
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 1792

<210> 4946

<211> 197

<212> PRT

<213> Homo sapiens

<400> 4946

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Pro Pro Gly Gln Glu Tyr Arg Met Tyr Asn Thr Tyr Asp Val His Phe
 35 40 45
Tyr Ala Ser Phe Ala Leu Ile Met Leu Trp Pro Lys Leu Glu Leu Ser
 50 55 60
Leu Gln Tyr Asp Met Ala Leu Ala Thr Leu Arg Glu Asp Leu Thr Arg
 65 70 75 80
Arg Arg Tyr Leu Met Ser Gly Val Met Ala Pro Val Lys Arg Arg Asn
 85 90 95
Val Ile Pro His Asp Ile Gly Asp Pro Asp Asp Glu Pro Trp Leu Arg
100 105 110
Val Asn Ala Tyr Leu Ile His Asp Thr Ala Asp Trp Lys Asp Leu Asn
115 120 125
Leu Lys Phe Val Leu Gln Val Tyr Arg Asp Tyr Tyr Leu Thr Gly Asp
130 135 140
Gln Asn Phe Leu Lys Asp Met Trp Pro Val Cys Leu Val Arg Asp Ala
145 150 155 160
His Ala Val Ala Ser Val Pro Gly Val Trp Leu Val Ser Gly Lys Ser
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180 185 190
Ser Leu Ser Arg Leu
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<210> 4947

<211> 2060

<212> DNA

<213> Homo sapiens

<400> 4947

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360
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420

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540
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600
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720
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780
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1020
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1080
tggcattacg ctggggacca gtccactgat tttaactggt acaccgccg agccatgctg
1140
gctgccatct acaacacaa acagctgggt atgatgcagg actcctctcc agactttgag
1200
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1260
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1320
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1380
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1440
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1560
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1620
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1680
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1740
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1800
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1920
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1980
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2040

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2060

<210> 4948

<211> 127

<212> PRT

<213> Homo sapiens

<400> 4948

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Ala Glu Leu Thr Pro Leu Pro Phe Ser Leu Gln Ala Leu Ser Ile Leu
 1              5              10              15
Met Leu Pro His Asn Ile Pro Ser Ser Leu Ser Leu Leu Thr Ser Met
                20              25              30
Val Asp Asp Met Trp His Tyr Ala Gly Asp Gln Ser Thr Asp Phe Asn
                35              40              45
Trp Tyr Thr Arg Arg Ala Met Leu Ala Ala Ile Tyr Asn Thr Thr Glu
 50              55              60
Leu Val Met Met Gln Asp Ser Ser Pro Asp Phe Glu Asp Thr Trp Arg
 65              70              75
Phe Leu Glu Asn Arg Val Asn Asp Ala Met Asn Met Gly His Thr Ala
                85              90              95
Lys Gln Val Lys Ser Thr Gly Glu Ala Leu Val Gln Gly Leu Met Gly
                100             105             110
Ala Ala Val Thr Leu Lys Asn Leu Thr Xaa Leu Asn Gln Arg Arg
                115             120             125

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<210> 4949

<211> 1259

<212> DNA

<213> Homo sapiens

<400> 4949

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 120
gcttgggagg aaaagacgct gtccaagtac gaggccagcg agattcgctt gctggagatc
 180
ctggagggggc tgtgcgagag cagcgacttc gaatgcaatc agatgctaga ggcgcaggag
 240
gagcacctgg aggcctggtg gctgcagctg aagagcgaat atcctgactt attcgagtgg
 300
ttttgtgtga agacactgaa agtgtgtgtgc totccaggaa cctacggtcc cgactgtctc
 360
gcatgccagg gcgatcccca gaggccctgc agcgggaatg gccactgcag cggagatggg
 420
agcagacagg gcgacgggtc ctgccggtgc cacatggggg accagggccc gctgtgcaact
 480
gactgcatgg acggctactt cagctcgttc cggaacgaga cccacagcat ctgcacagcc
 540
tgtgacgagt cctgcaagac gtgctcgggc ctgaccaaca gagactgcgg cgagtgtgaa
 600
gtgggctggg tgctggacga gggcgccctg gtggatgtgg acgagtgtgc ggcgagccg
 660

```

cctccctgca gcgctgcgca gttctgtaag aacgccaacy gctcctacac gtgcgaagag
 720
 tgtgactcca gctgtgtggg ctgcacaggg gaaggcccag gaaactgtaa agagtgtatc
 780
 tctggctacy cgagggagca cggacagtgt gcagatgtgg acgagtgtct actagcagaa
 840
 aaaacctgtg tgaggaaaaa cgaaaactgc tacaatactc caggagagcta cgtctgtgtg
 900
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 960
 cacagaagga gaaagcccga cacagctgcc ctcccgcgaa gacctgtaat gtgccggact
 1020
 taccctttaa attattcaga aggatgtccc gtggaaaatg tggccctgag gatgccgtct
 1080
 cctgcatgtg acagcggcgg ggagaggctg cctgctctct aacggttgat tctcatttgt
 1140
 cccttaaaca gctgcatttc ttggtgttc ttaaacagac ttgtatatatt tgatacagtt
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 1259

<210> 4950

<211> 318

<212> PRT

<213> Homo sapiens

<400> 4950

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Arg	Gly	Leu	Val	Asp	Lys	Phe	Asn	Gln	Gly	Met	Val	Asp	Thr	Ala	Lys
		20						25					30		
Lys	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Lys	Thr	Leu	Ser
	35					40						45			
Lys	Tyr	Glu	Ser	Ser	Glu	Ile	Arg	Leu	Leu	Glu	Ile	Leu	Glu	Gly	Leu
	50				55					60					
Cys	Glu	Ser	Ser	Asp	Phe	Glu	Cys	Asn	Gln	Met	Leu	Glu	Ala	Gln	Glu
65				70					75					80	
Glu	His	Leu	Glu	Ala	Trp	Trp	Leu	Gln	Leu	Lys	Ser	Glu	Tyr	Pro	Asp
		85						90					95		
Leu	Phe	Glu	Trp	Phe	Cys	Val	Lys	Thr	Leu	Lys	Val	Cys	Cys	Ser	Pro
		100					105					110			
Gly	Thr	Tyr	Gly	Pro	Asp	Cys	Leu	Ala	Cys	Gln	Gly	Gly	Ser	Gln	Arg
	115				120						125				
Pro	Cys	Ser	Gly	Asn	Gly	His	Cys	Ser	Gly	Asp	Gly	Ser	Arg	Gln	Gly
	130			135					140						
Asp	Gly	Ser	Cys	Arg	Cys	His	Met	Gly	Tyr	Gln	Gly	Pro	Leu	Cys	Thr
145				150					155					160	
Asp	Cys	Met	Asp	Gly	Tyr	Phe	Ser	Ser	Leu	Arg	Asn	Glu	Thr	His	Ser
		165						170					175		
Ile	Cys	Thr	Ala	Cys	Asp	Glu	Ser	Cys	Lys	Thr	Cys	Ser	Gly	Leu	Thr
		180					185					190			
Asn	Arg	Asp	Cys	Gly	Glu	Cys	Glu	Val	Gly	Trp	Val	Leu	Asp	Glu	Gly
	195				200						205				
Ala	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Ala	Glu	Pro	Pro	Pro	Cys	Ser

210	215	220
Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys Glu Glu		
225	230	235
Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly Asn Cys		240
	245	250
Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys Ala Asp		255
	260	265
Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys Asn Glu		270
	275	280
Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro Asp Gly		285
	290	295
Phe Glu Glu Xaa Gly Arg Cys Leu Cys Ala Ala Gly Arg Gly		300
305	310	315

<210> 4951

<211> 1835

<212> DNA

<213> Homo sapiens

<400> 4951

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 120
 agcgacgact tcgcacctcc ttagggccgt ggctccgtag ctaccggtag cgtcgccgtg
 180
 ggcgacgtgc ccgcttccaa aatggcgcg cgggcggtat ctgggtcgct tggccgggag
 240
 ggctggaggc tcctgcagct gcgatgcctg cccgtggccc gttgcccaga agccctgggtg
 300
 ccgcgtgcct tccatgcttc agctgtgggg ctaaggctct catgatgaga gaagcagcag
 360
 cctcccaact cattttctca gcagcattct gagacacagg gggcagaaaa acctgatcca
 420
 gactctcttc attcaccccc caggtatata gaccagggcg gcgaggagga ggaggactat
 480
 gaaagtggag agcagttgca gcaccgcac ctgacggcag cccttgagtt tgtgcccgcc
 540
 cacgggtgga cagcagaggc gattgcagaa ggagccagat ctctgggtct ctccagtcca
 600
 gcagccagca tggttggaag gatgggcagt gagctaatac tgcattttgt gaccagtgcc
 660
 aataccggcg tcacacgtgt gctagaagag gagcagaagc tggtacagtt gggccaggcg
 720
 gagaagagga agacagacca gttcctgagg gatgcagtg aaaccagact gagaatgctg
 780
 atcccatata ttgagcactg gcccggggcc ctccagcatcc tcatgctccc tcacaacatc
 840
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 960
 acagagctg tgatgatgca ggactcctct ccagactttg aggacacttg gcgcttcctg
 1020

gaaaaccggg ttaatgatgc aatgaacatg ggccacactg ccaagcaggt aaagtccaca
 1080
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 1140
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 1200
 gacagattga aagagctttg aaaagtataa ggtgccatcc acataacctg gtgttcacga
 1260
 gaacacacta aaggactcct gagtcactac cacagccacc tggaaaccac aaggcatttg
 1320
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 1380
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 1560
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 1620
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 1680
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 1740
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 1800
 agttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
 1835

<210> 4952

<211> 318

<212> PRT

<213> Homo sapiens

<400> 4952

Met	Ala	Ala	Ala	Ala	Val	Ser	Gly	Ala	Leu	Gly	Arg	Ala	Gly	Trp	Arg
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Leu	Leu	Gln	Leu	Arg	Cys	Leu	Pro	Val	Ala	Arg	Cys	Arg	Gln	Ala	Leu
			20					25						30	
Val	Pro	Arg	Ala	Phe	His	Ala	Ser	Ala	Val	Gly	Leu	Arg	Ser	Ser	Asp
			35				40					45			
Glu	Gln	Lys	Gln	Gln	Pro	Pro	Asn	Ser	Phe	Ser	Gln	Gln	His	Ser	Glu
			50			55					60				
Thr	Gln	Gly	Ala	Glu	Lys	Pro	Asp	Pro	Glu	Ser	Ser	His	Ser	Pro	Pro
65					70					75				80	
Arg	Tyr	Thr	Asp	Gln	Gly	Gly	Glu	Glu	Glu	Glu	Asp	Tyr	Glu	Ser	Glu
			85						90					95	
Glu	Gln	Leu	Gln	His	Arg	Ile	Leu	Thr	Ala	Ala	Leu	Glu	Phe	Val	Pro
			100					105					110		
Ala	His	Gly	Trp	Thr	Ala	Glu	Ala	Ile	Ala	Glu	Gly	Ala	Gln	Ser	Leu
			115				120					125			
Gly	Leu	Ser	Ser	Ala	Ala	Ala	Ser	Met	Phe	Gly	Arg	Met	Gly	Ser	Glu
			130				135				140				
Leu	Ile	Leu	His	Phe	Val	Thr	Gln	Cys	Asn	Thr	Arg	Leu	Thr	Arg	Val

```

145          150          155          160
Leu Glu Glu Glu Gln Lys Leu Val Gln Leu Gly Gln Ala Glu Lys Arg
          165          170          175
Lys Thr Asp Gln Phe Leu Arg Asp Ala Val Glu Thr Arg Leu Arg Met
          180          185          190
Leu Ile Pro Tyr Ile Glu His Trp Pro Arg Ala Leu Ser Ile Leu Met
          195          200          205
Leu Pro His Asn Ile Pro Ser Ser Leu Ser Leu Thr Ser Met Val
          210          215          220
Asp Asp Met Trp His Tyr Ala Gly Asp Gln Ser Thr Asp Phe Asn Trp
225          230          235          240
Tyr Thr Arg Arg Ala Met Leu Ala Ala Ile Tyr Asn Thr Thr Glu Leu
          245          250          255
Val Met Met Gln Asp Ser Ser Pro Asp Phe Glu Asp Thr Trp Arg Phe
          260          265          270
Leu Glu Asn Arg Val Asn Asp Ala Met Asn Met Gly His Thr Ala Lys
          275          280          285
Gln Val Lys Ser Thr Gly Glu Ala Leu Val Gln Gly Leu Met Gly Ala
          290          295          300
Ala Val Thr Leu Lys Asn Leu Thr Gly Leu Asn Gln Arg Arg
305          310          315

```

<210> 4953

<211> 355

<212> DNA

<213> Homo sapiens

<400> 4953

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gtgcacgcag gaaatggcgg gtgggaggca ggacaggaga gccacggcct ggacaccact
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120
ggtgccccct ggtggcagct tgaaggaagg acggggcagtg ggtcgcgacc agcgggggacc
180
tacccccga aacgcacata aaagctggaa tcagcttggtt acagctgcag gtccctctcg
240
tcgatttgg atagaccctc ttgggaccca ctgcaccagg gaaccccaaa tgcagctcag
300
cagcatggga ggagccctgt ctgctggggg tgtctgggat cgtcgagag aggcct
355

```

<210> 4954

<211> 114

<212> PRT

<213> Homo sapiens

<400> 4954

```

Met Ala Gly Gly Arg Gln Asp Arg Arg Ala Gln Ala Trp Thr Pro Leu
1          5          10          15
Ser Ala Trp Gly Cys Leu Ala Ala Ser Pro Val Leu Gly Ala Gly Ile
          20          25          30
Thr Trp Pro Arg Val Pro Pro Gly Gly Ser Leu Lys Glu Gly Arg Ala
          35          40          45
Val Gly Arg Ser Gln Arg Gly Pro Thr Pro Gln Asn Ala His Lys Ser

```

```

      50                      55                      60
Trp Asn Gln Leu Val Thr Ala Ala Gly Pro Ser Arg Pro Ile Trp Ile
65                      70                      75                      80
Asp Pro Leu Gly Thr His Cys Thr Arg Glu Pro Gln Met Gln Leu Ser
      85                      90                      95
Ser Met Gly Gly Ala Leu Ser Ala Gly Gly Val Trp Asp Arg Arg Arg
      100                      105                      110
Glu Ala

```

<210> 4955

<211> 364

<212> DNA

<213> Homo sapiens

<400> 4955

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agatctaagg ccctcgggag agatgggaac tgagcacctg ggtcttagac cggaggagca
60
aactgcaaga cagggtggcc ggggacacca gcctccgccc ttctgtgaca taaggacaag
120
agctcagcct gccaggaac aactctgggc aagagatgtg gaaagaaaga gctcangggg
180
gggcacgcat ggcacacctg ggggacatct gagggcaccc ccaccaacta ttctcccttc
240
caagggtggcc totgagtgtg aaggcagggg gaagcagaca cctgcccctc actctccctc
300
cctaccacat agctaccggg tggggggcgt ccctgggatg attcctgagg gcaggatcca
360
gggg
364

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<210> 4956

<211> 114

<212> PRT

<213> Homo sapiens

<400> 4956

```

Met Gly Thr Glu His Leu Gly Leu Arg Pro Glu Glu Gln Thr Ala Arg
1                      5                      10                      15
Gln Gly Gly Arg Gly His Gln Pro Pro Pro Phe Cys Asp Ile Arg Thr
      20                      25                      30
Arg Ala Gln Pro Ala Gln Glu Gln Leu Trp Ala Arg Asp Val Glu Arg
      35                      40                      45
Lys Ser Ser Xaa Gly Gly Thr His Gly Ile Leu Gly Gly His Leu Arg
      50                      55                      60
Ala Pro Pro Pro Thr Ile Pro Pro Ser Lys Val Ala Ser Glu Cys Glu
65                      70                      75                      80
Gly Arg Gly Lys Gln Thr Pro Ala Pro His Ser Pro Ser Leu Pro His
      85                      90                      95
Ser Tyr Arg Val Gly Gly Val Pro Gly Met Ile Pro Glu Gly Arg Ile
      100                      105                      110
Gln Gly

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<210> 4957

<211> 872

<212> DNA

<213> Homo sapiens

<400> 4957

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120
tcttgacaag actgtacagg gcttctcacc atacacaaac cctccacagc ccacggtccc
180
aaccacacagc acctcctgca gtcctggagg gaaaaggagc agtaacatga agtgtctgaa
240
gatccatttc acctcttttc catgtgaatc atgacgcttt caatgcattt cttgacagga
300
ttctattttt aaagaatgat gctcaatctg taccttttat gcttctgttt tcttctccat
360
caataatatg tcagtcaact gcttgtcaga gacacttagc tgctgacagg tcctcataac
420
ctgactcagg taaactgcc aagatgctt gcacaggatg ctgtcactct tccgtagcac
480
tgagaatgca aatgcaggac atgaacagta atgacaagaa gccaaacatg tgtatgtttt
540
actggaactt ccaaggacct ggtaaacacg ccttccactg ggtgatgaga ttaaggtgat
600
ggactgtcga tcaactaggt ccaaggcctg ggtggctgat gagccaaaga gaaacttcag
660
cgataacaga tattcatcag gaattcggtc ccgtacttcg cgcgctctcc tgcaccgcgc
720
ccgccatctc gctcaggagc tcctccacaa ccgcccggaa ctacggccat cgcgccgcag
780
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872

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<210> 4958

<211> 51

<212> PRT

<213> Homo sapiens

<400> 4958

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Gln Ile Phe Ile Arg Asn Ser Val Pro Tyr Phe Ala Arg Ser Pro Ala
1         5         10        15
Pro Pro Pro Pro Ser Arg Ser Gly Ala Pro Pro Gln Pro Pro Ala Thr
20        25        30
Thr Ala Ile Ala Pro Gln Asp Thr Pro Ser Thr Thr Arg Thr Ala Arg
35        40        45
Arg Ser Ser
50

```

<210> 4959

<211> 449

<212> DNA

<213> Homo sapiens

<400> 4959

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 120
 gcagggataa agaggagagc tggcatctgg agtcatgac tgctctgagag gcagtgccctc
 180
 cggccaccgt aggatggagg ccagcttcca gccctggctg atgggggaga agcagcgaat
 240
 tctccagatg tggatgggca gacctttgga agattcactc ggccctccact taacctttgtg
 300
 agaccaaagg ccacagcccc atgtgttctg cgtgctgttg aacatgtttg tatttcattg
 360
 gcgtggatga taatttgggt gaaaggagag atggtcacca gtggactcag tttaggaagg
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 449

<210> 4960

<211> 115

<212> PRT

<213> Homo sapiens

<400> 4960

Met	Phe	Asn	Ser	Thr	Gln	Asn	Thr	Trp	Gly	Cys	Gly	Leu	Trp	Ser	His
1			5						10					15	
Lys	Val	Lys	Trp	Arg	Pro	Ser	Glu	Ser	Ser	Lys	Gly	Leu	Pro	Tyr	His
		20						25					30		
Ile	Trp	Arg	Ile	Arg	Cys	Phe	Ser	Pro	Ile	Ser	Gln	Gly	Trp	Lys	Leu
		35					40					45			
Ala	Ser	Ile	Leu	Arg	Trp	Pro	Glu	Ala	Leu	Pro	Leu	Arg	Gln	Ile	Met
		50				55					60				
Thr	Pro	Asp	Ala	Ser	Ser	Pro	Leu	Tyr	Pro	Cys	His	Met	Glu	Gly	Pro
65					70					75				80	
Lys	His	Leu	Ala	Leu	Asn	Cys	Lys	Trp	Lys	Pro	Pro	Gln	Pro	Leu	His
			85						90				95		
Gln	Pro	Pro	Ala	Lys	Glu	Thr	Thr	Thr	Thr	Ile	Cys	Ile	Pro	Ser	Leu
			100					105					110		
Asp	Thr	Arg													
		115													

<210> 4961

<211> 4737

<212> DNA

<213> Homo sapiens

<400> 4961

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 120

tccaagaaca gcaagcgtgc ccgggagaag cgcgacagcc gcaacatgga agtacaggtc
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accaggagga tgcgcaacgt cagtatatggc atgggcagca gtgacgagtg gtctgatgtt
240
caagacatta ttgactccac gccagagctg gacatgtgtc cagagacccg cctggaccgc
300
acaggaagca gccaaccca gggcatcgtg aacaaagctt tcggcatcaa caccgactcc
360
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420
gacctcctag gggagttctc aggaatgggc aaagaagtgg ggaatctgct actggaaaac
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720
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780
atggcccctg tgctcatgga gcggaaccag tacaaggagc ggctgatgga gctgcaggag
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1260
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<210> 4962

<211> 1069

<212> PRT

<213> Homo sapiens

<400> 4962

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Pro Leu Gly Asp Tyr Gly Val Gly Ser Lys Asn Ser Lys Arg Ala Arg			
35	40	45	
Glu Lys Arg Asp Ser Arg Asn Met Glu Val Gln Val Thr Gln Glu Met			
50	55	60	
Arg Asn Val Ser Ile Gly Met Gly Ser Ser Asp Glu Trp Ser Asp Val			
65	70	75	80
Gln Asp Ile Ile Asp Ser Thr Pro Glu Leu Asp Met Cys Pro Glu Thr			
85	90	95	
Arg Leu Asp Arg Thr Gly Ser Ser Pro Thr Gln Gly Ile Val Asn Lys			
100	105	110	
Ala Phe Gly Ile Asn Thr Asp Ser Leu Tyr His Glu Leu Ser Thr Ala			
115	120	125	
Gly Ser Glu Val Ile Gly Asp Val Asp Glu Gly Ala Asp Leu Leu Gly			
130	135	140	
Glu Phe Ser Gly Met Gly Lys Glu Val Gly Asn Leu Leu Leu Glu Asn			
145	150	155	160
Ser Gln Leu Leu Glu Thr Lys Asn Ala Leu Asn Val Val Lys Asn Asp			
165	170	175	
Leu Ile Ala Lys Val Asp Gln Leu Ser Gly Glu Gln Glu Val Leu Arg			
180	185	190	
Gly Glu Leu Glu Ala Ala Lys Gln Ala Lys Val Lys Leu Glu Asn Arg			
195	200	205	
Ile Lys Glu Leu Glu Glu Glu Leu Lys Arg Val Lys Ser Glu Ala Ile			
210	215	220	
Ile Ala Arg Arg Glu Pro Lys Glu Glu Ala Glu Asp Val Ser Ser Tyr			
225	230	235	240
Leu Cys Thr Glu Ser Asp Lys Ile Pro Met Ala Gln Arg Arg Arg Phe			
245	250	255	
Thr Arg Val Glu Met Ala Arg Val Leu Met Glu Arg Asn Gln Tyr Lys			
260	265	270	
Glu Arg Leu Met Glu Leu Gln Glu Ala Val Arg Trp Thr Glu Met Ile			
275	280	285	
Arg Ala Ser Arg Glu His Pro Ser Val Gln Glu Lys Lys Lys Ser Thr			
290	295	300	
Ile Trp Gln Phe Phe Ser Arg Leu Phe Ser Ser Ser Ser Pro Pro			
305	310	315	320
Pro Ala Lys Arg Pro Tyr Pro Ser Val Asn Ile His Tyr Lys Ser Pro			
325	330	335	
Thr Thr Ala Gly Phe Ser Gln Arg Arg Asn His Ala Met Cys Pro Ile			
340	345	350	
Ser Ala Gly Ser Arg Pro Leu Glu Phe Phe Pro Asp Asp Asp Cys Thr			
355	360	365	
Ser Ser Ala Arg Arg Glu Gln Lys Arg Glu Gln Tyr Arg Gln Val Arg			
370	375	380	
Glu His Val Arg Asn Asp Asp Gly Arg Leu Gln Ala Cys Gly Trp Ser			
385	390	395	400
Leu Pro Ala Lys Tyr Lys Gln Leu Ser Pro Asn Gly Gly Gln Glu Asp			
405	410	415	
Thr Arg Met Lys Asn Val Pro Val Pro Val Tyr Cys Arg Pro Leu Val			
420	425	430	
Glu Lys Asp Pro Thr Met Lys Leu Trp Cys Ala Ala Gly Val Asn Leu			

435 440 445
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 Ala Pro Gly Arg Asp Pro Leu Thr Cys Asp Arg Glu Gly Asp Gly Glu
 465 470 475 480
 Pro Lys Ser Ala His Ala Ser Pro Glu Lys Lys Ala Lys Glu Leu
 485 490 495
 Pro Glu Met Asp Ala Thr Ser Ser Arg Val Trp Ile Leu Thr Ser Thr
 500 505 510
 Leu Thr Thr Ser Lys Val Val Ile Ile Asp Ala Asn Gln Pro Gly Thr
 515 520 525
 Val Val Asp Gln Phe Thr Val Cys Asn Ala His Val Leu Cys Ile Ser
 530 535 540
 Ser Ile Pro Ala Ala Ser Asp Ser Asp Tyr Pro Pro Gly Glu Met Phe
 545 550 555 560
 Leu Asp Ser Asp Val Asn Pro Glu Asp Pro Gly Ala Asp Gly Val Leu
 565 570 575
 Ala Gly Ile Thr Leu Val Gly Cys Ala Thr Arg Cys Asn Val Pro Arg
 580 585 590
 Ser Asn Cys Ser Ser Arg Gly Asp Thr Pro Val Leu Asp Lys Gly Gln
 595 600 605
 Gly Glu Val Ala Thr Ile Ala Asn Gly Lys Val Asn Pro Ser Gln Ser
 610 615 620
 Thr Glu Glu Ala Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser
 625 630 635 640
 Glu Pro Glu Thr Ala Thr Leu Arg Pro Gly Pro Leu Thr Glu His Val
 645 650 655
 Phe Thr Asp Pro Ala Pro Thr Pro Ser Ser Gly Pro Gln Pro Gly Ser
 660 665 670
 Glu Asn Gly Pro Glu Pro Asp Ser Ser Ser Thr Arg Pro Glu Pro Glu
 675 680 685
 Pro Ser Gly Asp Pro Thr Gly Ala Gly Ser Ser Ala Ala Pro Thr Met
 690 695 700
 Trp Leu Gly Ala Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala
 705 710 715 720
 Asn Trp Lys Lys Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu
 725 730 735
 Ser Leu Val His Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly
 740 745 750
 Thr Leu Ala Ile Phe His Arg Gly Glu Asp Gly Gln Trp Asp Leu Ser
 755 760 765
 Asn Tyr His Leu Met Asp Leu Gly His Pro His His Ser Ile Arg Cys
 770 775 780
 Met Ala Val Val Tyr Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val
 785 790 795 800
 His Val Ile Gln Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala
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 His Pro Arg Arg Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp
 820 825 830
 Gly Val Trp Val Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His
 835 840 845
 Ala His Thr His Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val
 850 855 860
 Ser Lys Met Leu Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile

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Thr Ala Leu Leu Val Ala Gly Ser Arg Leu Trp Val Gly Thr Gly Asn
      885                890                895
Gly Val Val Ile Ser Ile Pro Leu Thr Glu Thr Val Val Leu His Arg
      900                905                910
Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly
      915                920                925
Glu Gly Ala Arg Pro Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser
      930                935                940
Ser Asp Arg Ala Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln
      945                950                955                960
Ala Gln Leu Cys Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val
      965                970                975
Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp
      980                985                990
Ser Pro Ala Glu Gly Pro Gly Pro Ala Ala Pro Ala Ser Glu Val Glu
      995                1000                1005
Gly Gln Lys Leu Arg Asn Val Leu Val Leu Ser Gly Gly Glu Gly Tyr
      1010                1015                1020
Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Gly
      1025                1030                1035                1040
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<210> 4963

<211> 1575

<212> DNA

<213> Homo sapiens

<400> 4963

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120
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240
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420
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660

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<210> 4964

<211> 304

<212> PRT

<213> Homo sapiens

<400> 4964

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 20 25 30
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 35 40 45
 Asn Ser Arg Ala Leu Gly Val Met Asp Lys Ser Thr Ala Ile Pro Lys
 50 55 60
 Ala Ser Ser Ser Glu Ser Leu Ser Ala Lys Thr Cys Ser Leu Phe Leu
 65 70 75 80
 Pro Asn Tyr Val Gln Asp Lys Tyr Leu Leu Gln Leu Leu Arg Asn Ala
 85 90 95
 Asp Asp Val Ser Thr Trp Val Ala Ala Glu Ile Val Thr Ser His Thr
 100 105 110
 Ser Lys Leu Gln Val Asn Leu Leu Ser Lys Phe Xaa Leu Ile Ala Lys

115	120	125
Ser Cys Tyr Glu Gln Arg Asn Phe Ala Thr Ala Met Gln Ile Leu Ser		
130	135	140
Gly Leu Glu His Leu Ala Val Arg Gln Ser Pro Ala Trp Arg Ile Leu		
145	150	155
Pro Ala Lys Ile Ala Glu Val Met Glu Glu Leu Lys Ala Val Glu Val		
165	170	175
Phe Leu Lys Ser Asp Ser Leu Cys Leu Met Glu Gly Arg Arg Phe Arg		
180	185	190
Ala Gln Pro Thr Leu Pro Ser Ala His Leu Leu Ala Met His Ile Gln		
195	200	205
Gln Leu Glu Thr Gly Gly Phe Thr Met Thr Asn Gly Ala His Arg Trp		
210	215	220
Ser Lys Leu Arg Asn Ile Ala Lys Val Val Ser Gln Val His Ala Phe		
225	230	235
Gln Glu Asn Pro Tyr Thr Phe Ser Pro Asp Pro Lys Leu Gln Ser Tyr		
245	250	255
Leu Lys Gln Arg Ile Ala Arg Phe Ser Gly Ala Asp Ile Ser Thr Leu		
260	265	270
Ala Ala Asp Ser Arg Ala Asn Phe His Gln Val Ser Ser Glu Lys His		
275	280	285
Ser Arg Lys Ile Gln Asp Lys Leu Arg Arg Met Lys Ala Thr Phe Gln		
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<210> 4965

<211> 1474

<212> DNA

<213> Homo sapiens

<400> 4965

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720

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 1380
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 1440
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 1474

<210> 4966

<211> 212

<212> PRT

<213> Homo sapiens

<400> 4966

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 35 40 45
 Asn Asn Ile Ala Asn Leu Lys Ile Ser Leu Leu Asn Lys Asp Lys Ile
 50 55 60
 Glu Leu Asp Ser Ser Ser Pro Ala Ser Lys Glu Asn Glu Glu Lys Val
 65 70 75 80
 Cys Leu Glu Tyr Asn Glu Glu Leu Glu Lys Leu Cys Glu Glu Leu Gln
 85 90 95
 Ala Thr Leu Asp Gly Leu Thr Lys Ile Gln Val Lys Met Glu Lys Leu
 100 105 110
 Ser Ser Thr Thr Lys Gly Ile Cys Glu Leu Glu Asn Tyr His Tyr Gly
 115 120 125
 Glu Glu Ser Lys Arg Pro Pro Leu Phe His Thr Trp Pro Thr Thr His
 130 135 140
 Phe Tyr Glu Val Ser His Lys Leu Leu Glu Met Tyr Arg Lys Glu Leu
 145 150 155 160
 Leu Leu Lys Arg Thr Val Ala Lys Glu Leu Ala His Thr Gly Asp Pro

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Asp Leu Thr Leu Ser Tyr Leu Ser Met Trp Leu His Gln Pro Tyr Val
                180                185                190
Glu Ser Asp Ser Arg Leu His Leu Glu Ser Met Leu Leu Glu Thr Gly
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His Arg Ala Leu
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<210> 4967
 <211> 550
 <212> DNA
 <213> Homo sapiens

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<400> 4967
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120
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360
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420
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<210> 4968
 <211> 51
 <212> PRT
 <213> Homo sapiens

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<400> 4968
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Tyr Ser Ser Leu Gln Pro Arg Thr Pro Gly Leu Lys Gln Ser Phe Arg
20          25          30
Leu Asp Leu Gln Asn Ser Trp Xaa Tyr Thr Arg Glu Pro Pro Cys Pro
35          40          45
Ala Ser Gln
50

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<210> 4969
 <211> 2911
 <212> DNA
 <213> Homo sapiens

<400> 4969
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120
gatgagaagg gtgcgggggc ccttcccttc ctaccagggg tctttggcta cgcagtgaat
180
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240
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300
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360
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420
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540
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<213> Homo sapiens

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Pro Pro Ser Leu Asn Pro Pro Pro Leu Pro Ala Pro Trp Pro Pro Cys
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<212> PRT

<213> Homo sapiens

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<212> DNA

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<211> 298

<212> PRT

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<400> 4976

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 Arg Ala Leu Thr Lys Gly Leu Glu Gly Thr Ile Arg Ser Asp Met Asp
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Arg Leu Met Asn Leu Pro Leu His Ser Val Lys Met Glu Pro Cys Tyr		190
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Thr Lys Val Asn Leu Leu His Glu Arg Leu Gln Asp Leu Lys Ser Arg		205
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<212> DNA

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<400> 4977

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<212> PRT

<213> Homo sapiens

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 Ile Asp Ser Ser Asp Tyr Pro Leu Leu Pro Leu Asn Asn Phe Leu Glu
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 Cys Thr Tyr Asn Val Thr Val Tyr Thr Gly Tyr Gly Val Glu Leu Gln
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<211> 266

<212> PRT

<213> Homo sapiens

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<211> 1902

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 4986

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Ile Val Pro Thr Phe His Arg Arg Cys Tyr Trp Leu Leu Gln Asn Pro
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Asp Ile Val Leu Val His Tyr Leu Asn Val Pro Ala Leu Glu Asp Cys
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Gly Lys Gly Cys Ser Pro Ile Phe Cys Ser Ile Ser Ser Asp Arg Arg
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 <211> 828
 <212> DNA
 <213> Homo sapiens

<400> 4991

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<211> 69

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<213> Homo sapiens

<400> 4992

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<210> 4993

<211> 837

<212> DNA

<213> Homo sapiens

<400> 4993

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<213> Homo sapiens

<400> 4994

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Glu	Glu	Asp	Ser	Asp	Gly	Glu	Leu	Asn	Thr	Trp	Glu	Leu	Ser	Glu	Gly
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Ala	Pro	Gln	Gly	Asp	Met	Ile	Tyr	Asp	Pro	Ser	Trp	His	His	Pro	Pro
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<212> DNA

<213> Homo sapiens

<400> 4995

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<400> 4996
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 Leu Tyr Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr
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 <213> Homo sapiens

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<210> 4998
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 Ile Gly Lys Gly Asn Phe Ala Lys Val Lys Leu Ala Arg His Ile Leu
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 Thr Gly Arg Glu Val Ala Ile Lys Ile Ile Asp Lys Thr Gln Leu Asn
 85 90 95
 Pro Ser Ser Leu Gln Lys Leu Phe Arg Glu Val Arg Ile Met Lys Gly
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 Thr Leu Ser Ala Leu Pro Leu Cys His Leu Pro Leu Pro Leu His Leu
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 Thr Leu Thr Pro Leu Gly Leu Cys Pro Ala Gly Glu Val Phe Asp Tyr
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 His Arg Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Glu Ala Asn
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 Ile Lys Ile Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser
 225 230 235 240
 Lys Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu
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 Phe Gln Gly Lys Lys Tyr Asp Gly Pro Glu Val Asp Ile Trp Ser Leu
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 Gly Val Ile Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly
 275 280 285
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 325 330 335
 Asp Lys Trp Ile Asn Ile Gly Tyr Glu Gly Glu Leu Lys Pro Tyr

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<211> 1630

<212> DNA

<213> Homo sapiens

<400> 4999

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<211> 307

<212> PRT

<213> Homo sapiens

<400> 5000

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Leu	Asp	Val	Pro	Asp	Lys
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Val	Thr	Tyr	Ile	Lys	Lys
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Lys	Ala	Leu	Gly	His	Met
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Tyr	Thr	Gly	Ser	Asp	Gly
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<211> 3427

<212> DNA

<213> Homo sapiens

<400> 5001

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<212> PRT

<213> Homo sapiens

<400> 5002

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Arg	Ser	Gln	Tyr	Leu	Ser
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Phe	Lys	Pro	Arg	Leu	Gly
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Ser	Pro	Gln	Ala	Glu	Lys
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<211> 3729

<212> DNA

<213> Homo sapiens

<400> 5003

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<211> 642
 <212> PRT
 <213> Homo sapiens

<400> 5004

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Arg Glu Gly Arg Pro Gly Gly Glu Glu Arg Gly Ala Arg Val Gly Val
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<210> 5005

<211> 1120

<212> DNA

<213> Homo sapiens

<400> 5005

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<210> 5007

<211> 2165

<212> DNA

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<210> 5008

<211> 487

<212> PRT

<213> Homo sapiens

<400> 5008

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			20					25					30		
Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala
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Lys	Gly	Met	Phe	Ser	Met	Gly	Trp	Pro	Ala	Val	Leu	Ser	Ile	Thr	Pro
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Asn	Ile	Lys	Glu	Glu	Gly	Ala	Met	Lys	Glu	Asp	Ser	Gly	Met	Gln	Asp
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Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val	Glu	Gln	Leu	Tyr	Met	Cys	Val
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Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln
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225      230      235
Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Lys Glu Ile Glu
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Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His Gly Gly Val Ala
275      280      285
Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro
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Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu
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Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ser Glu
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355      360      365
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405      410      415
Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr Lys Asp Met Leu
420      425      430
Ser Glu Leu Ser Thr Val Met Asn Glu Gln Leu Cys Arg Gly Pro Cys
435      440      445
Leu Tyr Ser Phe Cys Ser Ser Val Ser Ser Ile Ser Leu Ser Thr Val
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<211> 426

<212> DNA

<213> Homo sapiens

<400> 5009

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<210> 5010

<211> 119

<212> PRT

<213> Homo sapiens

<400> 5010

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			20					25					30		
Asn	Leu	Pro	Gly	Arg	Val	His	Gln	Phe	Phe	Ile	Ser	Pro	Leu	Phe	Ile
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<213> Homo sapiens

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<211> 950

<212> PRT

<213> Homo sapiens

<400> 5012

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 50           55           60
Pro Glu Asp Lys Pro Ala Pro Lys Asn Glu Asp Glu Met Met Val Ala
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115           120           125
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145           150           155           160
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Tyr Ile Ala Asp Arg Leu Asn Asn Asp Pro Gly Trp Lys Asn Leu Thr
180           185           190
Val Ile Leu Ser Asp Ala Ser Ala Pro Gly Glu Gly Glu His Lys Ile
195           200           205
Met Asp Tyr Ile Arg Arg Gln Arg Ala Gln Pro Asn His Asp Pro Asn
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Thr His His Cys Leu Cys Gly Ala Asp Ala Asp Leu Ile Met Leu Gly
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Leu Ala Thr His Glu Pro Asn Phe Thr Ile Ile Arg Glu Glu Phe Lys
245           250           255
Pro Asn Lys Pro Lys Pro Cys Gly Leu Cys Asn Gln Phe Gly His Glu
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<212> DNA

<213> Homo sapiens

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<210> 5014

<211> 675

<212> PRT

<213> Homo sapiens

<400> 5014

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 50 55 60
 Ala Arg Glu Ala Ser Glu Glu Glu Leu Gly Leu Val His Ser Pro Glu
 65 70 75 80
 Tyr Val Ser Leu Val Arg Glu Thr Gln Val Leu Gly Lys Glu Glu Leu
 85 90 95
 Gln Ala Leu Ser Gly Gln Phe Asp Ala Ile Tyr Phe His Pro Ser Thr
 100 105 110
 Phe His Cys Ala Arg Leu Ala Ala Gly Ala Gly Leu Gln Leu Val Asp
 115 120 125
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 Pro Gly His His Gly Gln Arg Ala Ala Ala Asn Gly Phe Cys Val Phe
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 Asn Asn Val Ala Ile Ala Ala Ala His Ala Lys Gln Lys His Gly Leu
 165 170 175
 His Arg Ile Leu Val Val Asp Trp Asp Val His His Gly Gln Gly Ile
 180 185 190
 Gln Tyr Leu Phe Glu Asp Asp Pro Ser Val Leu Tyr Phe Ser Trp His
 195 200 205
 Arg Tyr Glu His Gly Arg Phe Trp Pro Phe Leu Arg Glu Ser Asp Ala
 210 215 220
 Asp Ala Val Gly Arg Gly Gln Gly Leu Gly Phe Thr Val Asn Leu Pro
 225 230 235 240
 Trp Asn Gln Val Gly Met Gly Asn Ala Asp Tyr Val Ala Ala Phe Leu
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 His Leu Leu Leu Pro Leu Ala Phe Glu Phe Asp Pro Glu Leu Val Leu
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 Val Ser Ala Gly Phe Asp Ser Ala Ile Gly Asp Pro Glu Gly Gln Met
 275 280 285
 Gln Ala Thr Pro Glu Cys Phe Ala His Leu Thr Gln Leu Leu Gln Val
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 Leu Ala Gly Gly Arg Val Cys Ala Val Leu Glu Gly Gly Tyr His Leu
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 325 330 335
 Asp Pro Ala Pro Pro Leu Ser Gly Pro Met Ala Pro Cys Gln Arg Cys
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 Glu Gly Ser Ala Leu Glu Ser Ile Gln Ser Ala Arg Ala Ala Gln Ala
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 Pro His Trp Lys Ser Leu Gln Gln Gln Asp Val Thr Ala Val Pro Met
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 Ser Pro Ser Ser His Ser Pro Glu Gly Arg Pro Pro Leu Leu Pro
 385 390 395 400
 Gly Gly Pro Val Cys Lys Ala Ala Ala Ser Ala Pro Ser Ser Leu Leu

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                405                410                415
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Leu Thr Thr Pro Asp Ile Thr Leu Val Leu Pro Pro Asp Val Ile Gln
                435                440                445
Gln Glu Ala Ser Ala Leu Arg Glu Glu Thr Glu Ala Trp Ala Arg Pro
                450                455                460
His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
                465                470                475
Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
                485                490                495
Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
                500                505                510
Arg Arg Gly Leu Ser His Gly Ala Gln Arg Leu Leu Cys Val Ala Leu
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Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
                530                535                540
Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His
                545                550                555
Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
                565                570                575
Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
                580                585                590
Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Ala Ala
                595                600                605
Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala
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Leu Leu Glu Glu Val Ser Trp Ala Gly Trp Arg Cys Cys Gly Val Gly
                625                630                635
Arg Gly Glu Gly Pro Val Thr Ala Ser Val Phe Ala Pro Gly Pro Glu
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Gly Thr Ser
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<210> 5015

<211> 1360

<212> DNA

<213> Homo sapiens

<400> 5015

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240
gaatgggtgc tgaacatcgg ccggggcaac ttcaagccca agcagcacac ggtcatctgc
300
tccgagcact tccggccaga gtgcttcagc gcctttggaa accgcaagaa cctaagcagc
360

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aatgccgtgc ccacggtgtt cgcctttcag gacccacac agcaggtgag ggagaacaca
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<210> 5016

<211> 284

<212> PRT

<213> Homo sapiens

<400> 5016

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		20						25					30		
Ala	Ala	Ile	Phe	Val	Gly	Gly	Ser	Gln	Ala	Trp	Leu	Glu	Met	Pro	Lys
		35					40					45			
Ser	Cys	Ala	Ala	Arg	Gln	Cys	Cys	Asn	Arg	Tyr	Ser	Ser	Arg	Arg	Lys
	50					55				60					
Gln	Leu	Thr	Phe	His	Arg	Phe	Pro	Phe	Ser	Arg	Pro	Glu	Leu	Leu	Lys
	65				70				75					80	
Glu	Trp	Val	Leu	Asn	Ile	Gly	Arg	Gly	Asn	Phe	Lys	Pro	Lys	Gln	His
			85					90					95		
Thr	Val	Ile	Cys	Ser	Glu	His	Phe	Arg	Pro	Glu	Cys	Phe	Ser	Ala	Phe

			100					105					110			
Gly	Asn	Arg	Lys	Asn	Leu	Lys	His	Asn	Ala	Val	Pro	Thr	Val	Phe	Ala	
			115					120					125			
Phe	Gln	Asp	Pro	Thr	Gln	Gln	Val	Arg	Glu	Asn	Thr	Asp	Pro	Ala	Ser	
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Glu	Arg	Gly	Asn	Ala	Ser	Ser	Ser	Gln	Lys	Glu	Lys	Val	Leu	Pro	Glu	
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Ala	Gly	Ala	Gly	Glu	Asp	Ser	Pro	Gly	Arg	Asn	Met	Asp	Thr	Ala	Leu	
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Glu	Glu	Leu	Gln	Leu	Pro	Pro	Asn	Ala	Glu	Gly	His	Val	Lys	Gln	Val	
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Ser	Pro	Arg	Arg	Pro	Gln	Ala	Thr	Glu	Ala	Val	Gly	Arg	Pro	Thr	Gly	
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Pro	Ala	Gly	Leu	Arg	Arg	Thr	Pro	Asn	Lys	Gln	Pro	Ser	Asp	His	Ser	
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Tyr	Ala	Leu	Leu	Asp	Leu	Asp	Ser	Leu	Lys	Lys	Lys	Leu	Phe	Leu	Thr	
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Leu	Lys	Glu	Asn	Glu	Lys	Leu	Arg	Lys	Arg	Leu	Gln	Ala	Gln	Arg	Leu	
				245					250						255	
Val	Met	Arg	Arg	Met	Ser	Ser	Arg	Leu	Arg	Ala	Cys	Lys	Gly	His	Arg	
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<210> 5017

<211> 785

<212> DNA

<213> Homo sapiens

<400> 5017

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180					
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360					
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660					
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<210> 5018

<211> 63

<212> PRT

<213> Homo sapiens

<400> 5018

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<210> 5019

<211> 2766

<212> DNA

<213> Homo sapiens

<400> 5019

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<210> 5020
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 <212> PRT
 <213> Homo sapiens

<400> 5020
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 Glu Gln His His Trp Asp Asp Arg Arg Arg Met Pro Asp Gly Gly Tyr
 35 40 45
 Pro His Gly Pro Pro Gly Pro Leu Gly Leu Leu Gly Val Arg Pro Gly
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 Met Pro Pro Gln Pro Gln Gly Pro Ala Pro Leu Arg Arg Pro Asp Ser
 65 70 75 80
 Ser Asp Asp Arg Tyr Val Met Thr Lys His Ala Thr Ile Tyr Pro Thr
 85 90 95
 Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val Ser Ile Thr Glu Arg
 100 105 110
 Ala Leu Lys Leu Val Ser Asp Ser Leu Ser Glu His Glu Lys Asn Lys
 115 120 125
 Asn Lys Glu Gly Asp Asp Lys Lys Glu Gly Gly Lys Asp Arg Ala Leu
 130 135 140
 Lys Gly Val Leu Arg Val Gly Val Phe Ala Lys Gly Leu Leu Leu Arg
 145 150 155 160
 Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys Ser Glu Lys Pro Ser
 165 170 175
 Lys Thr Leu Leu Ser Arg Ile Ala Glu Asn Leu Pro Lys Gln Leu Ala
 180 185 190
 Phe Ile Ser Pro Glu Lys Tyr Asp Ile Lys Cys Ala Val Ser Glu Ala
 195 200 205
 Ala Ile Ile Leu Asn Ser Cys Val Glu Pro Lys Met Gln Val Thr Ile
 210 215 220
 Thr Leu Thr Ser Pro Ile Ile Arg Glu Glu Asn Met Arg Glu Gly Asp
 225 230 235 240
 Val Thr Ser Gly Met Val Lys Asp Pro Pro Asp Val Leu Asp Arg Gln
 245 250 255
 Lys Cys Leu Asp Ala Leu Ala Ala Leu Arg His Ala Lys Trp Phe Gln
 260 265 270
 Ala Arg Ala Asn Gly Leu Gln Ser Cys Val Ile Ile Ile Arg Ile Leu

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Gln Ser Pro Gly Asp Ala Leu Arg Arg Val Phe Glu Cys Ile Ser Ser
      325              330              335
Gly Ile Ile Leu Lys Gly Ser Pro Gly Leu Leu Asp Pro Cys Glu Lys
      340              345              350
Asp Pro Phe Asp Thr Leu Ala Thr Met Thr Asp Gln Gln Arg Glu Asp
      355              360              365
Ile Thr Ser Ser Ala Gln Phe Ala Leu Arg Leu Leu Ala Phe Arg Gln
      370              375              380
Ile His Lys Val Leu Gly Met Asp Pro Leu Pro Gln Met Ser Gln Arg
 385              390              395
Phe Asn Ile His Asn Asn Arg Lys Arg Arg Arg Asp Ser Asp Gly Val
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Asp Gly Phe Glu Ala Glu Gly Lys Lys Asp Lys Asp Tyr Asp Asn
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<210> 5021

<211> 494

<212> DNA

<213> Homo sapiens

<400> 5021

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<210> 5022

<211> 124

<212> PRT

<213> Homo sapiens

<400> 5022

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Asp Tyr Lys Asn Tyr Leu Ala Leu Ile Asn His Arg Pro His Val Lys
      35           40           45
Gly Asn Ser Ser Cys Tyr Gly Val Leu Pro Thr Glu Pro Val Tyr
      50           55           60
Asn Trp Arg Thr Val Ile Asn Ser Ala Ala Asp Phe Tyr Phe Glu Gly
      65           70           75           80
Asn Ile His Gln Ser Leu Gln Asn Ile Thr Glu Asn Gln Leu Val Gln
      85           90           95
Pro Thr Ile Leu Gln Gln Lys Gly Gly Lys Gly Arg Lys Lys Leu Arg
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<210> 5023

<211> 3482

<212> DNA

<213> Homo sapiens

<400> 5023

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960

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<211> 323

<212> PRT

<213> Homo sapiens

<400> 5024

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<210> 5025

<211> 2596

<212> DNA

<213> Homo sapiens

<400> 5025

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<211> 136

<212> PRT

<213> Homo sapiens

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		100					105					110			
Pro	Arg	Lys	Gln	Arg	Leu	Lys	Lys	Cys	Leu	Ser	Leu	Thr	Leu	Glu	Trp
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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<213> Homo sapiens

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<211> 188

<212> PRT

<213> Homo sapiens

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Val	Ile	Leu	Ile	Phe	Cys	Leu	Met	Thr	Leu	Ile	Gly	Asn	Leu	Phe	Ile
			35				40					45			
Ile	Ile	Leu	Thr	Tyr	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Leu	Tyr	Phe
			50			55					60				
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Tyr	Thr	Thr	Ser	Ser
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Ile	Pro	Gln	Leu	Leu	Val	Ser	Leu	Trp	Gly	Val	Glu	Lys	Thr	Ile	Ser
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Tyr	Ala	Gly	Cys	Met	Val	Gln	Leu	Tyr	Phe	Phe	Leu	Thr	Leu	Gly	Thr
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			115					120				125			
Val	Cys	Arg	Pro	Leu	His	Tyr	Thr	Val	Leu	Met	His	Ser	Arg	Phe	Cys
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His	Leu	Leu	Ala	Val	Ala	Ser	Trp	Val	Ser	Gly	Phe	Thr	Asn	Pro	Ala
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 Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
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 100 105 110
 Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
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<212> DNA

<213> Homo sapiens

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<210> 5034

<211> 550

<212> PRT

<213> Homo sapiens

<400> 5034

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His Phe Tyr Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn
      35           40           45
Cys Val Glu Val Thr Gly Lys Phe Arg Gly Gly Val Asn Pro Phe Thr
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Arg Gly Cys Cys Gly Asn Val Glu His Val Leu Cys Ser Pro Leu Ala
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Pro Arg Tyr Val Val Glu Pro Pro Arg Leu Pro Leu Ala Val Ser Leu
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Lys Pro Pro Phe Leu Arg Pro Glu Leu Leu Asp Arg Ala Ala Pro Leu
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Lys Val Lys Leu Ser Asp Asn Gly Leu Lys Ala Gly Leu Gly Arg Ser
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Lys Ser Lys Gly Ser Leu Asp Arg Leu Asp Glu Lys Pro Leu Asp Leu
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Leu Gln Thr Pro Arg Pro Gly Ser Ala Glu Ser Ala Leu Ser Val Gln
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Arg Thr Ser Pro Pro Thr Pro Ala Met Tyr Lys Phe Arg Pro Ala Phe
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Pro Thr Gly Pro Lys Val Pro Phe Cys Gly Pro Gly Glu Gln Val Pro
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Gly Pro Asp Ser Leu Thr Leu Gly Asp Asp Asn Ile Arg Ser Leu Asp
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Phe Val Ser Glu Pro Ser Leu Asp Leu Pro Asp Tyr Gly Pro Gly Gly
225          230          235          240
Leu His Ala Ala Tyr Pro Pro Ser Pro Pro Leu Ser Ala Ser Asp Ala
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Phe Ser Gly Ala Leu Arg Ser Leu Ser Leu Lys Ala Ser Ser Arg Arg
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Gly Gly Asp His Val Ala Leu Gln Pro Leu Arg Ser Glu Gly Gly Pro
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Pro Thr Pro His Arg Ser Ile Phe Ala Pro His Ala Leu Pro Asn Arg
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Gly His Ala Cys Pro Ala His Pro Ala Val Gly Val Ala Gly Tyr His
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Ser Pro Tyr Leu His Pro Gly Ala Thr Gly Asp Pro Pro Arg Pro Leu
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Pro Arg Ser Phe Ser Pro Val Leu Gly Pro Arg Pro Arg Glu Pro Ser
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Pro Val Arg Tyr Asp Asn Leu Ser Arg Thr Ile Met Ala Ser Ile Gln
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Glu Arg Lys Asp Arg Glu Glu Arg Glu Arg Leu Leu Arg Ser Gln Ala
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Asp Ser Leu Phe Gly Asp Ser Gly Val Tyr Asp Ala Pro Ser Ser Tyr
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Ser Leu Gln Gln Ala Ser Val Leu Ser Glu Gly Pro Arg Gly Pro Ala

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Ser Val Ser Arg Ala Pro Arg Thr Ser Ser Ser Leu Gln Ala Asp
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Gln Ala Ser Ser Asn Ala Pro Gly Ala Pro Ala Gln Gln Trp Leu Thr
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Gln Val Thr Cys Thr Pro Gly Pro Ala Leu Pro Ala Arg His Ser Pro
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Leu Thr Ile Leu Arg Gly Pro Gln Ser Cys Arg Leu His Pro His Gly
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Pro Pro Arg Ala Thr Ala Leu Ala Asp Arg Ala Glu Gly Pro Pro Ser
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Ala Glu Asp Ser Pro Lys
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<210> 5035

<211> 2002

<212> DNA

<213> Homo sapiens

<400> 5035

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<210> 5036

<211> 384

<212> PRT

<213> Homo sapiens

<400> 5036

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 Leu Ala Arg Ala Asp Ser Thr Lys Asn Trp Thr Glu Lys Ile Leu Arg
 50 55 60
 Gln Thr Glu Val Leu Leu Gln Pro Asn Pro Ser Ala Arg Val Glu Glu

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Phe Leu Tyr Glu Lys Leu Asp Arg Lys Val Pro Ser Arg Val Thr Asn
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Pro Thr Thr Pro Tyr Gly Lys Thr Leu Ile Lys Val Ala Glu Ala Glu
115         120         125
Lys Gln Leu Gly Ala Ala Glu Arg Asp Phe Ile His Thr Ala Ser Ile
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Ser Phe Leu Thr Pro Leu Arg Asn Phe Leu Glu Gly Asp Trp Lys Thr
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Ile Ser Lys Glu Ser Arg Leu Leu Gln Asn Arg Arg Leu Asp Leu Asp
165         170         175
Ala Cys Lys Ala Arg Leu Lys Lys Ala Lys Ala Ala Glu Ala Lys Ala
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Thr Leu Trp Asn Asp Glu Val Asp Lys Ala Glu Gln Glu Leu Arg Val
195         200         205
Ala Gln Thr Glu Phe Asp Arg Gln Ala Glu Val Thr Arg Leu Leu Leu
210         215         220
Glu Gly Ile Ser Ser Thr His Val Asn His Leu Arg Cys Leu His Glu
225         230         235         240
Phe Val Lys Ser Gln Thr Thr Tyr Tyr Ala Gln Cys Tyr Arg His Met
245         250         255
Leu Asp Leu Gln Lys Gln Leu Gly Ser Ser Gln Gly Ala Ile Ser Arg
260         265         270
His Leu Arg Gly His His Arg Ala Arg Leu Pro Pro Leu Ser Ser Thr
275         280         285
Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser Val Ala
290         295         300
Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu Val Ala
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Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp Tyr Glu
325         330         335
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<210> 5037

<211> 2102

<212> DNA

<213> Homo sapiens

<400> 5037

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240

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<210> 5038

<211> 533

<212> PRT

<213> Homo sapiens

<400> 5038

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Leu	Ala	Gly	Asn	Leu	Trp	Glu	Lys	Leu	Arg	Glu	Lys	Ile	Arg	Ser	Phe
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Val	Ala	Tyr	Ser	Ile	Ala	Ile	Asp	Glu	Ile	Thr	Asp	Ile	Asn	Asn	Thr
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Thr	Gln	Leu	Ala	Ile	Phe	Ile	Arg	Gly	Val	Asp	Glu	Asn	Phe	Asp	Val
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Asn	Glu	Ile	Phe	Ser	Arg	Val	Glu	Lys	Ser	Leu	Lys	Lys	Phe	Cys	Ile
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Asp	Trp	Ser	Lys	Leu	Val	Ser	Val	Ala	Ser	Thr	Gly	Thr	Pro	Ala	Met
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Thr	Phe	Cys	Lys	Gly	Ala	Glu	Leu	Lys	Ser	Ile	Cys	Cys	Ile	Ile	His
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Pro	Glu	Ser	Leu	Cys	Ala	Gln	Lys	Leu	Lys	Met	Asp	His	Val	Met	Asp
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Val	Val	Val	Lys	Ser	Val	Asn	Trp	Ile	Cys	Ser	Arg	Gly	Leu	Asn	His
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Ser	Glu	Phe	Thr	Thr	Leu	Leu	Tyr	Glu	Leu	Asp	Ser	Gln	Tyr	Gly	Ser
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 Lys Tyr Asp Lys Val Gly Ile Pro Glu Phe Tyr Lys Tyr Leu Trp Gly
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 485 490 495
 Gly Ser Thr Tyr Ile Cys Glu Gln Leu Phe Ser Ile Met Lys Leu Ser
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<211> 3059

<212> DNA

<213> Homo sapiens

<400> 5039

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<212> PRT

<213> Homo sapiens

<400> 5040

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Ile Arg Arg Asp Ile Phe Gly Gly Leu Val Leu Leu Lys Val Lys Ala
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Lys Val Arg Gln Cys Leu Gln Glu Arg Arg Thr Val Pro Ile Leu Phe
65 70 75 80
Ala Ser Thr Val Arg Arg His Pro Asp Lys Thr Ala Leu Ile Phe Glu
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Gly Thr Asp Thr His Trp Thr Phe Arg Gln Leu Asp Glu Tyr Ser Ser
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<211> 686

<212> PRT

<213> Homo sapiens

<400> 5042

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Ala Arg Glu Ala Ser Glu Glu Glu Leu Gly Leu Val His Ser Pro Glu
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Tyr Val Ser Leu Val Arg Glu Thr Gln Val Leu Gly Lys Glu Glu Leu
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Gln Ala Leu Ser Gly Gln Phe Asp Ala Ile Tyr Phe His Pro Ser Thr
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Phe His Cys Ala Arg Leu Ala Ala Gly Ala Gly Leu Gln Leu Val Asp
115          120          125
Ala Val Leu Thr Gly Ala Val Gln Asn Gly Leu Ala Leu Val Arg Pro
130          135          140
Pro Gly His His Gly Gln Arg Ala Ala Ala Asn Gly Phe Cys Val Phe
145          150          155          160
Asn Asn Val Ala Ile Ala Ala Ala His Ala Lys Gln Lys His Gly Leu
165          170          175
His Arg Ile Leu Val Val Asp Trp Asp Val His His Gly Gln Gly Ile
180          185          190
Gln Tyr Leu Phe Glu Asp Asp Pro Ser Val Leu Tyr Phe Ser Trp His
195          200          205
Arg Tyr Glu His Gly Arg Phe Trp Pro Phe Leu Arg Glu Ser Asp Ala
210          215          220
Asp Ala Val Gly Arg Gly Gln Gly Leu Gly Phe Thr Val Asn Leu Pro
225          230          235          240
Trp Asn Gln Val Gly Met Gly Asn Ala Asp Tyr Val Ala Ala Phe Leu
245          250          255
His Leu Leu Leu Pro Leu Ala Phe Glu Phe Asp Pro Glu Leu Val Leu
260          265          270
Val Ser Ala Gly Phe Asp Ser Ala Ile Gly Asp Pro Glu Gly Gln Met
275          280          285
Gln Ala Thr Pro Glu Cys Phe Ala His Leu Thr Gln Leu Leu Gln Val
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Glu Gly Ser Ala Leu Glu Ser Ile Gln Ser Ala Arg Ala Ala Gln Ala
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Pro His Trp Lys Ser Leu Gln Gln Asp Val Thr Ala Val Pro Met
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Ser Pro Ser Ser His Ser Pro Glu Gly Arg Pro Pro Pro Leu Leu Pro
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Leu	Tyr	Leu	Leu	Asp	Gly	Met	Leu	Asp	Gly	Gln	Val	Asn	Ser	Gly	Ile														
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<210> 5043

<211> 1824

<212> DNA

<213> Homo sapiens

<400> 5043

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<211> 273

<212> PRT

<213> Homo sapiens

<400> 5044

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Thr Ser Lys Ser Leu Leu Pro Val Arg Ser Lys Glu Val Asp Val Ser
        65                70                75                80
Lys Gln Leu His Ser Gly Gly Pro Glu Asn Asp Val Thr Lys Ile Thr
                85                90                95
Lys Leu Arg Arg Glu Asn Gly Gln Met Lys Ala Thr Asp Thr Ala Thr
                100                105                110
Arg Arg Asn Val Arg Lys Gly Tyr Lys Pro Leu Ser Lys Gln Lys Ser
        115                120                125
Glu Glu Glu Leu Lys Asp Lys Asn Gln Leu Leu Glu Ala Val Asn Lys
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Gln Leu His Gln Lys Leu Thr Glu Thr Gln Gly Glu Leu Lys Asp Leu
        145                150                155                160
Thr Gln Lys Val Glu Leu Leu Glu Lys Phe Arg Asp Asn Cys Leu Ala
                165                170                175
Ile Leu Glu Ser Lys Gly Leu Asp Pro Ala Leu Gly Ser Glu Thr Leu
                180                185                190
Ala Ser Arg Gln Glu Ser Thr Thr Asp His Met Asp Ser Met Leu Leu
        195                200                205
Leu Glu Thr Leu Gln Glu Glu Leu Lys Leu Phe Asn Glu Thr Ala Lys
        210                215                220
Lys Gln Met Glu Glu Leu Gln Ala Leu Lys Val Lys Leu Glu Met Lys
        225                230                235                240
Glu Glu Arg Val Arg Phe Leu Glu Gln Gln Thr Leu Cys Asn Asn Gln
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<210> 5045

<211> 462

<212> DNA

<213> Homo sapiens

<400> 5045

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<211> 92

<212> PRT

<213> Homo sapiens

<400> 5046

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		20						25				30			
Ser	Leu	Arg	Leu	Thr	Ala	Pro	Ser	Leu	Trp	Gly	Gly	Ser	Val	Ala	Arg
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Asp	Met	Val	Ala	Cys	Cys	Leu	Phe	Ser	Cys	Ser	Ser	Lys	His	Tyr	Pro
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Leu	Tyr	Ser	Leu	Asn	Val	Ala	Ser	Met	Trp	Leu	Lys	Leu	Gly	Arg	Leu
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<213> Homo sapiens

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<213> Homo sapiens

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Gln Glu Lys Met Ser Ser Val Phe Glu Asp Ser Asn Val Tyr Met Leu
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<400> 5049

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<212> PRT

<213> Homo sapiens

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<211> 4125

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<400> 5051

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<212> DNA

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<210> 5054

<211> 156

<212> PRT

<213> Homo sapiens

<400> 5054

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Val	Gly	Pro	Cys	Pro	Lys	Met	Ser	Pro	Leu	Arg	Pro	Leu	Leu	Leu	Ala
			20					25					30		
Leu	Ala	Leu	Ala	Ser	Val	Pro	Cys	Ala	Gln	Gly	Ala	Cys	Pro	Ala	Ser
		35					40					45			
Ala	Asp	Leu	Lys	His	Ser	Asp	Gly	Thr	Arg	Thr	Cys	Ala	Lys	Leu	Tyr
		50				55					60				
Asp	Lys	Ser	Asp	Pro	Tyr	Tyr	Glu	Asn	Cys	Cys	Gly	Gly	Ala	Glu	Leu
65					70				75					80	
Ser	Leu	Glu	Ser	Gly	Ala	Asp	Leu	Pro	Tyr	Leu	Pro	Ser	Asn	Trp	Ala
			85					90					95		
Asn	Thr	Ala	Ser	Ser	Leu	Val	Val	Ala	Pro	Arg	Cys	Glu	Leu	Thr	Val
			100					105					110		
Trp	Ser	Arg	Gln	Gly	Lys	Ala	Gly	Lys	Thr	His	Lys	Phe	Ser	Ala	Gly
			115				120					125			
Thr	Tyr	Pro	Arg	Leu	Glu	Glu	Tyr	Arg	Arg	Gly	Ile	Leu	Gly	Asp	Trp
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145

150

155

<210> 5055

<211> 2520

<212> DNA

<213> Homo sapiens

<400> 5055

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780
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1260
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1320
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1380

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 2400
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<210> 5056

<211> 672

<212> PRT

<213> Homo sapiens

<400> 5056

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 20 25 30
 Asp Val Thr Val Ile Val Glu Asp Arg Lys Phe Arg Ala His Lys Asn
 35 40 45
 Ile Leu Ser Ala Ser Ser Thr Tyr Phe His Gln Leu Phe Ser Val Ala
 50 55 60
 Gly Gln Val Val Glu Leu Ser Phe Ile Arg Ala Glu Ile Phe Ala Glu

65					70					75					80
Ile	Leu	Asn	Tyr	Ile	Tyr	Ser	Ser	Lys	Ile	Val	Arg	Val	Arg	Ser	Asp
				85					90					95	
Leu	Leu	Asp	Glu	Leu	Ile	Lys	Ser	Gly	Gln	Leu	Leu	Gly	Val	Lys	Phe
			100					105					110		
Ile	Ala	Glu	Leu	Gly	Val	Pro	Leu	Ser	Gln	Val	Lys	Ser	Ile	Ser	Gly
			115					120					125		
Thr	Ala	Gln	Asp	Gly	Asn	Thr	Glu	Pro	Leu	Pro	Pro	Asp	Ser	Gly	Asp
			130					135					140		
Lys	Asn	Leu	Val	Ile	Gln	Lys	Ser	Lys	Asp	Glu	Ala	Gln	Asp	Asn	Gly
			145					150					155		160
Ala	Thr	Ile	Met	Pro	Ile	Ile	Thr	Glu	Ser	Phe	Ser	Leu	Ser	Ala	Glu
			165					170						175	
Asp	Tyr	Glu	Met	Lys	Lys	Ile	Ile	Val	Thr	Asp	Ser	Asp	Asp	Asp	Asp
			180					185						190	
Asp	Asp	Val	Ile	Phe	Cys	Ser	Glu	Ile	Leu	Pro	Thr	Lys	Glu	Thr	Leu
			195					200					205		
Pro	Ser	Asn	Asn	Thr	Val	Ala	Gln	Val	Gln	Ser	Asn	Pro	Gly	Pro	Val
			210					215					220		
Ala	Ile	Ser	Asp	Val	Ala	Pro	Ser	Ala	Ser	Asn	Asn	Ser	Pro	Pro	Leu
			225					230					235		240
Thr	Asn	Ile	Thr	Pro	Thr	Gln	Lys	Leu	Pro	Thr	Pro	Val	Asn	Gln	Ala
			245					250						255	
Thr	Leu	Ser	Gln	Thr	Gln	Gly	Ser	Glu	Lys	Leu	Leu	Val	Ser	Ser	Ala
			260					265						270	
Pro	Thr	His	Leu	Thr	Pro	Asn	Ile	Ile	Leu	Leu	Asn	Gln	Thr	Pro	Leu
			275					280						285	
Ser	Thr	Pro	Pro	Asn	Val	Ser	Ser	Ser	Leu	Pro	Asn	His	Met	Pro	Ser
			290					295				300			
Ser	Ile	Asn	Leu	Leu	Val	Gln	Asn	Gln	Gln	Thr	Pro	Asn	Ser	Ala	Ile
			305					310						320	
Leu	Thr	Gly	Asn	Lys	Ala	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Ile	Ile	Asp
			325					330						335	
Asp	Asp	Asp	Asp	Thr	Ile	Ser	Ser	Ser	Pro	Asp	Ser	Ala	Val	Ser	Asn
			340					345						350	
Thr	Ser	Leu	Val	Pro	Gln	Ala	Asp	Thr	Ser	Gln	Asn	Thr	Ser	Phe	Asp
			355					360					365		
Gly	Ser	Leu	Ile	Gln	Lys	Met	Gln	Ile	Pro	Thr	Leu	Gln	Gln	Glu	Pro
			370					375					380		
Leu	Ser	Asn	Ser	Leu	Lys	Ile	Ser	Asp	Ile	Ile	Thr	Arg	Asn	Thr	Asn
			385					390					395		400
Asp	Pro	Gly	Val	Gly	Ser	Lys	His	Leu	Met	Glu	Gly	Gln	Lys	Ile	Ile
			405					410						415	
Thr	Leu	Asp	Thr	Ala	Thr	Glu	Ile	Glu	Gly	Leu	Ser	Thr	Gly	Cys	Lys
			420												

500										505					510				
Phe	Asn	Ile	His	Ser	Trp	Glu	Lys	Lys	Tyr	Pro	Cys	Arg	Tyr	Cys	Glu				
515										520					525				
Lys	Val	Phe	Pro	Leu	Ala	Glu	Tyr	Arg	Thr	Lys	His	Glu	Ile	His	His				
530										535					540				
Thr	Gly	Glu	Arg	Arg	Tyr	Gln	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Phe	Ile				
545										550					555				
Asn	Tyr	Gln	Phe	Met	Ser	Ser	His	Ile	Lys	Ser	Val	His	Ser	Gln	Asp				
565										570					575				
Pro	Ser	Gly	Asp	Ser	Lys	Leu	Tyr	Arg	Leu	His	Pro	Cys	Arg	Ser	Leu				
580										585					590				
Gln	Ile	Arg	Gln	Tyr	Ala	Tyr	His	Ser	Asp	Arg	Ser	Ser	Thr	Ile	Pro				
595										600					605				
Ala	Met	Lys	Asp	Asp	Gly	Ile	Gly	Tyr	Lys	Val	Asp	Thr	Gly	Lys	Glu				
610										615					620				
Pro	Pro	Val	Gly	Thr	Thr	Ser	Thr	Gln	Asn	Lys	Pro	Met	Thr	Trp					
625										630					635				
Glu	Asp	Ile	Phe	Ile	Gln	Gln	Glu	Asn	Asp	Ser	Ile	Phe	Lys	Gln	Asn				
645										650					655				
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<210> 5057
<211> 673
<212> DNA
<213> Homo sapiens
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<400> 5057
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180
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240
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360
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480
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<210> 5058

<211> 122

<212> PRT

<213> Homo sapiens

<400> 5058

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Met Val Ser Ile Pro Glu Tyr Tyr Glu Gly Lys Asn Val Leu Leu Thr
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Gly Ala Thr Gly Phe Leu Gly Lys Val Leu Leu Glu Lys Leu Leu Arg
          20           25           30
Ser Cys Pro Lys Val Asn Ser Val Tyr Val Leu Val Arg Gln Lys Ala
          35           40           45
Gly Gln Thr Pro Gln Glu Arg Val Glu Glu Val Leu Ser Gly Lys Leu
          50           55           60
Phe Asp Arg Leu Arg Asp Glu Asn Pro Asp Phe Arg Glu Lys Ile Ile
65          70          75          80
Ala Ile Asn Ser Glu Leu Thr Gln Pro Lys Leu Ala Leu Ser Glu Glu
          85          90          95
Asp Lys Glu Val Ile Ile Asp Ser Thr Asn Ile Ile Phe His Cys Ala
          100         105         110
Ala Thr Val Arg Phe Asn Glu Asn Leu Arg
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<210> 5059

<211> 480

<212> DNA

<213> Homo sapiens

<400> 5059

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120
cagctgtgag tctttctcca gggacagtcg gcagccggcc ctaggtgcag agccgatgac
180
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300
cagagagatg gggaggagag ggagcaggag gggactggcc atctctgaga cagaagcgtg
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<210> 5060

<211> 114

<212> PRT

<213> Homo sapiens

<400> 5060

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Met Ala Ser Pro Leu Leu Leu Pro Leu Leu Pro Ile Ser Leu Pro Ala
 1           5           10           15
Phe Ala Ser Trp Leu Ser Leu Asp Ile Met Thr Gly Gly Leu Ala Pro

```


ggctttggat tggacagtca aagggaagtg ggcaaaacca gctgagaacc cgggagctgg
 1080
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 1140
 ctctctgcta agtaaatcaa tgaccattca ttgagaactg atggggacc cgcgtgtggc
 1200
 ccaatgagtg gcagtttttt cctagccagc ttctgtggcc aaatttggag gattttccaa
 1260
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 1320
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 1380
 aagccctttt tcagccttca cacaattttt ctttctagaa gacatcgcgt tctggaagcc
 1440
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 1560
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 2462

<210> 5062

<211> 136

<212> PRT

<213> Homo sapiens

<400> 5062

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Met Ala Gly Trp Gly Leu Val Asp Val Ser Asp Ala Pro Glu Pro Trp
1          5          10          15
Arg Ile Pro His Gly Ile Pro Leu Pro Ala Leu Ser Gly Leu Cys Gly
20          25          30
Val Arg Arg Ser Pro Ser Ser Arg Phe Ser Phe Phe Pro Pro Gln Gln
35          40          45
Arg Asn Trp Arg Lys Asp Ile Lys Leu Ser Ala Val Asp Leu Ser Ala
50          55          60
Glu Ile Phe Pro Glu Ser Met Val Val Leu Asn Tyr Leu His Val Ser
65          70          75          80
Ser Ile Phe Asn Ser Gly Val Gly Leu Phe Leu Ile Ser Ser Gln Lys
85          90          95
Cys Ser Ala Leu Gly Glu Gly Thr Ser Pro Leu Ala Cys His Phe Pro
100          105          110
Gly Val Leu Tyr His Phe Asp Gly Thr Leu Trp Ser Ala Glu Asn Ala
115          120          125
Leu Ser Trp His Ala Ser Arg Leu
130          135

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<210> 5063

<211> 561

<212> DNA

<213> Homo sapiens

<400> 5063

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120
tctcccttct tagagagaga gtggaagctt ctgagtgtgg cttgggtcgt tctgaaccat
180
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240
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300
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360
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420
gagagggcgg agaagttccg gcagaagtac tggaacaagc ttcagaccct gaggcagcag
480
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540
aacgagttca acttcccgga t
561

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<210> 5064

<211> 110

<212> PRT

<213> Homo sapiens

<400> 5064

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Pro Pro Ser Tyr Val Pro Asp Thr Val Asp Leu Thr Asp Asp Ala Leu
           20           25           30
Ala Arg Lys Tyr Trp Leu Thr Cys Phe Glu Glu Ala Leu Asp Gly Val
 35           40           45
Val Lys Arg Ala Val Ala Ser Gln Pro Asp Ser Val Asp Ala Ala Glu
 50           55           60
Arg Ala Glu Lys Phe Arg Gln Lys Tyr Trp Asn Lys Leu Gln Thr Leu
65           70           75           80
Arg Gln Gln Pro Phe Ala Tyr Gly Thr Leu Thr Val Arg Ser Leu Leu
           85           90           95
Asp Thr Arg Glu His Cys Leu Asn Glu Phe Asn Phe Pro Asp
100          105          110

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<210> 5065

<211> 370

<212> DNA

<213> Homo sapiens

<400> 5065

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120
gagaaaaaaca agatggaacc ccggaacctg gccttggtct tggggccgac actggtgagg
180
acgtctgagg acaacatgac agacatgggtg acccacatgc ctgaccgcta caagatcgtg
240
gagacactga tccagcactc agactggttc ttcagtgcag aagaggacaa gggagagaga
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acgccccggg
370

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<210> 5066

<211> 123

<212> PRT

<213> Homo sapiens

<400> 5066

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Ile Glu Asp Ala Arg Glu Arg Met Arg Thr Leu Arg Lys Leu Ile Arg
 1           5           10           15
Asp Leu Pro Gly His Tyr Tyr Glu Thr Leu Lys Phe Leu Val Gly His
           20           25           30
Leu Lys Thr Ile Ala Asp His Ser Glu Lys Asn Lys Met Glu Pro Arg
 35           40           45
Asn Leu Ala Leu Val Phe Gly Pro Thr Leu Val Arg Thr Ser Glu Asp
 50           55           60
Asn Met Thr Asp Met Val Thr His Met Pro Asp Arg Tyr Lys Ile Val
65           70           75           80
Glu Thr Leu Ile Gln His Ser Asp Trp Phe Phe Ser Asp Glu Glu Asp

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			85					90				95			
Lys	Gly	Glu	Arg	Ile	Leu	Pro	Pro	Val	Val	Gln	Ser	Ser	Pro	Arg	Val
			100					105					110		
Arg	Gly	Pro	Pro	Arg	Arg	Ser	Arg	Thr	Pro	Gly					
			115					120							

<210> 5067

<211> 2023

<212> DNA

<213> Homo sapiens

<400> 5067

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 120
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 180
 atgagactag gtttttagtaa tatggctcctt tctaatctct cccctgaggc attcagccac
 240
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 300
 ggtcatccca tgggtggccc accacaagct tggggccatc caatgcaagg tggaccccg
 360
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<211> 179

<212> PRT

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<400> 5074

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<211> 444

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 5076

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<212> DNA

<213> Homo sapiens

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<210> 5078

<211> 558

<212> PRT

<213> Homo sapiens

<400> 5078

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Leu	Gln	Gln	Phe	Asp	Phe	Asn	Val	Asp	Lys	Ala	Val	Gln	Ala	Phe	Val
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Asp	Gly	Ser	Ala	Ile	Gln	Val	Leu	Lys	Glu	Trp	Asn	Met	Thr	Gly	Lys
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Lys	Lys	Asn	Asn	Lys	Arg	Lys	Arg	Ser	Lys	Ser	Lys	Gln	His	Gln	Gly
			65					70				75			80
Asn	Lys	Asp	Ala	Lys	Asp	Lys	Val	Glu	Arg	Pro	Glu	Ala	Gly	Pro	Leu
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Lys	Asp	Ser	Ser	Ser	Thr	Asp	Ser	Ala	Asn	Glu	Lys	Pro	Ala	Leu	Ile
				115				120				125			
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				130				135				140			
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				145				150				155			160
Asp	Gly	Asn	Pro	Lys	Pro	Ile	His	Gly	Thr	Thr	Glu	Arg	Ser	Asp	Gly
				165					170					175	
Leu	Gln	Trp	Ser	Ala	Glu	Gln	Pro	Cys	Asn	Pro	Ser	Lys	Pro	Lys	Ala
				180					185				190		
Lys	Thr	Ser	Pro	Val	Lys	Ser	Asn	Thr	Pro	Ala	Ala	His	Leu	Glu	Ile
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Val	Lys	Asp	Leu	Gln	Arg	Cys	Thr	Val	Ser	Leu	Thr	Arg	Tyr	Arg	Val
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305                310                315                320
Phe Val Ser Glu Arg Lys Tyr Asp Glu Glu Leu Gly Lys Ala Ala Arg
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Phe Ser Cys Asp Ile Glu Gln Leu Lys Ala Gln Ile Met Leu Cys Gly
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Glu Ile Thr His Pro Lys Asn Asn Tyr Ser Ser Arg Thr Pro Cys Ser
      355                360                365
Ser Leu Leu Pro Leu Leu Asn Ala His Ala Ala Thr Ser Gly Lys Gln
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Ser Asn Phe Ser Arg Lys Ser Ser Thr His Asn Lys Pro Ser Glu Gly
385                390                395                400
Lys Ala Ala Asn Pro Lys Met Val Ser Ser Leu Pro Ser Thr Ala Asp
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      420                425                430
Gln Arg Arg Arg Phe Asn Pro Gln Tyr His Asn Asn Arg Leu Asn Gly
      435                440                445
Pro Ala Lys Ser Gln Gly Ser Gly Asn Glu Ala Glu Pro Leu Gly Lys
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Gly Asn Ser Arg His Glu His Arg Arg Gln Pro His Asn Gly Phe Arg
465                470                475                480
Pro Lys Asn Lys Gly Gly Ala Lys Asn Gln Glu Ala Ser Leu Gly Met
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Lys Thr Pro Glu Ala Pro Ala His Ser Glu Lys Pro Arg Arg Arg Gln
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His Ala Ala Asp Thr Ser Glu Ala Arg Pro Phe Arg Gly Ser Val Gly
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<210> 5079

<211> 1338

<212> DNA

<213> Homo sapiens

<400> 5079

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<210> 5080

<211> 165

<212> PRT

<213> Homo sapiens

<400> 5080

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 Ile Pro Asp Val Asp Ile Asp Ser Asp Gly Val Phe Lys Tyr Val Leu
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 Ile Arg Val His Ser Ala Pro Arg Ser Gly Ala Pro Ala Ala Glu Ser
 65 70 75 80
 Lys Glu Ile Val Arg Gly Tyr Lys Trp Ala Glu Tyr His Ala Asp Ile

					85						90						95
Tyr	Asp	Lys	Val	Ser	Gly	Asp	Met	Gln	Lys	Gln	Gly	Cys	Asp	Cys	Glu		
					100						105						110
Cys	Leu	Gly	Gly	Gly	Arg	Ile	Ser	His	Gln	Ser	Gln	Asp	Lys	Lys	Ile		
					115						120						125
His	Val	Tyr	Gly	Tyr	Ser	Met	Val	Ser	Arg	Ser	Pro	Val	Pro	Pro	Cys		
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Arg	Arg	Pro	Gln	Tyr	Gln	Leu	Arg	Gly	Pro	Pro	Glu	Pro	Ala	Ala	Leu		
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<210> 5081

<211> 561

<212> DNA

<213> Homo sapiens

<400> 5081

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<210> 5082

$\langle 211 \rangle$ 111

<212> PRT

<213> Homo sapiens

<400> 5082

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		20						25					30		
Asp	Ala	Val	Arg	Met	Pro	Leu	Gly	Ala	Gly	Thr	Pro	Val	Asn	Val	Gln
		35					40					45			
Arg	Arg	Glu	Asp	Ser	Ala	Thr	Glu	Gly	Ser	His	Arg	Leu	Ile	Leu	Ala
		50				55					60				
Ala	Asn	Arg	Asp	Glu	Phe	Tyr	Ser	Arg	Pro	Ser	Lys	Leu	Ala	Asp	Phe

65					70					75				80
Trp	Gly	Asn	Asn	Asn	Glu	Ile	Leu	Ser	Gly	Leu	Asp	Met	Glu	Gly
				85					90				95	
Lys	Glu	Gly	Gly	Thr	Trp	Leu	Gly	Ile	Ser	Thr	Arg	Gly	Lys	Leu
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<210> 5083

<211> 1856

<212> DNA

<213> Homo sapiens

<400> 5083

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 1856

<210> 5084

<211> 396

<212> PRT

<213> Homo sapiens

<400> 5084

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 50 55 60
 Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser
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 Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp
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 Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile
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	245		250	255
Asp Phe Leu Lys Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln				
	260		265	270
Val Gln Pro Phe Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro				
	275		280	285
Arg Leu Leu Ile Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu				
	290		295	300
Gly Met Ile Met Gly Leu Gly Gly Met Asp Phe Asp Ser Lys Lys				
305		310		315
Ala Tyr Arg Asp Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu				
	325		330	335
Ala Leu Ala Glu Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val				
	340		345	350
Arg Arg Glu His Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro				
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<210> 5085

<211> 2964

<212> DNA

<213> Homo sapiens

<400> 5085

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<211> 792

<212> PRT

<213> Homo sapiens

<400> 5086

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<210> 5087

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<212> DNA

<213> Homo sapiens

<400> 5087

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<211> 465

<212> PRT

<213> Homo sapiens

<400> 5088

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<212> DNA

<213> Homo sapiens

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<211> 632
 <212> PRT
 <213> Homo sapiens

<400> 5092

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Met Ala Pro Arg Glu Leu Pro Thr Cys Ser Ile Cys Leu Glu Arg Leu
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Arg Asp Pro Ile Ser Leu Asp Cys Gly His Asp Phe Cys Ile Arg Cys
65          70          75          80
Phe Ser Thr His Arg Leu Pro Gly Cys Glu Pro Pro Cys Cys Pro Glu
          85          90          95
Cys Arg Lys Ile Cys Lys Gln Lys Arg Gly Leu Arg Ser Leu Gly Glu
          100          105          110
Lys Met Lys Leu Leu Pro Gln Arg Pro Leu Pro Pro Ala Leu Gln Glu
          115          120          125
Thr Cys Pro Val Arg Ala Glu Pro Leu Leu Leu Val Arg Ile Asn Ala
          130          135          140
Ser Gly Gly Leu Ile Leu Arg Met Gly Ala Ile Asn Arg Cys Leu Lys
145          150          155          160
His Pro Leu Ala Arg Asp Thr Pro Val Cys Leu Leu Ala Val Leu Gly
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Glu Gln His Ser Gly Lys Ser Phe Leu Leu Asn His Leu Leu Gln Gly
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Leu Pro Gly Leu Glu Ser Gly Glu Gly Arg Pro Arg Gly Gly Glu
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Ala Ser Leu Gln Gly Cys Arg Trp Gly Ala Asn Gly Leu Ala Gly Gly
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Ile Trp Met Trp Ser His Pro Phe Leu Leu Gly Lys Glu Gly Lys Lys
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Val Ala Val Phe Leu Val Asp Thr Gly Asp Ala Met Ser Pro Glu Leu
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Ser Arg Glu Thr Arg Ile Lys Leu Cys Ala Leu Thr Thr Met Leu Ser
          260          265          270
Ser Tyr Gln Ile Leu Ser Thr Ser Gln Glu Leu Lys Asp Thr Asp Leu
          275          280          285
Asp Tyr Leu Glu Met Phe Val His Val Ala Glu Val Met Gly Lys His
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Tyr Gly Met Val Pro Ile Gln His Leu Asp Leu Leu Val Arg Asp Ser
305          310          315          320
Ser His Pro Asn Lys Ala Gly Gln Gly His Val Gly Asn Ile Phe Gln
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Arg Leu Ser Gly Arg Tyr Pro Lys Val Gln Glu Leu Leu Gln Gly Lys
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Arg Ala Arg Cys Cys Leu Leu Pro Ala Pro Gly Arg Arg Arg Met Asn
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Gln Gly His Ala Ser Pro Gly Gly Asp Thr Asp Asp Asp Phe Arg His
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Lys Asn Leu Ser Gly Trp Met Gly Arg Thr Gly Pro Gly Phe Thr Ser
          435          440          445
Pro Asp Glu Met Ala Ala Gln Leu His Asp Leu Arg Lys Val Glu Ala
          450          455          460
Ala Lys Arg Glu Phe Glu Glu Tyr Val Arg Gln Gln Asp Val Ala Thr
          465          470          475          480
Lys Arg Ile Phe Ser Ala Leu Arg Val Leu Pro Asp Thr Met Arg Asn
          485          490          495
Leu Leu Ser Thr Gln Lys Asp Ala Ile Leu Ala Arg His Gly Val Ala
          500          505          510
Leu Leu Cys Lys Gly Arg Asp Gln Thr Leu Glu Ala Leu Glu Ala Glu
          515          520          525
Leu Gln Ala Thr Ala Lys Ala Phe Met Asp Ser Tyr Thr Met Arg Phe
          530          535          540
Cys Gly His Leu Ala Ala Val Gly Gly Ala Val Gly Ala Gly Leu Met
          545          550          555          560
Gly Leu Ala Gly Gly Val Val Gly Ala Gly Met Ala Ala Ala Ala Leu
          565          570          575
Ala Ala Glu Ala Gly Met Val Ala Ala Gly Ala Ala Val Gly Ala Thr
          580          585          590
Gly Ala Ala Val Val Gly Gly Gly Val Gly Ala Gly Leu Ala Ala Thr
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<210> 5093

<211> 1662

<212> DNA

<213> Homo sapiens

<400> 5093

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<210> 5094

<211> 365

<212> PRT

<213> Homo sapiens

<400> 5094

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Asp Val Val Lys Val Arg Leu Gln Ser Gln Arg Pro Ser Met Ala Ser
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Glu Leu Met Pro Ser Ser Arg Leu Trp Ser Leu Ser Tyr Thr Lys Leu

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Pro Ser Leu Ser Tyr Thr Lys Trp Lys Cys Leu Tyr Cys Asn Gly
65              70              75              80
Val Leu Glu Pro Leu Tyr Leu Cys Pro Asn Gly Ala Arg Cys Ala Thr
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Trp Phe Gln Asp Pro Thr Arg Phe Thr Gly Thr Met Asp Ala Phe Val
      100              105              110
Lys Ile Val Arg His Glu Gly Thr Arg Thr Leu Trp Ser Gly Leu Pro
      115              120              125
Ala Thr Leu Val Met Thr Val Pro Ala Thr Ala Ile Tyr Phe Thr Ala
      130              135              140
Tyr Asp Gln Leu Lys Ala Phe Leu Cys Gly Arg Ala Leu Thr Ser Asp
145              150              155              160
Leu Tyr Ala Pro Met Val Ala Gly Ala Leu Ala Arg Leu Gly Thr Val
      165              170              175
Thr Val Ile Ser Pro Leu Glu Leu Met Arg Thr Lys Leu Gln Ala Gln
      180              185              190
His Val Ser Tyr Arg Glu Leu Gly Ala Cys Val Arg Thr Ala Val Ala
      195              200              205
Gln Gly Gly Trp Arg Ser Leu Trp Leu Gly Trp Gly Pro Thr Ala Leu
      210              215              220
Arg Asp Val Pro Phe Ser Val His Pro Pro Pro Gln Ala Leu Tyr Trp
225              230              235              240
Phe Asn Tyr Glu Leu Val Lys Ser Trp Leu Asn Gly Leu Arg Pro Lys
      245              250              255
Asp Gln Thr Ser Val Gly Met Ser Phe Val Ala Gly Gly Ile Ser Gly
      260              265              270
Thr Val Ala Val Leu Thr Leu Pro Phe Asp Val Val Lys Thr Gln
      275              280              285
Arg Gln Val Ala Leu Gly Ala Met Glu Ala Val Arg Val Asn Pro Leu
290              295              300
His Val Asp Ser Thr Trp Leu Leu Leu Arg Arg Ile Arg Ala Glu Ser
305              310              315              320
Gly Thr Lys Gly Leu Phe Ala Gly Phe Leu Pro Arg Ile Ile Lys Ala
      325              330              335
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<210> 5095

<211> 2230

<212> DNA

<213> Homo sapiens

<400> 5095

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<210> 5096

<211> 153

<212> PRT

<213> Homo sapiens

<400> 5096

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Gln	Gln	His	Phe	Pro	Val	Gly	Thr	Ala	Pro	Gly	Asn	Pro	Val	Pro	Ser
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Glu	Gln	Gly	Gly	Arg	Thr	His	Pro	Ser	Leu	Ile	Arg	Ile	Trp	Ala	Arg
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Arg	Ala	Gln	Gln	Gly	Arg	Leu	Leu	Arg	Leu	Pro	Thr	Ser	Gln	His	Arg
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Leu	Ser	Gly	Leu	Asn	Pro	Ser	Val	Leu	Phe	Pro	Ser	Trp	Leu	Ile	Gly
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Arg	Pro	Phe	Ala	Gly	Thr	His	Cys	Phe	Asn	Leu	Thr	Leu	Pro	Pro	Pro
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Ala	Thr	Leu	Leu	His	Thr	Pro	Leu	Arg	Ser	Ala	Ser	Leu	Pro	Cys	Gln
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<211> 3074

<212> DNA

<213> Homo sapiens

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 2340
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 2400
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 2580
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 2880
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 2940
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 3060
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 3074

<210> 5098

<211> 114

<212> PRT

<213> Homo sapiens

<400> 5098

Met Ala Val Pro Gln Leu Gly Pro Ile Pro Val His Val Arg Thr Lys
 1 5 10 15
 Gly Val Phe Ala Ile Met Leu Pro Thr Lys Ser Lys Glu Cys Trp Phe

```

                20                25                30
Pro Ser Phe Gln Pro Gln His Phe Gln Lys Ala Leu Phe Leu Glu
      35                40                45
Thr Glu Ser Arg Cys Val Ser Gln Ala Gly Val Gln Arg Gly Asp Leu
      50                55                60
Ser Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Gln Phe Ser Cys Leu
      65                70                75                80
Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Val Pro Pro His Pro Ala
      85                90                95
Asn Phe Cys Ile Phe Ser Arg Asn Gly Val Ser Pro His Trp Pro Gly
      100                105                110
Trp Ser

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<210> 5099

<211> 801

<212> DNA

<213> Homo sapiens

<400> 5099

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ttgcatcttt acccactaga cttctgcact gaccagggg ctggagcgaa tcccagacca
180
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240
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360
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420
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480
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540
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600
gtcgccccac ctcccacccc tacctggagc ggcccagggt tggggactct gagctgtgtt
660
aaggagaaca agggcaagga gacctccctt tgtgctccct cactccctaa taaacatgag
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780
aaaaaaaaaa aaaaaaaaaa a
801

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<210> 5100

<211> 102

<212> PRT

<213> Homo sapiens

<400> 5100

Ala Cys Arg Arg Ala Arg Val Gly Glu Ala Asp Trp Val Leu Gly Leu
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 20 25 30
 Gly Pro Ser Ala Arg Pro Pro Thr Thr Trp Thr Gly Pro Gly
 35 40 45
 Leu Gly Thr Leu Ser Cys Val Lys Glu Asn Lys Gly Lys Glu Thr Ser
 50 55 60
 Leu Cys Ala Pro Ser Leu Pro Asn Lys His Glu Ser Asp Val Leu Gln
 65 70 75 80
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 85 90 95
 Lys Lys Lys Lys Lys Lys
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<210> 5101

<211> 1711

<212> DNA

<213> Homo sapiens

<400> 5101

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 120
 agcgtccctg agacgccaac ggcagtcact gccccccatt ccagctccctg ggatacgtac
 180
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 300
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 420
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 480
 aactacaact ttgacttccg gagctggcca gtcgacttcc actgggaaga acccagcagc
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 660
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 720
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 960

ctgggctgga atcatccagg ctttgctgga agcacggggg taccattccc acagaatgag
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 1080
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 1140
 taccagatg ttagtgccat gatcctggat gcctcctttg atgacctggt gcccttgggc
 1200
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 1320
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 1380
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 1620
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 1711

<210> 5102

<211> 436

<212> PRT

<213> Homo sapiens

<400> 5102

Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
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 Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
 20 25 30
 Pro Thr Ala Val Thr Ala Pro His Ser Ser Trp Asp Thr Tyr Tyr
 35 40 45
 Gln Pro Arg Ala Leu Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala
 50 55 60
 Ser Val Phe Trp Ser Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe
 65 70 75 80
 Tyr Leu Tyr Arg Lys Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe
 85 90 95
 Ser His Tyr Ala Gly Thr Leu Leu Leu Leu Ala Gly Val Ala Cys
 100 105 110
 Leu Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile
 115 120 125
 Thr Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg
 130 135 140
 Gln Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe
 145 150 155 160
 His Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser


```

165      170      175
Arg Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr
180      185      190
Ala Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr
195      200      205
Ser Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly
210      215      220
Ser Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Ala Leu Leu Gln Gly
225      230      235      240
Gln Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu
245      250      255
Ala Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly
260      265      270
Thr Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn
275      280      285
Ala Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly
290      295      300
Tyr Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly
305      310      315      320
Val Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln
325      330      335
Phe Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Val Ile Tyr
340      345      350
Ala Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr
355      360      365
Pro Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val
370      375      380
Pro Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr
385      390      395      400
Arg Thr Val Arg Gln His Leu Asn Leu Asn Ala Glu Gln Leu Cys
405      410      415
Arg Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile
420      425      430
Ile Thr Thr Thr
435

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<210> 5103

<211> 1982

<212> DNA

<213> Homo sapiens

<400> 5103

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120
aathtaggcc aatacataac tagatttgaa taaagtcaga tgaagcaata attcctcctc
180
tgtgtttgaa aggaatgagt gtggttacaa agtcacagga tgagtcctgt ggaatctgggg
240
tgggagaagg ggtggatcaa gaatgacttg ggtttgtcac tccctagcag gctgagggcg
300
tgacacagca gctcgggtgc ggagaggtct attctagttt ctaacactcc aatgctaact
360

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ttttggatgt atttccttct agcatgtaga aagggtcttt ctgggtgcc aggaagtagg
420
gagcagggat gtggcatggt gatgatctga ggacagccag gcatatgtctc agacactttg
480
gaaaactggg gagggggaac agggagacag aatcttcate ttcttcttt ttgtgaactgg
540
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600
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660
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720
tcctttagctg gtaagatcta gcactgaaac aactcttaat ttttaacttg tgaggggtctt
780
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840
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1800
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1860
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1920
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1980

gg
1982

<210> 5104

<211> 167

<212> PRT

<213> Homo sapiens

<400> 5104

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Met Phe Ile Leu Lys His Thr Ser Lys Gln Asp Lys Gln Gln Tyr Val
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Ser Leu Leu His Cys Arg Ser Ser Leu Asn Leu Pro Arg His Pro Pro
      20           25           30
Leu His Leu Phe Pro Gln Glu Leu Leu Gly His Phe Phe Cys Leu Trp
  35           40           45
Pro Ala Ala Ser Leu Lys Thr Thr Lys Asp Leu Met Ser Lys Ser Leu
  50           55           60
Ser Gly Val Cys Pro Ala Ser Ser Gly Leu Leu Arg Thr Pro His Pro
  65           70           75           80
Glu Gly Ala Arg Arg Pro Ala Gly Leu Ala Gly Pro Gly Ser Ser Leu
      85           90           95
Thr Ala Gly Trp Thr Ala Phe Arg Thr Cys Pro Gly Cys Ser Ala Phe
  100           105           110
Val Ala Gly Ser Asn Trp Arg Asn Leu Glu Arg Gly Ser Cys Ala Cys
  115           120           125
Lys Asp Gly Phe Cys Val Ser Ser Gly Phe Leu Leu Ser Gly Pro Gly
  130           135           140
Ser Ser Leu Val Pro Tyr Arg Pro Leu Phe Val His Gly Leu Ala Leu
  145           150           155           160
Tyr Glu Arg Ala Met Cys Phe
      165
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<210> 5105

<211> 1359

<212> DNA

<213> Homo sapiens

<400> 5105

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  120
tccagttccc cccacaccca gcaaagtgga caagaccccc cagaggtggt tctctctgtt
  180
ctggcttggt gcaggttcgg agggcagccc tgagtgtctg ccatccgctc aactcagtg
  240
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  300
catcatcttc ttttaagttt atcctcgccc tgtttccaaa aacgcgtaca ggctcatctt
  360
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  420
caacaacgag atcctcagtg ggctggacat ggaggaaggc aaggaaggag gcatatggct
  480
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540
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600
ggggagcctg atcctatcgt tttgacgccc ggcaagctac ggctgagcaa cgcgctgctg
660
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720
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840
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900
atcatcctgg tagatgcgga cggccacgtg accttcaactg agcgtagcat gatggacaag
960
gacctctccc actgggagac cagaacctat gagttcacac tgcagagcta accccacctc
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1080
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1140
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1200
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1260
catgtggata gacctgagcc cactcttgca catgtacaca ggcaactcaca tggcacacac
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<210> 5106

<211> 178

<212> PRT

<213> Homo sapiens

<400> 5106

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Met Ala Gly His Gln His Thr Trp Gln Ala Gly Ser Thr His Gln Leu
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Pro Ala Ala Ala Ala Gly Leu Ala Gly Pro Arg Ala Ser Thr Ala Lys
                20             25             30
Gly Asp Val Ile Cys Tyr Tyr Gly Asn Arg Gly Glu Pro Asp Pro Ile
                35             40             45
Val Leu Thr Pro Gly Thr Tyr Gly Leu Ser Asn Ala Leu Leu Glu Thr
                50             55             60
Pro Trp Arg Lys Leu Cys Phe Gly Lys Gln Leu Phe Leu Glu Ala Val
 65             70             75             80
Glu Arg Ser Gln Ala Leu Pro Lys Asp Val Leu Ile Ala Ser Leu Leu
                85             90             95
Asp Val Leu Asn Asn Glu Glu Ala Gln Leu Pro Asp Pro Ala Ile Glu
                100            105            110
Asp Gln Gly Gly Glu Tyr Val Gln Pro Met Leu Ser Lys Tyr Ala Ala
                115            120            125
Val Cys Val Arg Cys Pro Gly Tyr Gly Thr Arg Thr Asn Thr Ile Ile

```

130		135		140	
Leu Val Asp Ala Asp Gly His Val Thr Phe Thr Glu Arg Ser Met Met					
145		150		155	160
Asp Lys Asp Leu Ser His Trp Glu Thr Arg Thr Tyr Glu Phe Thr Leu					
	165		170		175
Gln Ser					

<210> 5107

<211> 1207

<212> DNA

<213> Homo sapiens

<400> 5107

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120
acaggggatga ccaccacctg gaacgggggac agccacagtg gccatttccc cccgcagctt
180
tctgccagca ctcccaacag tctttccaca gaaccgagca ctgctcgggtg aatgaggact
240
ggacgctcca gggcaccgcg cccagtttgt atttatttat ttatttattt atttagagac
300
agagtctcgc tctgtcgcnc taggggggtg cagtggcgca atctcagctc actgcaacct
360
ccacctcccg ggttaacagg attctcctgc ctcagcctcc tgagtagctg ggattacagg
420
cgtgtgccac catgcccgcc taatttttgt attttttagta gagacagggt ttcaccgtgt
480
tagccagggt ggtcttgatc tctgacctc atgacctgc cgcctcagcc tcccagagtg
540
ctgggattac aggcgatgag cactgcgcct ggcccaattt attttttttt gtatgttcat
600
tctcttcaca tccaaacagc tacagcttcc ctcttttgtt ggggtcccca aaccaagtct
660
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720
gtcagctggg ttgggtcttc ccatgtgagg gaggtgatg gcactcgag gtttttgctt
780
catctatgta caaaggctca gaaaatttct tcggcatttg ggacctcgt gttctgtage
840
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960
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1020
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1080
tgctcactcc ccacagggat gaccaccacc tggaaacggg acagccacag tggcccttta
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1200

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ggccggc
1207

<210> 5108
<211> 83
<212> PRT
<213> Homo sapiens

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<400> 5108
Met Arg Thr Gly Arg Ser Arg Ala Pro Ala Pro Val Cys Ile Tyr Leu
 1             5             10             15
Phe Ile Tyr Leu Phe Arg Asp Arg Val Ser Leu Cys Arg Xaa Arg Gly
      20             25             30
Val Gln Trp Arg Asn Leu Ser Ser Leu Gln Pro Pro Pro Gly Phe
      35             40             45
Lys Arg Phe Ser Cys Leu Ser Leu Leu Ser Ser Trp Asp Tyr Arg Arg
      50             55             60
Val Pro Pro Cys Pro Ala Asn Phe Cys Ile Phe Ser Arg Asp Arg Val
      65             70             75             80
Ser Pro Cys

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<210> 5109
<211> 651
<212> DNA
<213> Homo sapiens

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<400> 5109
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ctgcagnatg cgcaaggac ttttgaatca gctgtgcaag agaatatcag cattaatggg
 120
caagcatggc aggaagcttc agataattgt tttatggatt ctgacatcaa agtacttgaa
 180
gatcagtttg atgaaatcat agtagatata gccacaaaaa gtaagcagta tcccagaaa
 240
atcctggaat gtgtcatcaa aaccataaaa gcaaaaacag aaattctgaa gcagtaccac
 300
cctgtttgtac atccactgga cctaaaatat gacctgtac cagttctcaa cggaatgct
 360
ttcaactttt cccattcaa catgatgttg gctgtggatt tgtcatatat ggtttttatt
 420
acttcggccc ctcatatgga aaatttgaaa tgcagagggg aaacagtagc aaaggagatc
 480
agtgaagcca tgaagtcctt gcctgcatta attgaacaag gagagggatt ttcccaagtt
 540
ctcaggatgc agcctgttat ccacctccag aggattcacc aagaagtctt ttccagttgt
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cataggaaac cagatgctaa acctgagaac ttataaac agatagaaac c
 651

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<210> 5110
<211> 206
<212> PRT

<213> Homo sapiens

<400> 5110

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Phe Glu Ser Ala Val Gln Glu Asn Ile Ser Ile Asn Gly Gln Ala Trp
 20           25           30
Gln Glu Ala Ser Asp Asn Cys Phe Met Asp Ser Asp Ile Lys Val Leu
 35           40           45
Glu Asp Gln Phe Asp Glu Ile Ile Val Asp Ile Ala Thr Lys Arg Lys
 50           55           60
Gln Tyr Pro Arg Lys Ile Leu Glu Cys Val Ile Lys Thr Ile Lys Ala
 65           70           75           80
Lys Gln Glu Ile Leu Lys Gln Tyr His Pro Val Val His Pro Leu Asp
 85           90           95
Leu Lys Tyr Asp Pro Asp Pro Val Leu Asn Gly Asn Ala Phe Asn Phe
100           105           110
Ser Pro Phe Asn Met Met Leu Ala Val Asp Leu Ser Tyr Met Val Phe
115           120           125
Ile Thr Ser Ala Pro His Met Glu Asn Leu Lys Cys Arg Gly Glu Thr
130           135           140
Val Ala Lys Glu Ile Ser Glu Ala Met Lys Ser Leu Pro Ala Leu Ile
145           150           155           160
Glu Gln Gly Glu Gly Phe Ser Gln Val Leu Arg Met Gln Pro Val Ile
165           170           175
His Leu Gln Arg Ile His Gln Glu Val Phe Ser Ser Cys His Arg Lys
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Pro Asp Ala Lys Pro Glu Asn Phe Ile Thr Gln Ile Glu Thr
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<210> 5111

<211> 2247

<212> DNA

<213> Homo sapiens

<400> 5111

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540

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2160

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<210> 5112

<211> 581

<212> PRT

<213> Homo sapiens

<400> 5112

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Thr	Phe	Pro	His	85	Val	Ala	Ala	Lys	Thr	Gly	Ser	Gly	Ala	Ser	Ile	Gly
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Cys	Thr	Pro	Thr	100	Ser	Thr	Gln	Ala	Lys	Met	Val	Ser	Lys	Arg	Ile	Ala
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Tyr	Leu	Thr	Arg	195	Phe	Cys	Asp	Gln	Cys	Lys	Gln	Asp	Lys	Ala	Cys	Arg
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Lys	Leu	Ala	Thr	225	Ala	Gly	Asp	Gln	Gly	Leu	Leu	Leu	Gln	Ser	Leu	Asn
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Gly	Leu	Gln	Leu	260	Leu	Val	Ala	Thr	Leu	Thr	Gln	Asn	Ala	Asp	Glu	Ala
									265					270		
Asp	Leu	Thr	Cys	275	Ser	Gly	Ile	Arg	Cys	Val	Arg	His	Ala	Cys	Leu	Lys
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Leu	Thr	Gly	Ala	305	Ile	Thr	His	His	Gly	His	His	Thr	Asp	Val	Val	Arg
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Glu	Ala	Cys	Trp	325	Ala	Leu	Arg	Val	Met	Thr	Phe	Asp	Asp	Asp	Ile	Arg
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Val	Pro	Phe	Gly		His	Ala	His	Asn	His	Ala	Lys	Met	Ile	Val	Gln	Glu

340 345 350
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 355 360 365
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 370 375 380
 Ile Arg Asn Glu Phe Cys Gln Glu Val Val Asp Leu Gly Gly Leu Ser
 385 390 395 400
 Ile Leu Val Ser Leu Leu Ala Asp Cys Asn Asp His Gln Met Arg Asp
 405 410 415
 Gln Ser Gly Val Gln Glu Leu Val Lys Gln Val Leu Ser Thr Leu Arg
 420 425 430
 Ala Ile Ala Gly Asn Asp Asp Val Lys Asp Ala Ile Val Arg Ala Gly
 435 440 445
 Gly Thr Glu Ser Ile Val Ala Ala Met Thr Gln His Leu Thr Ser Pro
 450 455 460
 Gln Val Trp Glu Gln Ser Cys Ala Ala Leu Cys Phe Leu Ala Leu Arg
 465 470 475 480
 Lys Pro Asp Asn Ser Arg Ile Ile Val Glu Gly Gly Gly Ala Val Ala
 485 490 495
 Ala Leu Gln Ala Met Lys Ala His Pro Gln Lys Ala Gly Val Gln Lys
 500 505 510
 Gln Ala Cys Met Leu Ile Arg Asn Leu Val Ala His Gly Gln Ala Phe
 515 520 525
 Ser Lys Pro Ile Leu Asp Leu Gly Ala Glu Ala Leu Ile Met Gln Ala
 530 535 540
 Arg Ser Ala His Arg Asp Cys Glu Asp Val Ala Lys Ala Ala Leu Arg
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 Asp Leu Gly Cys His Val Glu Leu Arg Glu Leu Trp Thr Gly Gln Arg
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 Gly Asn Leu Ala Pro
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<210> 5113

<211> 472

<212> DNA

<213> Homo sapiens

<400> 5113

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 180
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 240
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<210> 5114
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 5114
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 Met His Leu Thr Pro Val Ile Gly Thr Gln Arg Gly Ala Trp His Leu
 35 40 45
 Gln Cys Arg His Thr Gly His Arg Ser Val Gln Glu Gly Pro Phe Ala
 50 55 60
 Asn Val His Ser Ser Leu Cys Leu Phe Ser Tyr Ala Phe Leu Asp Trp
 65 70 75 80
 Ser Lys Arg Phe Phe Phe Pro Ser Lys Glu Gln Phe Met Phe Leu Asn
 85 90 95
 Thr Phe Phe Pro
 100

<210> 5115
 <211> 1003
 <212> DNA
 <213> Homo sapiens

<400> 5115
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 120
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 180
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<210> 5116

<211> 226

<212> PRT

<213> Homo sapiens

<400> 5116

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Ser Pro Gly Pro Gln Ala Leu Lys Gly Gly Ala Arg Gly Ser Gly His
35 40 45
Val Leu Thr Ser Ser Ser Gly Ser Ala Cys Ala Gly Ser Pro Leu Cys
50 55 60
Pro Ala Met Ser His Leu Gly Val Ser His Val Arg Glu Gln Leu Leu
65 70 75 80
Leu Ser Ile Met Gln Phe Leu Ser Trp Val Ile Ala Val His Gly Glu
85 90 95
Gln Val His Ala Gln Pro Val His Pro Leu Phe Leu Leu Tyr Ile His
100 105 110
Tyr His Ser His His His Pro Asp Gln Gly Asp Glu Glu Glu Gly Pro
115 120 125
Gln His Ile Ala His His Gly Val Ala Val Gly Leu Gly Gly Ile Gly
130 135 140
His Ser Gly Val Thr His Asp Ile Ser Ser Arg Arg Ala Gly Trp Ser
145 150 155 160
Ala Trp Ala Val Ala Leu Arg Glu Gly Ala Ser Thr Gly Leu Pro Ser
165 170 175
Arg Met Leu Ile Val Pro Gly Gln Gly Gly Met Pro Gly Trp Gly Gly
180 185 190
Arg Gln Ala Ala Ala Arg Met Arg Ala Ser Asn Ser Gly Xaa Gly Gly
195 200 205
Gly Ser His Gly Ala Gly Xaa Ala His Ala Gly Gly Gly Gly Val Gly
210 215 220
Gly Cys
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<210> 5117

<211> 1180

<212> DNA

<213> Homo sapiens

<400> 5117

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 240
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<210> 5118

<211> 300

<212> PRT

<213> Homo sapiens

<400> 5118

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 35 40 45
 Lys Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
 50 55 60
 Pro Gly Leu Phe Asp Thr Lys Glu Ser Leu Asp Thr Thr Cys Lys Glu

65		70		75		80
Ile Ser Arg Cys	Ile Ile Ser Ser Cys	Pro Gly Pro His Ala	Ile Val			
	85	90	95			
Leu Val Leu Leu	Leu Gly Arg Tyr Thr	Glu Glu Glu Gln	Lys Thr Val			
	100	105	110			
Ala Leu Ile Lys	Ala Val Phe Gly Lys Ser	Ala Met Lys His	Met Val			
	115	120	125			
Ile Leu Phe Thr	Arg Lys Glu Glu Leu	Glu Gly Gln Ser	Phe His Asp			
	130	135	140			
Phe Ile Ala Asp	Ala Asp Val Gly Leu	Lys Ser Ile Val	Lys Glu Cys			
	145	150	155			
Gly Asn Arg Cys	Cys Ala Phe Ser Asn	Ser Lys Lys Thr	Ser Lys Ala			
	165	170	175			
Glu Lys Glu Ser	Gln Val Gln Glu Leu	Val Glu Ile Glu	Lys Met			
	180	185	190			
Val Gln Cys Asn	Glu Gly Ala Tyr Phe	Ser Asp Asp Ile	Tyr Lys Asp			
	195	200	205			
Thr Glu Glu Arg	Leu Lys Gln Arg	Glu Glu Val Leu	Arg Lys Ile Tyr			
	210	215	220			
Thr Asp Gln Leu	Asn Glu Glu Ile Lys	Leu Val Glu Glu	Asp Lys His			
	225	230	235			
Lys Ser Glu Glu	Glu Lys Glu Lys Glu	Ile Lys Leu Leu	Lys Leu Lys			
	245	250	255			
Tyr Asp Glu Lys	Ile Lys Asn Ile Arg	Glu Glu Ala Glu	Arg Asn Ile			
	260	265	270			
Phe Lys Asp Val	Phe Asn Arg Ile Trp	Lys Met Leu Ser	Glu Ile Trp			
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His Arg Phe Leu	Ser Lys Cys Lys Phe	Tyr Ser Ser				
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<210> 5119

<211> 1450

<212> DNA

<213> Homo sapiens

<400> 5119

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420
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 1020
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 1450

<210> 5120

<211> 314

<212> PRT

<213> Homo sapiens

<400> 5120

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 20 25 30
 Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val Leu Val
 35 40 45
 Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val Pro Gln
 65 70 75 80
 Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ile Gly
 85 90 95
 Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Tyr
 100 105 110
 Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val Cys His

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      115              120              125
Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu Gln Leu
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Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile Gln Ser
145              150              155              160
Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val Asp Asp
165              170              175
Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr Asp Thr
180              185              190
Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu Leu Val
195              200              205
Met Pro Leu Ile Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala Lys Ala
210              215              220
Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe Gly Thr
225              230              235              240
Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr Val Thr
245              250              255
Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp Gly Lys
260              265              270
Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu
275              280              285
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Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn
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<210> 5121

<211> 944

<212> DNA

<213> Homo sapiens

<400> 5121

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120
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180
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240
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<210> 5122

<211> 172

<212> PRT

<213> Homo sapiens

<400> 5122

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 Glu Glu Lys Asp Pro Arg Arg Cys Leu Glu Glu Gly Lys Leu Val Asn
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 Phe Arg His Cys Arg Lys Gln Gln Ala Lys Phe Asp Glu Cys Val Leu
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 Asp Lys Leu Gly Trp Val Arg Pro Asp Leu Gly Glu Leu Ser Lys Val
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 Thr Lys Val Lys Thr Asp Arg Pro Leu Pro Glu Asn Pro Tyr His Ser
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<211> 1139

<212> DNA

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<400> 5123

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<211> 101

<212> PRT

<213> Homo sapiens

<400> 5124

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 Gln Ala Cys Met Leu Ile Arg Asn Leu Val Ala His Gly Gln Ala Phe
 35 40 45
 Ser Lys Pro Ile Leu Asp Leu Gly Ala Glu Ala Leu Ile Met Gln Ala
 50 55 60
 Arg Ser Ala His Arg Asp Cys Glu Asp Val Ala Lys Ala Ala Leu Arg
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<210> 5125

<211> 6244

<212> DNA

<213> Homo sapiens

<400> 5125

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<211> 117

<212> PRT

<213> Homo sapiens

<400> 5126

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Thr Phe Ser Gly Leu Val Ser Thr Phe Glu Val Val Leu Trp Leu Asn
          20           25           30
Phe Ser Cys Ser Phe Cys Val Val Phe Arg Gly Gly Ser Pro His Ala
          35           40           45
Glu Ile Leu Cys Met Gln Pro Thr Gly Lys Arg Pro Pro Gly Ser Gln
          50           55           60
Asp Phe Ser Phe Ser Cys Leu Cys Pro Ala Thr Cys Ser Leu Pro Leu
65           70           75           80
Phe Arg Cys Gln Arg Gly Asp Phe Arg Ala Val Cys Phe Asn Pro Gly
          85           90           95
Arg Ser Asp Thr Leu Val Ser Phe Phe Gln Glu Thr Ile Ala Phe Thr
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Asp Val Leu Val Val
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<210> 5127

<211> 400

<212> DNA

<213> Homo sapiens

<400> 5127

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<210> 5128

<211> 55

<212> PRT

<213> Homo sapiens

<400> 5128

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          20           25           30
Trp Gly Trp Thr Phe Thr Gly Thr Met Ser Ala Gly Ser Ala Ala Pro

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35 40 45
Ala Ser Ser Thr Thr Ile Ser
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<210> 5129
<211> 745
<212> DNA
<213> Homo sapiens

<400> 5129
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<210> 5130
<211> 111
<212> PRT
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<400> 5130
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Ser Arg Gln Leu His Phe Arg Leu Leu Glu Glu Arg Gln Gly Val Gly
35 40 45
Gly Val Gly Leu Ser Ala Lys Gly Gly Lys His Pro Gln Asp Arg Asn
50 55 60
Leu Ala Ala Val Gly Pro Glu Val Gln Ala Cys Gly Trp Ala Arg Pro
65 70 75 80
Asp Pro Ala Cys Ala Gly Gly Gln Val Ala Gly Gly Gly Glu Pro Gly

4313

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Ala Gly Lys Thr Glu Ala Ser Lys His Ile Met Gln Tyr Ile Ala Ala
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Val Thr Asn Pro Ser Gln Arg Ala Glu Val Glu Arg Val Lys Asp Val
      100             105             110
Leu Leu Lys Ser Thr Cys Val Leu Glu Ala Phe Gly Asn Ala Arg Thr
      115             120             125
Asn Arg Asn His Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Ile Asn
      130             135             140
Phe Asp Phe Lys Gly Asp Pro Ile Gly Gly His Ile His Ser Tyr Leu
145      150             155             160
Leu Glu Lys Ser Arg Val Leu Lys Gln His Val Gly Glu Arg Asn Phe
      165             170             175
His Ala Phe Tyr Gln Leu Leu Arg Gly Ser Glu Asp Lys Gln Leu His
      180             185             190
Glu Leu His Leu Glu Arg Asn Pro Ala Val Tyr Asn Phe Thr His Gln
      195             200             205
Gly Ala Gly Leu Asn Met Thr Val His Ser Ala Leu Asp Ser Asp Glu
      210             215             220
Gln Ser His Gln Ala Val Thr Glu Ala Met Arg Val Ile Gly Phe Ser
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Pro Glu Glu Val Glu Ser Val His Arg Ile Leu Ala Ala Ile Leu His
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<210> 5133

<211> 581

<212> DNA

<213> Homo sapiens

<400> 5133

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<210> 5134

<211> 157

<212> PRT

<213> Homo sapiens

<400> 5134

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 20           25           30
His Leu Ser His Pro Asp His Tyr His His Gly Lys Ser Asp Leu
 35           40           45
Ser Arg Gly Ser Pro Tyr Arg Glu Ser Pro Leu Gly His Phe Glu Ser
 50           55           60
Tyr Gly Gly Met Pro Phe Phe Gln Ala Gln Lys Met Phe Val Asp Val
 65           70           75           80
Pro Glu Asn Thr Val Ile Leu Asp Glu Met Thr Leu Arg His Met Val
 85           90           95
Gln Asp Cys Thr Ala Val Lys Thr Gln Leu Leu Lys Leu Lys Arg Leu
100           105           110
Leu His Gln His Asp Gly Ser Gly Ser Leu His Asp Ile Gln Leu Ser
115           120           125
Leu Pro Ser Ser Pro Glu Pro Glu Asp Gly Asp Lys Val Tyr Lys Asn
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Glu Asp Leu Leu Asn Glu Ile Lys Gln Leu Lys Asp Glu
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<210> 5135

<211> 1696

<212> DNA

<213> Homo sapiens

<400> 5135

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<210> 5136

<211> 341

<212> PRT

<213> Homo sapiens

<400> 5136

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 Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro Pro Glu

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Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile Tyr Val
      130              135              140
Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn
      145              150              155
Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His
      165              170              175
Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro
      180              185              190
Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr
      195              200              205
His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His
      210              215              220
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly Arg
      225              230              235
Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu Gln Leu
      245              250              255
Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg His Leu
      260              265              270
His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala Ala Gln
      275              280              285
Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn Thr Val
      290              295              300
Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly Ala Pro
      305              310              315
Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala Thr Pro
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Trp Cys Thr Phe Ser
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<210> 5137

<211> 3090

<212> DNA

<213> Homo sapiens

<400> 5137

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420

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<210> 5138

<211> 371

<212> PRT

<213> Homo sapiens

<400> 5138

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 Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
 35 40 45
 Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
 50 55 60
 Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
 65 70 75 80
 Tyr Ser Leu Pro Arg Glu Thr Val Ser Met Asp Leu Glu Ser Glu Ser

85 90 95
 Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
 100 105 110
 Ala Glu Gln Glu Ile Ala Arg Leu Val Leu Thr Asp Glu Glu Lys Ser
 115 120 125
 Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
 130 135 140
 Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Arg Lys Ile Arg Asn
 145 150 155 160
 Lys Arg Ser Ala Gln Glu Ser Arg Arg Lys Lys Val Tyr Val Gly
 165 170 175
 Gly Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu
 180 185 190
 Gln Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp
 195 200 205
 Gln Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr
 210 215 220
 Ser Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu
 225 230 235 240
 Leu Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro
 245 250 255
 Ala Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu
 260 265 270
 Asp Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys
 275 280 285
 Asp Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala
 290 295 300
 Pro Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser
 305 310 315 320
 Ala Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro
 325 330 335
 Leu Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys
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<210> 5139

<211> 1968

<212> DNA

<213> Homo sapiens

<400> 5139

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<210> 5140

<211> 443

<212> PRT

<213> Homo sapiens

<400> 5140

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Asn His Thr Gly Glu Leu Leu Ala Thr Gly Asp Lys Gly Arg Val
          35           40           45
Val Ile Phe Gln Arg Glu Gln Glu Ser Lys Asn Gln Val His Arg Arg
          50           55           60
Gly Glu Tyr Asn Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe
65          70          75          80
Asp Tyr Leu Lys Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Arg
          85          90          95
Trp Leu Pro Gln Gln Asn Ala Ala Tyr Phe Leu Leu Ser Thr Asn Asp
          100         105         110
Lys Thr Val Lys Leu Trp Lys Val Ser Glu Arg Asp Lys Arg Pro Glu
          115         120         125
Gly Tyr Asn Leu Lys Asp Glu Glu Gly Arg Leu Arg Asp Pro Ala Thr
          130         135         140
Ile Thr Thr Leu Arg Val Pro Val Leu Arg Pro Met Asp Leu Met Val
          145         150         155
Glu Ala Thr Pro Arg Arg Val Phe Ala Asn Ala His Thr Tyr His Ile
          165         170         175
Asn Ser Ile Ser Val Asn Ser Asp Tyr Glu Thr Tyr Met Ser Ala Asp
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Asp Leu Arg Ile Asn Leu Trp Asn Phe Glu Ile Thr Asn Gln Ser Phe
          195         200         205
Asn Ile Val Asp Ile Lys Pro Ala Asn Met Glu Glu Leu Thr Glu Val
          210         215         220
Ile Thr Ala Ala Glu Phe His Pro His His Cys Asn Thr Phe Val Tyr
          225         230         235
Ser Ser Ser Lys Gly Thr Ile Arg Leu Cys Asp Met Arg Ala Ser Ala
          245         250         255
Leu Cys Asp Arg His Thr Lys Phe Phe Glu Glu Pro Glu Asp Pro Ser
          260         265         270
Asn Arg Ser Phe Phe Ser Glu Ile Ile Ser Ser Ile Ser Asp Val Lys
          275         280         285
Phe Ser His Ser Gly Arg Tyr Ile Met Thr Arg Asp Tyr Leu Thr Val
          290         295         300
Lys Val Trp Asp Leu Asn Met Glu Ser Arg Pro Val Glu Thr His Gln
          305         310         315
Val His Asp Tyr Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp
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Cys Ile Phe Asp Lys Phe Glu Cys Val Trp Asn Gly Ser Asp Ser Val
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Lys	Asp	Glu	Ile	Ser	Val	Asp	Ser	Leu	Asp	Phe	Ser	Lys	Lys	Ile	Leu
405					410					415					
His	Thr	Ala	Trp	His	Pro	Val	Asp	Asn	Val	Ile	Ala	Val	Ala	Ala	Thr
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<210> 5141

<211> 928

<212> DNA

<213> Homo sapiens

<400> 5141

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<210> 5142

<211> 227

<212> PRT

<213> Homo sapiens

<400> 5142

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Pro Leu Val Val Asn Val Leu Glu Asn Leu Asp Ser Val Leu Ser Glu
 35           40           45
Asn Gln Glu His Glu Val Glu Leu Glu Leu Arg Glu Asp Asn Glu
 50           55           60
Gln Leu Leu Thr Gln Tyr Glu Arg Glu Lys Ala Leu Arg Arg Gln Ala
 65           70           75           80
Glu Glu Lys Phe Ile Glu Phe Glu Asp Ala Leu Glu Gln Glu Lys Lys
 85           90           95
Glu Leu Gln Ile Gln Val Glu His Tyr Glu Phe Gln Thr Arg Gln Leu
100           105           110
Glu Leu Lys Ala Lys Asn Tyr Ala Asp Gln Ile Ser Arg Leu Glu Glu
115           120           125
Arg Glu Ser Glu Met Lys Lys Glu Tyr Asn Ala Leu His Gln Arg His
130           135           140
Thr Glu Met Ile Gln Thr Tyr Val Glu His Ile Glu Arg Ser Lys Met
145           150           155           160
Gln Gln Val Gly Gly Asn Ser Gln Thr Glu Ser Ser Leu Pro Gly Arg
165           170           175
Ser Arg Lys Glu Arg Pro Thr Ser Leu Asn Val Phe Pro Leu Ala Asp
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Gly Thr Val Arg Ala Gln Ile Gly Gly Lys Leu Val Pro Ala Gly Asp
195           200           205
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Gln Val Leu
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<210> 5143

<211> 1666

<212> DNA

<213> Homo sapiens

<400> 5143

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420

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 960
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 1020
 atatgatata atattgtatt tccttactgt tttatctatt gtaataaaaa agcattttaa
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 1320
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 1560
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<210> 5144

<211> 218

<212> PRT

<213> Homo sapiens

<400> 5144

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 20 25 30
 Gln Glu Ala Ser Asp Asn Cys Phe Met Asp Ser Asp Ile Lys Val Leu

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      35              40              45
Glu Asp Gln Phe Asp Glu Ile Ile Val Asp Ile Ala Thr Lys Arg Lys
  50              55              60
Gln Tyr Pro Arg Lys Ile Leu Glu Cys Val Ile Lys Thr Ile Lys Ala
  65              70              75              80
Lys Gln Glu Ile Leu Lys Gln Tyr His Pro Val Val His Pro Leu Asp
      85              90              95
Leu Lys Tyr Asp Pro Asp Pro Ala Pro His Met Glu Asn Leu Lys Cys
      100              105              110
Arg Gly Glu Thr Val Ala Lys Glu Ile Ser Glu Ala Met Lys Ser Leu
      115              120              125
Pro Ala Leu Ile Glu Gln Gly Glu Gly Phe Ser Gln Val Leu Arg Met
      130              135              140
Gln Pro Val Ile His Leu Gln Arg Ile His Gln Glu Val Phe Ser Ser
      145              150              155              160
Cys His Arg Lys Pro Asp Ala Lys Pro Glu Asn Phe Ile Thr Gln Ile
      165              170              175
Glu Thr Thr Pro Thr Glu Thr Ala Ser Arg Lys Thr Ser Asp Met Val
      180              185              190
Leu Lys Arg Lys Gln Thr Lys Asp Cys Pro Gln Arg Lys Trp Tyr Pro
      195              200              205
Leu Arg Pro Lys Lys Ile Asn Leu Asp Thr
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<210> 5145

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 5145

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  180
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  480
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  600
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  720

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 1740
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 1860
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 1885

<210> 5146

<211> 312

<212> PRT

<213> Homo sapiens

<400> 5146

Pro Ala Thr Ser Glu Lys Glu Ser Ile Leu Leu Phe Pro Asp Leu Arg
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 Cys Ala Leu Ala Gly His Asn Asp Leu Val Glu Ile His Leu Ser Gly
 20 25 30
 Arg Leu Gly Val Cys Thr Gly Leu Ala Cys Ala Tyr His Leu Leu Cys
 35 40 45
 Thr Pro Pro Thr Pro Cys Ile Pro Thr Pro Gly Leu Val Ala Pro Ala

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<210> 5147

<211> 2943

<212> DNA

<213> Homo sapiens

<400> 5147

<400> 5147
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120

120
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180

180
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240

240
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300

300
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360

360
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420

gaacctcagc ttgctagtct ttgtctagat acaatagaca aaagcacaat ggatgcaata
480
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540
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 2340
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 2700
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 2820
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 2943

<210> 5148

<211> 296

<212> PRT

<213> Homo sapiens

<400> 5148

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 20 25 30
 Ile Asp Ile Asp Thr Leu Cys Ala Val Leu Glu Arg Asp Thr Leu Ser
 35 40 45
 Ile Arg Glu Ser Arg Leu Phe Gly Ala Val Val Arg Trp Ala Glu Ala
 50 55 60
 Glu Cys Gln Arg Gln Gln Leu Pro Val Thr Phe Gly Asn Lys Gln Lys
 65 70 75 80
 Val Leu Gly Lys Ala Leu Ser Leu Ile Arg Phe Pro Leu Met Thr Ile
 85 90 95
 Glu Glu Phe Ala Ala Gly Pro Ala Gln Ser Gly Ile Leu Ser Asp Arg
 100 105 110
 Glu Val Val Asn Leu Phe Leu His Phe Thr Val Asn Pro Lys Pro Arg

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      115              120              125
Val Glu Tyr Ile Asp Arg Pro Arg Cys Cys Leu Arg Gly Lys Glu Cys
      130              135              140
Cys Ile Asn Arg Phe Gln Gln Val Glu Ser Arg Trp Gly Tyr Ser Gly
145              150              155              160
Thr Ser Asp Arg Ile Arg Phe Thr Val Asn Arg Arg Ile Ser Ile Val
      165              170              175
Gly Phe Gly Leu Tyr Gly Ser Ile His Gly Pro Thr Asp Tyr Gln Val
      180              185              190
Asn Ile Gln Ile Ile Glu Tyr Glu Lys Lys Gln Thr Leu Gly Gln Asn
      195              200              205
Asp Thr Gly Phe Ser Cys Asp Gly Thr Ala Asn Thr Phe Arg Val Met
      210              215              220
Phe Lys Glu Pro Ile Glu Ile Leu Pro Asn Val Cys Tyr Thr Ala Cys
225              230              235              240
Ala Thr Leu Lys Gly Pro Asp Ser His Tyr Gly Thr Lys Gly Leu Lys
      245              250              255
Lys Val Val His Glu Thr Pro Ala Ala Ser Lys Thr Val Phe Phe Phe
      260              265              270
Phe Ser Ser Pro Gly Asn Asn Asn Gly Thr Ser Ile Glu Asp Gly Gln
      275              280              285
Ile Pro Glu Ile Ile Phe Tyr Thr
      290              295

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<210> 5149

<211> 533

<212> DNA

<213> Homo sapiens

<400> 5149

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120
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180
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360
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420
agaagcacta acatagctgc agctgccagt gagccacact cctgagacac tctctaaatt
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533

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<210> 5150

<211> 154

<212> PRT

<213> Homo sapiens

<400> 5150

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 20 25 30
 Ile Val Gly Asp Ile Ala Pro Ala Asp Asn Ile Pro Lys Glu Glu Lys
 35 40 45
 His Arg Arg Glu Glu Glu Ala Met Lys Gln Ile Thr Gln Leu Leu Pro
 50 55 60
 Glu Asp Leu Arg Lys Glu Leu Tyr Glu Leu Trp Glu Glu Tyr Glu Thr
 65 70 75 80
 Gln Ser Ser Ala Glu Ala Lys Phe Val Lys Gln Leu Asp Gln Cys Glu
 85 90 95
 Met Ile Leu Gln Ala Ser Glu Tyr Glu Asp Leu Glu His Lys Pro Gly
 100 105 110
 Arg Leu Gln Asp Phe Tyr Asp Ser Thr Ala Gly Lys Phe Asn His Pro
 115 120 125
 Glu Ile Val Gln Leu Val Ser Glu Leu Glu Ala Glu Arg Ser Thr Asn
 130 135 140
 Ile Ala Ala Ala Ser Glu Pro His Ser
 145 150

<210> 5151

<211> 2273

<212> DNA

<213> Homo sapiens

<400> 5151

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 120
 gaggcctgagg cggcgagctc ccggggcagc cctgtgcgcg tgaagcggga gttcgagccg
 180
 gcgagcgcgc gcgagggccc ggcttctgtt gtcccgtttg tcggggtgaa gcgggagcgc
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 660
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 720
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 780

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<210> 5152

<211> 324

<212> PRT

<213> Homo sapiens

<400> 5152

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Lys Pro Thr Phe Thr Lys Gln Gln Ile Ala Asn Leu Asp Lys Gln Ala
 35              40              45
Lys Leu Ser Arg Ala Tyr Asp Gly Thr Thr Tyr Leu Pro Gly Ile Val
 50              55              60
Gly Leu Asn Asn Ile Lys Ala Asn Asp Tyr Ala Asn Ala Val Leu Gln
 65              70              75              80
Ala Leu Ser Asn Val Pro Pro Leu Arg Asn Tyr Phe Leu Glu Glu Asp
              85              90              95
Asn Tyr Lys Asn Ile Lys Arg Pro Pro Gly Asp Ile Met Phe Leu Leu
 100              105              110
Val Gln Arg Phe Gly Glu Leu Met Arg Lys Leu Trp Asn Pro Arg Asn
 115              120              125
Phe Lys Ala His Val Ser Pro His Glu Met Leu Gln Ala Val Val Leu
 130              135              140
Cys Ser Lys Lys Thr Phe Gln Ile Thr Lys Gln Gly Asp Gly Val Asp
 145              150              155              160
Phe Leu Ser Trp Phe Leu Asn Ala Leu His Ser Ala Leu Gly Gly Thr
              165              170              175
Lys Lys Lys Lys Lys Thr Ile Val Thr Asp Val Phe Gln Gly Ser Met
 180              185              190
Arg Ile Phe Thr Lys Lys Leu Pro His Pro Asp Leu Pro Ala Glu Glu
 195              200              205
Lys Glu Gln Leu Leu His Asn Asp Glu Tyr Gln Glu Thr Met Val Glu
 210              215              220
Ser Thr Phe Met Tyr Leu Thr Leu Asp Leu Pro Thr Ala Pro Leu Tyr
 225              230              235              240
Lys Asp Glu Lys Glu Gln Leu Ile Ile Pro Gln Val Pro Leu Phe Asn
              245              250              255
Ile Leu Ala Lys Phe Asn Gly Ile Thr Glu Lys Glu Tyr Lys Thr Tyr
 260              265              270
Lys Glu Asn Phe Leu Lys Arg Phe Gln Leu Thr Lys Leu Pro Pro Tyr
 275              280              285
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Arg Ile Leu Val

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<210> 5153

<211> 640

<212> DNA

<213> Homo sapiens

<400> 5153

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<210> 5154

<211> 162

<212> PRT

<213> Homo sapiens

<400> 5154

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Leu Glu Arg Thr Thr Ser Pro Thr Ile Pro Ser Phe Tyr Thr Phe Ser
      20             25             30
Ala Cys His Arg Trp Leu Gln Glu Gly Ser Thr Leu Gly Gly Thr Gly
      35             40             45
Glu Leu Ala Phe Gly Ala Asp Thr Leu Leu Thr Leu Pro Phe Leu Leu
      50             55             60
Gln Gly Val Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val
      65             70             75             80
Val Gln Phe Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile
      85             90             95
Ile Tyr Ala Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met
      100            105            110
Ser Tyr Pro Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp
      115            120            125
Leu Val Pro Leu Ala Leu Lys Val Met Pro Asp Ser Trp Ser Glu Cys
      130            135            140
Ser Ser Gln Ala Cys Pro Ser Trp Glu Gly Val Gly Trp Asn Trp Glu
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Leu Phe

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<210> 5155

<211> 1402

<212> DNA

<213> Homo sapiens

<400> 5155
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240
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420
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1020
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1080
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1140
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1200
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1260
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1380
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1402

<210> 5156

<211> 118

<212> PRT

<213> Homo sapiens

<400> 5156

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Met Asp Leu Ala Gln Met His Ala Cys Gln Gly Pro Gly Asn Asp Leu
 1             5             10             15
Tyr Ile Glu Ala Ser Ala Ala Leu Cys Ala Gly Ser Asp Phe Ser Val
          20             25             30
Ser Gly Gly Leu Gln Trp Val Gln Leu Val Ala His Gly Ser Ala Gly
 35             40             45
Asp Asp Asn Gly Trp Leu Arg Cys His Arg Pro Pro Trp Gln Gly Leu
 50             55             60
Gly Asp Asn Glu Leu Asp Gly Cys Ser Gly Glu Val Asn Val Ser Gln
 65             70             75             80
Asp Phe Val Lys Thr Leu Leu Arg Ile Cys Asn Ala Ile Pro Ser Phe
          85             90             95
Arg Gly Leu Leu Glu Ser Cys Met Phe Gly Cys Arg Ala Arg Val Thr
          100             105             110
Arg Asn Phe Trp Thr Leu
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<210> 5157

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 5157

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cggggcaggg gaattgcatc tgcaggaag agatgcagca tgctcctcac tcttgagtgc
180
ccacctgtcc tgcttctctg caggtgaaaa ctctggggga tgctgatcaa tagagcttgg
240
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420
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540
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600
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660
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720
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780
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840

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 1020
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 1080
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 tactccaggc ttctggacac acatacccat ggggtgattt tgctcctcag gcccaatatt
 1200
 ctcagacagc ccagcagtgt gaacacacaa tgccaggcca gggaaactggg gaccaccatc
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 1310

<210> 5158
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 5158
 Met Thr Ser His Met Val Arg Leu Gly Ser Ser His Pro Gln Ala Gly
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 Thr Ser Ser Cys Leu Ser Ser Asn Ala Ser Arg Met Leu His Cys Ser
 20 25 30
 Gln Glu Leu Ala Ile Arg Tyr Val Leu Cys Gly Gln Ser Ala Ser Gln
 35 40 45
 Thr His Arg Cys Ser Pro Ala Trp Leu Ser Trp Asp Leu Asn Leu Leu
 50 55 60
 Val Lys Ser Phe Ser Leu Ser Glu Val Pro Ser Leu Gln Met Leu Asn
 65 70 75 80
 Leu Ala

<210> 5159
 <211> 3233
 <212> DNA
 <213> Homo sapiens

<400> 5159
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 120
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 180
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 240
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 cagcgagtgt gtttgaggat agtgagcgaa cagtttgtct gttcacggac atctgtccag
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480
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1380
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1980

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 2160
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 3120
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 3233

<210> 5160

<211> 849

<212> PRT

<213> Homo sapiens

<400> 5160

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 20 25 30
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35 40 45
 Tyr Ala Met Val Asp Pro Glu Asp Ile Ser Ile Thr Glu Leu Tyr Arg
 50 55 60
 Leu Ser Met Leu Ile Met Phe Leu Leu Gly Gly Val Ile Gln Met Glu
 65 70 75 80
 His Arg His Arg Lys Lys Asp Thr Pro Val Gln Ala Ser Ser His His
 85 90 95
 Leu Phe Val Gln Met Lys Ser Leu Met Cys Ser Asn Leu Gly Glu Glu
 100 105 110
 Leu Glu Val Ile Phe Ser Leu Phe Asp Ser Lys Glu Asn Arg Pro Ile
 115 120 125
 Ser Glu Arg Phe Phe Leu Arg Leu Asn Arg Asn Gly Leu Pro Lys Ala
 130 135 140
 Pro Asp Lys Pro Glu Arg His Cys Ser Leu Phe Val Asp Leu Gly Ser
 145 150 155 160
 Ser Glu Leu Arg Lys Asp Ile Tyr Ile Thr Val His Ile Ile Arg Ile
 165 170 175
 Gly Arg Met Gly Ala Gly Glu Lys Lys Asn Ala Cys Ser Val Gln Tyr
 180 185 190
 Arg Arg Pro Phe Gly Cys Ala Val Leu Ser Ile Ala Asp Leu Leu Thr
 195 200 205
 Gly Glu Thr Lys Asp Asp Leu Ile Leu Lys Val Tyr Met Cys Asn Thr
 210 215 220
 Glu Ser Glu Trp Tyr Gln Ile His Glu Asn Ile Ile Lys Lys Leu Asn
 225 230 235 240
 Ala Arg Tyr Asn Leu Thr Gly Ser Asn Ala Gly Leu Ala Val Ser Leu
 245 250 255
 Gln Leu Leu His Gly Asp Ile Glu Gln Ile Arg Arg Glu Tyr Ser Ser
 260 265 270
 Val Phe Ser His Gly Val Ser Ile Thr Arg Lys Leu Gly Phe Ser Asn
 275 280 285
 Ile Ile Met Pro Gly Glu Met Arg Asn Asp Leu Tyr Ile Thr Ile Glu
 290 295 300
 Arg Gly Glu Phe Glu Lys Gly Gly Lys Ser Val Ala Arg Asn Val Glu
 305 310 315 320
 Val Thr Met Phe Ile Val Asp Ser Ser Gly Gln Thr Leu Lys Asp Phe
 325 330 335
 Ile Ser Phe Gly Ser Gly Glu Pro Pro Ala Ser Glu Tyr His Ser Phe
 340 345 350
 Val Leu Tyr His Asn Asn Ser Pro Arg Trp Ser Glu Leu Lys Leu
 355 360 365
 Pro Ile Pro Val Asp Lys Phe Arg Gly Ala His Ile Arg Phe Glu Phe
 370 375 380
 Arg His Cys Ser Thr Lys Glu Lys Gly Glu Lys Lys Leu Phe Gly Phe
 385 390 395 400
 Ser Phe Val Pro Leu Met Gln Glu Asp Gly Arg Thr Leu Pro Asp Gly
 405 410 415
 Thr His Glu Leu Ile Val His Lys Cys Glu Glu Asn Thr Asn Leu Gln
 420 425 430
 Asp Thr Thr Arg Tyr Leu Lys Leu Pro Phe Ser Lys Gly Ile Phe Leu
 435 440 445
 Gly Asn Asn Asn Gln Ala Met Lys Ala Thr Lys Glu Ser Phe Cys Ile
 450 455 460
 Thr Ser Phe Leu Cys Ser Thr Lys Leu Thr Gln Asn Gly Asp Met Leu

[illegible]

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<210> 5161
<211> 1645
<212> DNA
<213> Homo sapiens
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<400> 5161
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120
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180
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 1620
 aaaaaaaaaa aaaaaaaaaa aaaaa
 1645

<210> 5162
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 5162
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 Lys Thr Gly Leu Arg Leu Arg Lys Val Asp Gln Gly Leu Phe Val Gln
 35 40 45
 Leu Val Gln Ala Asn Thr Pro Ala Ser Leu Val Gly Leu Arg Phe Gly
 50 55 60
 Asp Gln Leu Leu Gln Ile Asp Gly Arg Asp Cys Ala Gly Trp Ser Ser
 65 70 75 80
 His Lys Ala His Gln Val Val Lys Lys Ala Ser Gly Asp Lys Ile Val
 85 90 95
 Val Val Val Arg Asp Arg Pro Phe Gln Arg Thr Val Thr Met His Lys
 100 105 110
 Asp Ser Met Gly His Val Gly Phe Val Ile Lys Lys Gly Lys Ile Val
 115 120 125
 Ser Leu Val Lys Gly Ser Ser Ala Ala Cys Asn Gly Leu Leu Thr Asn
 130 135 140
 His Tyr Val Cys Glu Val Asp Gly Gln Asn Val Ile Gly Leu Lys Asp
 145 150 155 160
 Lys Lys Ile Met Glu Ile Leu Ala Thr Ala Gly Asn Val Val Thr Leu
 165 170 175
 Thr Ile Ile Pro Ser Val Ile Tyr Glu His Met Val Lys Lys Leu Pro
 180 185 190
 Pro Val Leu Leu His His Thr Met Asp His Ser Ile Pro Asp Ala
 195 200 205

<210> 5163
 <211> 1187
 <212> DNA
 <213> Homo sapiens

<400> 5163
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 120
 tttttatttt taaatacatg tatagcatga gtgatggagc caaacacaag ttttgaagcc
 180
 aagctcttgg ttctgagaaa caggcccaac actgcacagt gtcatttcga gtcaacccaa
 240
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 300

gatggcagtt attacgaagg ggcgtttgtg gacggagaga tcacgggaga aggccgccgg
 360
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<210> 5164

<211> 213

<212> PRT

<213> Homo sapiens

<400> 5164

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 20 25 30
 Arg His Trp Ala Trp Ser Gly Asp Thr Phe Ser Gly Gln Phe Val Leu
 35 40 45
 Gly Glu Pro Gln Gly Tyr Gly Val Met Glu Tyr Lys Ala Gly Gly Cys
 50 55 60
 Tyr Glu Gly Glu Val Ser His Gly Met Arg Glu Gly His Gly Phe Leu
 65 70 75 80
 Val Asp Arg Asp Gly Gln Val Tyr Gln Gly Ser Phe His Asp Asn Lys
 85 90 95
 Arg His Gly Pro Gly Gln Met Leu Phe Gln Asn Gly Asp Lys Tyr Asp
 100 105 110
 Gly Asp Trp Val Arg Asp Arg Arg Gln Gly His Gly Val Leu Arg Cys
 115 120 125
 Ala Asp Gly Ser Thr Tyr Lys Gly Gln Trp His Ser Asp Val Phe Ser

130		135		140
Gly Leu Gly Ser Met	Ala His Cys Ser Gly Val Thr Tyr Tyr Gly Leu			
145	150		155	160
Trp Ile Asn Gly His Pro	Ala Glu Gln Ala Thr Arg Ile Val Ile Leu			
	165		170	175
Gly Pro Glu Val Met	Glu Val Ala Gln Gly Ser Pro Phe Ser Val Asn			
	180		185	190
Val Gln Leu Leu Gln Asp His	Gly Glu Ile Ala Lys Ser Lys His Leu			
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Gln Gly Glu Met Thr				
210				

<210> 5165

<211> 2370

<212> DNA

<213> Homo sapiens

<400> 5165

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 120
 actcacctga gcctgcagga cagatcagag atgcagctgc agagcgaagc cgacagggcg
 180
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 240
 gtgcgcaggt gcctgcagca acagtgtgaa cagactgtgc ggatcctgca tgccaagggt
 300
 gcccagaaat catacggaaa tgagaagcgg ttcttctgcc cccgcacctg tgtctacctc
 360
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 420
 gggcccacgg tctgcggtta catgggactg gacagcgcgt ccggcagcgc cactgagacg
 480
 cagaagctga atttcagca gcagccggac tccagggaat tcggctgcgc caagaccctg
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 660
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 840
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 960
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 1020
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 1080

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 1200
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 1260
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 1320
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 1380
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 1560
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 1680
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 1860
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 2040
 aagtttggga catttaccct ccaggcatct atgtcccttc ttgaagagaa aacacacagc
 2100
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 2160
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 2220
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 2280
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 2340
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 2370

<210> 5166

<211> 521

<212> PRT

<213> Homo sapiens

<400> 5166

Met Asp Pro Ala Gly Ala Ala Asp Pro Ser Val Pro Pro Asn Pro Leu
 1 5 10 15
 Thr His Leu Ser Leu Gln Asp Arg Ser Glu Met Gln Leu Gln Ser Glu

[illegible]

```

      450              455              460
Arg Ala Asp Gly Leu Phe Tyr Pro Ser Ala Phe Ser Phe Thr Tyr Thr
465              470              475              480
Pro Glu Tyr Ser Val Arg Pro Gly His Pro Gly Val Pro Glu Pro Ala
      485              490              495
Thr Asp Ala Asp Ala Leu Leu Glu Ser Ile His Gln Glu Phe Thr Arg
      500              505              510
Thr Asn Phe His Leu Phe Ile Gln Thr
      515              520

```

<210> 5167
 <211> 878
 <212> DNA
 <213> Homo sapiens

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<400> 5167
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120
ttggactgtg tgtctgcagac acaatatccc aggtctatga gaattgtcaat acagacttca
180
cgtgggaaat ggtgaggcaa taaggatcgt ttcccttgat gaaatggagc ttgcagaaga
240
aggcagggtc agtttgtggg agctctgggt ggaggtggag ggagtgcaatt ccaagctgag
300
ccaagctatg acacctgagt ttccctgcctc tgtgtcgcct cctgttttc cattcccggt
360
tttcagcttc acttgtgggc tgagagtcctc tgcgtgggtt atttttctgc ctttctcagg
420
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480
ggcatgatat gatgtatgta aaatgcttgg cacaagggtt ctcaccgaag tctggaggag
540
ctgtccaggg ttctggagac gaaacggagc ccgctgggaa ctgtcctgag ccccggtgct
600
gaaacagatc gcggttctct tctcggacct cccgagaggc gctgtccgga tatttggtgc
660
tcccaagcag tcagccctgc tgggtctctgc ttccagacc gtcaaaacttc gccatctctg
720
tccctttttg ggaaaatgtc catgcgccaa cctgcaaacc agcctcattc ccggcatccc
780
acgtccctca gaccacccct cctccacgc agctgcggga ctccccctct gtgtgcctca
840
cctgcttcca gtcttggttg cagatgcagg tgtcccg
878

```

<210> 5168
 <211> 199
 <212> PRT
 <213> Homo sapiens

```

<400> 5168
Met Pro Gly Met Arg Leu Val Cys Arg Leu Ala His Gly His Phe Pro

```

1	5	10	15
Lys Lys Gly Gln Arg Trp Arg Ser Leu Thr Val Trp Lys Ala Glu Thr			
	20	25	30
Ser Arg Ala Asp Cys Leu Gly Ala Pro Asn Ile Arg Thr Ala Pro Leu			
	35	40	45
Gly Arg Ser Glu Lys Arg Thr Ala Ile Cys Phe Ser Thr Gly Ala Gln			
	50	55	60
Asp Ser Ser Gln Arg Ala Pro Phe Arg Leu Gln Asn Pro Gly Gln Leu			
	65	70	75
Leu Gln Thr Ser Val Arg Asn Leu Val Pro Ser Ile Leu His Thr Ser			
	85	90	95
Tyr His Ala Ile Phe Asn Pro Arg Thr Trp Val Leu Leu Cys Pro Cys			
	100	105	110
Asp Ile Trp Gly Thr Gln Gly Pro Glu Lys Gly Arg Lys Ile Thr His			
	115	120	125
Ala Gly Thr Leu Ser Pro Gln Val Lys Leu Arg Thr Gly Asn Gly Lys			
	130	135	140
Gln Gly Gly Ser Thr Glu Ala Gly Asn Ser Gly Val Ile Ala Trp Leu			
	145	150	155
Ser Leu Glu Cys Thr Pro Ser Thr Ser Thr Gln Ser Ser Pro Gln Leu			
	165	170	175
Thr Leu Pro Ser Ser Ala Ser Ser Ile Ser Ser Arg Glu Thr Ile Leu			
	180	185	190
Ile Ala Ser Pro Phe Pro Thr			
195			

<210> 5169

<211> 609

<212> DNA

<213> Homo sapiens

<400> 5169

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120
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180
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240
gggtatgcgg cccctacct gacagtgttc agcgagaact ccatcgatgt gtttgacgtg
300
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360
ggctccctgt tcctctacgg cacogagaag gtcgcgctga cctacctcag gaaccagctg
420
gcagagaagg acgagttcga catcccgga ctcacgaca acagccggcg ccagctgttc
480
ctaccaaga gcaagcgccg cttctttttc cgcgtgtcgg aggagcagca gaagcagcag
540
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600
ttcaaccac
609

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<210> 5170
 <211> 203
 <212> PRT
 <213> Homo sapiens

<400> 5170
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 Ala Leu Gly Ala Gly Leu Val Pro Glu Leu Pro Pro Ser Arg Gly
 20 25 30
 Gly Leu Gly Glu Ala Leu Gly Ala Val Glu Leu Ser Leu Ser Glu Phe
 35 40 45
 Leu Leu Leu Phe Thr Thr Ala Gly Ile Tyr Val Asp Gly Ala Gly Arg
 50 55 60
 Lys Ser Arg Gly His Glu Leu Leu Trp Pro Ala Ala Pro Met Gly Trp
 65 70 75 80
 Gly Tyr Ala Ala Pro Tyr Leu Thr Val Phe Ser Glu Asn Ser Ile Asp
 85 90 95
 Val Phe Asp Val Arg Arg Ala Glu Trp Val Gln Thr Val Pro Leu Lys
 100 105 110
 Lys Val Arg Pro Leu Asn Pro Glu Gly Ser Leu Phe Leu Tyr Gly Thr
 115 120 125
 Glu Lys Val Arg Leu Thr Tyr Leu Arg Asn Gln Leu Ala Glu Lys Asp
 130 135 140
 Glu Phe Asp Ile Pro Asp Leu Thr Asp Asn Ser Arg Arg Gln Leu Phe
 145 150 155 160
 Leu Thr Lys Ser Lys Arg Arg Phe Phe Phe Arg Val Ser Glu Glu Gln
 165 170 175
 Gln Lys Gln Gln Arg Arg Glu Met Leu Lys Asp Pro Phe Val Arg Ser
 180 185 190
 Lys Leu Ile Ser Pro Pro Thr Asn Phe Asn His
 195 200

<210> 5171
 <211> 2060
 <212> DNA
 <213> Homo sapiens

<400> 5171
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 ctctagtgtc tgactttgag atgcattata tttttaacac ataaatgagg ggatccatat
 120
 cacattcttt cttgtggacc accaaattga aggttttctt gtaattcaca agcagcagct
 180
 ctccagcatc tctccgtagc ctgggtgaag tcccagaagc tgggtgtgcat cattttccaa
 240
 ggtggcagag ctgcttgc tcgagatcat tcctttgaga gaggagtaca agtgaagaaa
 300
 caaggagcca ctctctgtag gagcactgat gtgccttgtc cacactcccc tctgagcttt
 360
 actggttaaga gagctccgac tgaacatgct gagcagttga gcacttttcc atcagcaaca
 420

acagcgagga tggaaatgga aaggaaccga actaaaatgc atttcccttt gcagggcaga
480
gagctaagct cttaggaata gtgttataga aataagcacc ctaacttcaa ttccctgaaaa
540
gttggtgtaa tggagagaat tttggagttt cacttaatat ttcccatcgc gtcgccataa
600
ataagcttctc aggcgcctcct agaagagtcc cagcccaagg ctcgattaag gaccacactg
660
caggctctgag gctcactgct ctgagtcctg aacaccagag cctgcgagag agtgggtgata
720
acacatcatc tctgcaaaga ggaacctctc ccccgccgcg cacttcactc aggcctctac
780
tgagcagcaa ggacagcctg ggtttcaaat gccacttccc ctgctttagg gatccagggtg
840
tcttgatagc gtgacctgc tgaggcaagg tatcaactcc gagagtgact gagtcaactga
900
gcgtggcaca tgaacaaacg tcatgacaaa gattctctga gtgaagttaa caccacgtat
960
tttacccttg caaaaaaaa actggcaccc tgagttctaa ctacggacgg acgatatactt
1020
tgcctccaca ccagattcc tggaaatggc taacgtttcc tttctagggg aagggtcgag
1080
gaataactca gtgctagctt agcagctttg ttcagtccag atcagagctg ttaggtaaag
1140
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1320
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1380
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1440
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1500
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1560
ccacctacca gattctggaa atgcgctctt ctagaaaaag atggcgtttg tgggtgtctt
1620
cttttgaaag gaacagtaat ttgtgtggat attgttaaag tgtttaaaga atattttgac
1680
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1740
accctatttc actgttgttc aagtaaatct aaaccttgta gacaagttag tcacctgata
1800
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1860
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1920
tttaaatggt ttttatgtaa tagaaatcac gcaaaatag gaaggattta aaatatgtat
1980
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2040

aaaaaaaaa aaaaaaaaaa

2060

<210> 5172

<211> 104

<212> PRT

<213> Homo sapiens

<400> 5172

```

Met Leu Val Asn Gly Glu Asn Phe Gly Val Ser Leu Asn Ile Phe Pro
 1             5             10             15
Ser Val Ala Ile Asn Lys Ser Ser Gly Ala Pro Arg Arg Val Pro Ala
      20             25             30
Gln Gly Ser Ile Lys Asp His Thr Ala Gly Leu Arg Leu Thr Ala Leu
      35             40             45
Ser Pro Glu His Gln Ser Pro Ala Glu Ser Gly Asp Asn Thr Ser Ser
      50             55             60
Leu Gln Arg Gly Thr Ser Pro Pro Ala Ala Thr Ser Leu Arg Leu Leu
      65             70             75             80
Leu Ser Ser Lys Asp Ser Leu Gly Phe Lys Cys His Phe Pro Cys Phe
      85             90             95
Arg Asp Pro Gly Val Leu Ile Ala
      100

```

<210> 5173

<211> 557

<212> DNA

<213> Homo sapiens

<400> 5173

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120
tcacagtgtg acaggggagac aaatagacct gtcagtagat aacatgaaaa taattggact
180
atgtgctgca gacacaatat cccagggtcta tgagaatgtc aatacagact tcacgtggga
240
aatgggtgag caataaggat cgtttccctt gatgaaatgg agcttcgaga agaaggcagg
300
gtcagttgtg gggagctctg gttggaggtg gagggagtgc attccaagct ggaggagctg
360
tccaggggtt tggagactaa acggagcccc ctgggaactg tcctgagccc cgggtgctgaa
420
acagatcgcg gttctctctt cggacctccc gagaagcgct gtccggatat ttggtgctcc
480
caagcagtcg gccctgctgg ttctctgctt ccagaccggc aaacttcgcc gtctctgtcc
540
ctttctggga aaatggc
557

```

<210> 5174

<211> 93

<212> PRT

<213> Homo sapiens

<400> 5174

```

Met Glu Leu Ala Glu Gly Arg Val Ser Cys Gly Glu Leu Trp Leu
 1              5              10              15
Glu Val Glu Gly Val His Ser Lys Leu Glu Leu Ser Arg Val Leu
              20              25              30
Glu Thr Lys Arg Ser Pro Leu Gly Thr Val Leu Ser Pro Gly Ala Glu
              35              40              45
Thr Asp Arg Gly Ser Leu Leu Gly Pro Pro Glu Lys Arg Cys Pro Asp
              50              55              60
Ile Trp Cys Ser Gln Ala Val Ser Pro Ala Gly Leu Cys Phe Pro Asp
65              70              75              80
Arg Gln Thr Ser Pro Ser Leu Ser Leu Ser Gly Lys Met
              85              90

```

<210> 5175

<211> 272

<212> DNA

<213> Homo sapiens

<400> 5175

```

ccatggcagc tccagagacc aggtggagg gaaatcaccc cacgtcccg agcagagagc
60
ttcggagcca gccagcctca ctgtgcgtgg cccacaacag ctgtctccat gtgtcacgtg
120
agggtgtccc aacaccagggt agggcagcaa cgcccaagcc ctgcgccggc acagcctccc
180
agaggtcact gccatgccgc actgaccgga gagagggcag tggtagagagg tgcattgccac
240
cccaggcttg ttccgaaggc cennnnnncc nc
272

```

<210> 5176

<211> 90

<212> PRT

<213> Homo sapiens

<400> 5176

```

Met Ala Ala Pro Glu Thr Arg Trp Arg Gly Asn His Pro Thr Leu Pro
 1              5              10              15
Ser Arg Glu Leu Arg Ser Gln Pro Ala Ser Leu Cys Val Ala His Asn
              20              25              30
Ser Cys Leu His Val Ser Arg Glu Gly Cys Pro Thr Pro Gly Arg Ala
              35              40              45
Ala Thr Pro Thr Pro Ser Pro Gly Thr Ala Ser Gln Arg Ser Leu Pro
              50              55              60
Cys Arg Thr Asp Arg Glu Gly Ser Gly Glu Arg Cys Met Pro Pro
65              70              75              80
Gln Ala Cys Ser Glu Gly Pro Xaa Xaa Xaa
              85              90

```

<210> 5177

<211> 637

<212> DNA

<213> Homo sapiens

<400> 5177

```

ntcctagtga gtatcgagtt ggtcttatta tcgctgaac tgggagcett tgtttcctgc
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gtgtcgcagg aagtgcagtt tcgggtacag ccgctaccag agtcccttctc tcgcgaggcg
120
gaagaacccc gatcgcctgag gagcaagggg gcgctaggaa aggggaactgg gttgcgacgg
180
tccggcgaga gagagctggg gtgctggggg gcggggaagt tggggagcag aggccgcttg
240
gtgtccgagt agggtaagac cgcaccgacc cagtccgtta ggaaagaagg gaaacgaggc
300
aattgtcggg cggatccccg gacggagggc taaggttgtg tggaaggcgc tgcctcccg
360
atggcgacgg cagatactcc gggcccgccc tccagtggcc tctcgccgaa ggaagaaggg
420
gagcttgaag atggggaaat cagtgcagac gataataaca gccagatacg ggtcggagc
480
agcagcagca gcagcggcgg cgggctgtta ccctatccgc ggcaaggcc tcctcactcg
540
gcccgggggc gtggatctgg cggagcggt ggctcttctc cgtcatcgtc ctcttctcag
600
cagcagctga ggaatttctc acgctcgcgg caccgct
637

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<210> 5178

<211> 92

<212> PRT

<213> Homo sapiens

<400> 5178

```

Met Ala Thr Ala Asp Thr Pro Ala Pro Ala Ser Ser Gly Leu Ser Pro
1      5      10
Lys Glu Glu Gly Glu Leu Glu Asp Gly Glu Ile Ser Asp Asp Asp Asn
20     25     30
Asn Ser Gln Ile Arg Ser Arg Ser Ser Ser Ser Ser Gly Gly Gly
35     40     45
Leu Leu Pro Tyr Pro Arg Arg Arg Pro Pro His Ser Ala Arg Gly Gly
50     55     60
Gly Ser Gly Gly Gly Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Gln
65     70     75     80
Gln Gln Leu Arg Asn Phe Ser Arg Ser Arg His Ala
85     90

```

<210> 5179

<211> 1527

<212> DNA

<213> Homo sapiens

<400> 5179

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ggaacacagg ccatgcgcgc tcctctctct tgggattacc accagtgcac ctggaactat
60

```

gaagttgagc cggatgtaaa agcagtggat gcaggggttg atgggcatga cattccttat
120
gatgccatgt ggctggacat agagcacact gagggaaga ggtacttcac ctgggacaaa
180
aacagattcc ctaaccccaa gaggatgcaa gagctgctca ggaacaaaaa gcgtaagctt
240
gtgggtcatca gtgatcccca catcaagatt gaacctgact actcagtata tgtgaagggc
300
aaagatcagg gcttctttgt gaagaatcag gaaggggaag actttgaagg ggtgtgttgg
360
ccagggtctct cctcttacct ggatttcacc aatcccaagg tcagagagtg gtattcaagt
420
ctttttgctt tccctgttta tcagggatct acggacatcc tcttcttttg gaatgacatg
480
aatgagcctt ctgtcttttag agggccagag caaacatgc agaagaatgc cattcatcat
540
ggcaattggg agcacagaga gctccacaac atctacggtt ttatcatca aatggctact
600
gcagaaggac tgataaaacg atctaaaggg aaggagagac cttttgttct tacacgttct
660
ttctttgctg gatcacaaaa gtatggtgac gtgtggacag gcgacaacac agcagaatgg
720
agcaacttga aaatttctat cccaatgtta ctactctca gcattactgg gatctctttt
780
tgcgaggctg acataggcgg gttcattggg aatccagaga cagagctgct agtgcgttgg
840
taccaggctg gagcctacca gcccttcttc cgtggccatg ccaccatgaa caccaagcga
900
cgagagccct ggctcttttg ggaggaacac acccgactca tccgagaagc catcagagag
960
cgctatggcc tcctgccata ttggtattct ctgttctacc atgcacacgt ggcttccaa
1020
cctgtcatga ggctctctgt ggtagagtgc cctgatgaac taaagacttt tgatatggaa
1080
gatgaatata tgctggggag tgcattattg gtcatccag tcacagaacc aaaagccacc
1140
acagttgatg tgtttcttcc aggatcaaat gaggtctggt atgactataa gacatttgc
1200
cattgggaag gaggggtgac tgtaaagatc ccagtgcct tggacactat tccagtgttt
1260
cagcgagggtg gaagtgtgat accaataaag acaactgtag gaaaaaccac aggctggatg
1320
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1380
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1500
cccagcaagt gtgtggtgga gaagatc
1527

<210> 5180

<211> 444

<212> PRT

<213> Homo sapiens

<400> 5180

Gly Thr Gln Ala Met Pro Pro Pro Leu Ser Trp Asp Tyr His Gln Cys
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 Thr Trp Asn Tyr Glu Val Glu Pro Asp Val Lys Ala Val Asp Ala Gly
 20 25 30
 Phe Asp Gly His Asp Ile Pro Tyr Asp Ala Met Trp Leu Asp Ile Glu
 35 40 45
 His Thr Glu Gly Lys Arg Tyr Phe Thr Trp Asp Lys Asn Arg Phe Pro
 50 55 60
 Asn Pro Lys Arg Met Gln Glu Leu Leu Arg Asn Lys Lys Arg Lys Leu
 65 70 75 80
 Val Val Ile Ser Asp Pro His Ile Lys Ile Glu Pro Asp Tyr Ser Val
 85 90 95
 Tyr Val Lys Ala Lys Asp Gln Gly Phe Phe Val Lys Asn Gln Glu Gly
 100 105 110
 Glu Asp Phe Glu Gly Val Cys Trp Pro Gly Leu Ser Ser Tyr Leu Asp
 115 120 125
 Phe Thr Asn Pro Lys Val Arg Glu Trp Tyr Ser Ser Leu Phe Ala Phe
 130 135 140
 Pro Val Tyr Gln Gly Ser Thr Asp Ile Leu Phe Leu Trp Asn Asp Met
 145 150 155 160
 Asn Glu Pro Ser Val Phe Arg Gly Pro Glu Gln Thr Met Gln Lys Asn
 165 170 175
 Ala Ile His His Gly Asn Trp Glu His Arg Glu Leu His Asn Ile Tyr
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<211> 4961

<212> DNA

<213> Homo sapiens

<400> 5181

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<212> PRT

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 5184

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<212> DNA

<213> Homo sapiens

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120

cggtattccca tgagaaactc tctggatcta gttcctctac gtcacatgag tgtgcaaaca
180
ggagactaca agagttaa aatactggga ctgctggaga tttccctggc catatatagt
240
tcacttggtt cacagatctc actctgtcac ccagggtgga gtacagtggg gcgatctcaa
300
cttactgcaa cctccgcctc cgggttcaag cgattcgctt gcctctgcct tagctatgtc
360
cctttcagaa aaattctact tcaagagaag atttgggttc aggatgtctc ctggactgga
420
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480
agcgtttcag atcacatgta ccggtatggc gttatggcta tgggtatcaa agatgaccgt
540
cttaacaaag acncggaagc tatgaagcag ataaccagc tctaccaga ggacctcaga
600
aaggagctct atgaactttg ggaagagtac gagaccaat ctagtgcaga agccaaattt
660
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720
cacaaacctg ggagactgca agacttctat gattccacag cagggaaaatt caatcacctt
780
gagatagtcc agctgttttc tgaacttgag gcagaaagaa gcaactaat agctgcagct
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gccagtgage cacactcctg agacactctc taaattgctg cactcctgta acaaacatta
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960
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1020
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1080
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1140
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1200
ttgaataata gaaaatttca ttatgattgc ttttaagaac agattcttca gctgatttag
1260
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1320
tgcccttatte agatttactc tcttgagcca gattttgaat ttactgcag actgcttcag
1380
acttctaate ataggcttgt aaacctacta ataggctctg cccctcttcc caatactttt
1440
tgtcatttag agatataaac cggggcatat aaaaatgcaa cttgtattcc tttgtatatt
1500
tttccctgtc tgacttataa atcttgagac ctttattgta aaagcattta tcactcaggtg
1560
agaaatataa ataggaactg ggggtcattga gcctcaggta gggaatatat caaccggatt
1620
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1657

<211> 243
 <212> PRT
 <213> Homo sapiens

<400> 5186
 Met Arg Asn Ser Leu Asp Leu Val Pro Leu Arg His Met Ser Val Gln
 1 5 10 15
 Thr Gly Asp Tyr Lys Ser Leu Lys Ile Leu Gly Leu Leu Glu Ile Ser
 20 25 30
 Leu Ala Ile Tyr Ser Ser Leu Val Ser Gln Ile Ser Leu Cys His Pro
 35 40 45
 Gly Trp Ser Thr Val Val Arg Ser Gln Leu Thr Ala Thr Ser Ala Ser
 50 55 60
 Arg Phe Lys Arg Phe Ala Cys Leu Cys Leu Ser Tyr Val Pro Phe Arg
 65 70 75 80
 Lys Ile Leu Leu Gln Glu Lys Ile Trp Phe Gln Asp Val Ser Trp Thr
 85 90 95
 Gly Gly His Val Pro Arg Val Pro Arg Thr Gly Trp Val Tyr Arg Asn
 100 105 110
 Val Gln Arg Pro Glu Ser Val Ser Asp His Met Tyr Arg Met Ala Val
 115 120 125
 Met Ala Met Val Ile Lys Asp Asp Arg Leu Asn Lys Asp Xaa Glu Ala
 130 135 140
 Met Lys Gln Ile Thr Gln Leu Leu Pro Glu Asp Leu Arg Lys Glu Leu
 145 150 155 160
 Tyr Glu Leu Trp Glu Glu Tyr Glu Thr Gln Ser Ser Ala Glu Ala Lys
 165 170 175
 Phe Val Lys Gln Leu Asp Gln Cys Glu Met Ile Leu Gln Ala Ser Glu
 180 185 190
 Tyr Glu Asp Leu Glu His Lys Pro Gly Arg Leu Gln Asp Phe Tyr Asp
 195 200 205
 Ser Thr Ala Gly Lys Phe Asn His Pro Glu Ile Val Gln Leu Val Ser
 210 215 220
 Glu Leu Glu Ala Glu Arg Ser Thr Asn Ile Ala Ala Ala Ser Glu
 225 230 235 240
 Pro His Ser

<210> 5187
 <211> 1712
 <212> DNA
 <213> Homo sapiens

<400> 5187
 ntttgtctt gtcggctcct gtgtgttagga gggatttcgg cctgagagcg gcccaggag
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 attggcgacg gtgtgcgccg tgttttcggt ggcgggtgcc tgggctggtg ggaacagccg
 120
 cccgaaggaa gcaccatgat ttcggccgcg cagttgttgg atgagttaat gggccgggac
 180
 cgaaccttag ccccggaaga gaagcgcagc aacgtgcggt gggaccacga gacgctttgt
 240
 aaatattatc tctgtggttt ttgtcctgcg gaattgttca caaatacag ttctgatctt
 300

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ggtcggtgtg aaaaaattca tgatgaaaat ctacgaaaac agtatgagaa gagctctcgt
360
ttcatgaaa gttggtatga gagagatttt ttgcgatact tacagagctt acttgacagaa
420
gtagaacgta ggatcagacg aggcctatgct cgtttggcat tatctcaaaa ccagcagctt
480
tctggggcgc ctggcccaac agggcaaaaat gaagaaaaaa ttcaggttct aacagacaaa
540
attgatgtac ttctgcaaca gattgaagaa ttaggggtctg aaggaaaagt agaagaagcc
600
caggggatga tgaatttagt tgagcaatta aaagaagaga gagaactgct aagggtccaca
660
acgtcgacaa ttgaaagctt tgctgcacaa gaaaaacaaa tggaagtgtg tgaagtatgt
720
ggagcctttt taatagtagg agatgcccag tcccgggtag atgaccattt gatgggaaaa
780
caacacatgg gctatgccaa aattaaagct actgtagaag aattaaaga aaagttaagg
840
aaaagaaccg aagaacctga tcgtgatgag cgtctaaaaa aggagaagca agaagagaa
900
gaaagagaaa aagaacggga gagagaaaag gaagaaagag aaaggaaaag acgaagggaa
960
gaggaagaaa gagaaaaaga aagggtcgtg gacagagaaa gaagaaagag aagtcgttca
1020
cgaagtagac actcaagccg aacatcagac agaagatgca gcagggtctcg ggaccacaaa
1080
aggtcacgaa gtatagaaa gaggcggagc agaagtagag atcgacgaag aagcagaagc
1140
catgatcgat cagaagaaa acacagatct cgaagtcggg atcgaagaag atcaaaaagc
1200
cgggatcgaa agtcatataa gcacaggagc aaaagtcggg acagagaaca agatagaaaa
1260
tccaaggaga aagaaaagag gggatctgat gataaaaaaa gtagtgtgaa gtccggtagt
1320
cgagaaaagc agagtgaaga cacaacact gaatcgaagg aaagtgtac taagaatgag
1380
gtcaatggga ccagtgaaga cattaatctt gaagtgcagc gtaagtatgc acagatgaag
1440
atggaactaa gccgagtaag aagacataca aaagcctctt ctgaaggaaa agacagtgtg
1500
gtcctgcaaa acatttttagt gtacattgtt ttgtctcagc tatttttagt cagactcgtg
1560
ccccattag tgtgcctctt tggaaattat cgcgccattt tgtaatatag tcgccattga
1620
aaagttaatt atcctttttt tagggatttt gatgtcgttt cttttttttt ttaatacaaa
1680
ggttgaactg tttttttttt ccttttttgg tt
1712

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<210> 5188

<211> 489

<212> PRT

<213> Homo sapiens

<400> 5188

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Met Ile Ser Ala Ala Gln Leu Leu Asp Glu Leu Met Gly Arg Asp Arg
 1           5           10           15
Asn Leu Ala Pro Asp Glu Lys Arg Ser Asn Val Arg Trp Asp His Glu
          20           25           30
Ser Val Cys Lys Tyr Tyr Leu Cys Gly Phe Cys Pro Ala Glu Leu Phe
          35           40           45
Thr Asn Thr Arg Ser Asp Leu Gly Pro Cys Glu Lys Ile His Asp Glu
          50           55           60
Asn Leu Arg Lys Gln Tyr Glu Lys Ser Ser Arg Phe Met Lys Val Gly
65           70           75           80
Tyr Glu Arg Asp Phe Leu Arg Tyr Leu Gln Ser Leu Leu Ala Glu Val
          85           90           95
Glu Arg Arg Ile Arg Arg Gly His Ala Arg Leu Ala Leu Ser Gln Asn
          100          105          110
Gln Gln Ser Ser Gly Ala Ala Gly Pro Thr Gly Lys Asn Glu Glu Lys
          115          120          125
Ile Gln Val Leu Thr Asp Lys Ile Asp Val Leu Leu Gln Gln Ile Glu
          130          135          140
Glu Leu Gly Ser Glu Gly Lys Val Glu Glu Ala Gln Gly Met Met Lys
145          150          155          160
Leu Val Glu Gln Leu Lys Glu Glu Arg Glu Leu Leu Arg Ser Thr Thr
          165          170          175
Ser Thr Ile Glu Ser Phe Ala Ala Gln Glu Lys Gln Met Glu Val Cys
          180          185          190
Glu Val Cys Gly Ala Phe Leu Ile Val Gly Asp Ala Gln Ser Arg Val
          195          200          205
Asp Asp His Leu Met Gly Lys Gln His Met Gly Tyr Ala Lys Ile Lys
210          215          220
Ala Thr Val Glu Glu Leu Lys Glu Lys Leu Arg Lys Arg Thr Glu Glu
225          230          235          240
Pro Asp Arg Asp Glu Arg Leu Lys Lys Glu Lys Gln Glu Arg Glu Glu
          245          250          255
Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Lys Arg
          260          265          270
Arg Arg Glu Glu Glu Arg Glu Lys Glu Arg Ala Arg Asp Arg Glu
          275          280          285
Arg Arg Lys Arg Ser Arg Ser Arg Ser Arg His Ser Ser Arg Thr Ser
290          295          300
Asp Arg Arg Cys Ser Arg Ser Arg Asp His Lys Arg Ser Arg Ser Arg
305          310          315          320
Glu Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Ser Arg Ser His
          325          330          335
Asp Arg Ser Glu Arg Lys His Arg Ser Arg Ser Arg Asp Arg Arg Arg
          340          345          350
Ser Lys Ser Arg Asp Arg Lys Ser Tyr Lys His Arg Ser Lys Ser Arg
          355          360          365
Asp Arg Glu Gln Asp Arg Lys Ser Lys Glu Lys Glu Lys Arg Gly Ser
          370          375          380
Asp Asp Lys Lys Ser Ser Val Lys Ser Gly Ser Arg Glu Lys Gln Ser
385          390          395          400
Glu Asp Thr Asn Thr Glu Ser Lys Glu Ser Asp Thr Lys Asn Glu Val
          405          410          415
Asn Gly Thr Ser Glu Asp Ile Lys Ser Glu Val Gln Arg Lys Tyr Ala

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                420                425                430
Gln Met Lys Met Glu Leu Ser Arg Val Arg Arg His Thr Lys Ala Ser
                435                440                445
Ser Glu Gly Lys Asp Ser Val Val Leu Gln Asn Ile Leu Arg Tyr Ile
                450                455                460
Val Leu Ser Gln Leu Phe Cys Ser Arg Leu Val Pro Pro Leu Val Cys
465                470                475                480
Leu Phe Gly Asn Tyr Arg Pro His Leu
                485

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<210> 5189
 <211> 323
 <212> DNA
 <213> Homo sapiens

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<400> 5189
acgcgtgaag ggattacagg catgagccac tgcacctggc caggagaaat tgtttttata
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acgtatgaca aatgccttgag taattcctgg cttgaaagtg ggctcacaaat aaataactgg
120
aatccaaaaa taacaaaatg ttttagcaatt caggtaatgt caagcagtat tcaaacacat
180
gaagttaatc attccttaat tcctgtttat ttatatattca tttttgcttt ctttttactc
240
catgtgttat tcctacagaa gtcacaagtt aaatgttttt ggggaacttt gggggggggg
300
gacaaacatc catgtgctgc taa
323

```

<210> 5190
 <211> 100
 <212> PRT
 <213> Homo sapiens

```

<400> 5190
Met Ser His Cys Thr Trp Pro Gly Glu Ile Val Phe Ile Thr Tyr Asp
1                5                10                15
Lys Cys Leu Ser Asn Ser Trp Leu Glu Ser Gly Leu Thr Ile Asn Asn
20                25                30
Trp Asn Pro Lys Ile Thr Lys Cys Leu Ala Ile Gln Val Met Ser Ser
35                40                45
Ser Ile Gln Thr His Glu Val Asn His Ser Leu Ile Pro Val Tyr Leu
50                55                60
Tyr Phe Ile Phe Ala Phe Phe Leu Leu His Val Leu Phe Leu Gln Lys
65                70                75                80
Ser Gln Val Lys Cys Phe Trp Gly Thr Leu Gly Gly Gly Asp Lys His
85                90                95
Pro Cys Ala Ala
100

```

<210> 5191
 <211> 1632
 <212> DNA
 <213> Homo sapiens

<400> 5191
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60
cggtgcatcg gggagccct tcccaagccc cgcaaacacc tgcatgcaaa gaggcaggct
120
tccttctgac agcagataac atgtcgccgtg cggcgtcagc aagaggcgca tgcgccttgc
180
cgtgggagcg cgggtgcgca ggactggaac gcggttctc cttcttcccc gccccgcccc
240
gcttccggcg gaagcggcct caacaaggga aactttattg ttcccgtggg gcagtcgagg
300
atgtcgggtg attacgcggc ggggctgtcg cgtacgcgg acaagggcaa gtgcggcctc
360
ccggagatct tcgaccccc ggaggagctg gagcggaagg tgtgggaact ggcgaggctg
420
gtctggcagt cttccagtgt ggtgttccac acgggtgccg gcatcagcac tgcccttgcc
480
atccccgact tcaggggtcc ccacggagtc tggaccatgg aggagcgagg tctggcccc
540
aagttcgcaca ccaccttga gagcgcgcgg ccacgcaga ccacatggc gctggtgcag
600
ctggagcgcg tgggcctcct ccgcttctg gtcagccaga acgtggacgg gctccatgtg
660
cgctcaggct tccccaggga caaactggca gagctccacg ggaacatgtt tgtggaagaa
720
tgtgccaagt gtaagacgca gtacgtccga gacacagtcg tgggcaccat gggcctgaag
780
gccacggggc ggctctgcac cgtggctaag gcaagggggc tgcgagcctg caggggaggc
840
tgcgaggccc ctgaggactc tcctcagctt cctcattgca ggggagagct gagggaaccc
900
atcctagact gggaggactc cctgcccgc cgggacctgg cactcgccga tgaggccagc
960
aggaaacgcg acctgtccat cacgctgggt acatcgctgc agatccggcc cagcgggaac
1020
ctgcgctggt ctaccaagcg ccggggaggc cgcctgtgca tcgtcaacct cgagcccacc
1080
aagcacgacc gccatgtga cctccgcac catggctacg ttgacagagt catgaccgg
1140
ctcatgaagc acctggggct ggagatcccc gcctgggacg gccccgtgt gctggagagg
1200
gcgctgccac cctgccccg ccgcccacc cccaagctgg agcccaagga ggaatctccc
1260
acccggatca acggtctat cccgcgcggc cccaagcagg agccctgcgc ccagcacaac
1320
ggctcagagc ccgcagccc caaacgggag cggcccacca gccctgcccc ccacagacc
1380
cccaaaaggg ggctctggt gcggttccgg gaagaagcca cccccagag gtgacagctg
1440
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1500
ccctggtctc cagcttaaac aggagtgaac tcctctgtc ccaggggcct ccctctggg
1560

ccccctacag cccaccctac ccctcctcca tgggcccctgc aggaggggag accccaccttg
 1620
 aagtggggga tc
 1632

<210> 5192
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 5192
 Met Ser Val Asn Tyr Ala Ala Gly Leu Ser Pro Tyr Ala Asp Lys Gly
 1 5 10 15
 Lys Cys Gly Leu Pro Glu Ile Phe Asp Pro Pro Glu Glu Leu Glu Arg
 20 25 30
 Lys Val Trp Glu Leu Ala Arg Leu Val Trp Gln Ser Ser Ser Val Val
 35 40 45
 Phe His Thr Gly Ala Gly Ile Ser Thr Ala Ser Gly Ile Pro Asp Phe
 50 55 60
 Arg Gly Pro His Gly Val Trp Thr Met Glu Glu Arg Gly Leu Ala Pro
 65 70 75 80
 Lys Phe Asp Thr Thr Phe Glu Ser Ala Arg Pro Thr Gln Thr His Met
 85 90 95
 Ala Leu Val Gln Leu Glu Arg Val Gly Leu Leu Arg Phe Leu Val Ser
 100 105 110
 Gln Asn Val Asp Gly Leu His Val Arg Ser Gly Phe Pro Arg Asp Lys
 115 120 125
 Leu Ala Glu Leu His Gly Asn Met Phe Val Glu Glu Cys Ala Lys Cys
 130 135 140
 Lys Thr Gln Tyr Val Arg Asp Thr Val Val Gly Thr Met Gly Leu Lys
 145 150 155 160
 Ala Thr Gly Arg Leu Cys Thr Val Ala Lys Ala Arg Gly Leu Arg Ala
 165 170 175
 Cys Arg Gly Gly Cys Glu Ala Pro Glu Asp Ser Pro Gln Leu Pro His
 180 185 190
 Cys Arg Gly Glu Leu Arg Asp Thr Ile Leu Asp Trp Glu Asp Ser Leu
 195 200 205
 Pro Asp Arg Asp Leu Ala Leu Ala Asp Glu Ala Ser Arg Asn Ala Asp
 210 215 220
 Leu Ser Ile Thr Leu Gly Thr Ser Leu Gln Ile Arg Pro Ser Gly Asn
 225 230 235 240
 Leu Pro Leu Ala Thr Lys Arg Arg Gly Gly Arg Leu Val Ile Val Asn
 245 250 255
 Leu Gln Pro Thr Lys His Asp Arg His Ala Asp Leu Arg Ile His Gly
 260 265 270
 Tyr Val Asp Glu Val Met Thr Arg Leu Met Lys His Leu Gly Leu Glu
 275 280 285
 Ile Pro Ala Trp Asp Gly Pro Arg Val Leu Glu Arg Ala Leu Pro Pro
 290 295 300
 Leu Pro Arg Pro Pro Thr Pro Lys Leu Glu Pro Lys Glu Glu Ser Pro
 305 310 315 320
 Thr Arg Ile Asn Gly Ser Ile Pro Ala Gly Pro Lys Gln Glu Pro Cys
 325 330 335
 Ala Gln His Asn Gly Ser Glu Pro Ala Ser Pro Lys Arg Glu Arg Pro

```

          340          345          350
Thr Ser Pro Ala Pro His Arg Pro Pro Lys Arg Gly Pro Leu Val Arg
          355          360          365
Phe Arg Glu Glu Ala Thr Pro Gln Arg
          370          375

```

<210> 5193
 <211> 554
 <212> DNA
 <213> Homo sapiens

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<400> 5193
acgcgtccct tccccagggt ccaggcggac gtgtcccttc ccgaggttct aggcggacat
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gtcttttgag agggcctcag gttaacccac tactgtgtct gaatctgtcc cttccccaag
120
cagcagctct gtgtcccgcc atggccactg tggggcagag acacagcagg tccacatct
180
ctgtgccctg cagaccctgc agccctgggg atgctgggtc gggacggacc cctagatatc
240
acacagccga gaggtaggtc agcgctttaa gatgctgata ccgctgggtc agctcctgga
300
gcagaattct cagggtaggt ttccagcaac gcctcctggg agggtcagca ggggctgggg
360
tccgtggggg ggtctccggg aggtttgcct gtgtcaggcc tgtgtgctt ctggcggagg
420
cgcttgtcca gcctcatcca gcctggtgtc tccggtgcca cgcgtaaca ctttcagtgc
480
acgctcggga acgcgcctgg aaggccctgc cctgccccgc ccagggtcc agccagatgc
540
tgccagcacc cggg
554

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<210> 5194
 <211> 94
 <212> PRT
 <213> Homo sapiens

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<400> 5194
Met Leu Ile Pro Leu Val Gln Leu Leu Glu Asn Ser Gln Gly Gly
1          5          10          15
Phe Pro Ala Thr Pro Pro Gly Arg Val Ser Arg Gly Trp Gly Pro Trp
          20          25          30
Gly Gly Leu Arg Glu Val Cys Leu Cys Gln Ala Cys Ala Ala Ser Gly
          35          40          45
Gly Gly Ala Cys Pro Ala Ser Ser Ser Leu Val Ser Pro Val Pro Arg
          50          55          60
Ala Asn Thr Phe Ser Ala Arg Ser Gly Thr Arg Leu Glu Gly Pro Ala
65          70          75          80
Leu Pro Arg Pro Arg Leu Gln Pro Asp Ala Ala Ser Thr Arg
          85          90

```

<210> 5195
 <211> 964

<212> DNA
 <213> Homo sapiens

<400> 5195
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 ccagcctcgc ttcaatgctg ggaggctgac gtcttccttt ttgtctcttg cccagggcag
 120
 ctgcgggcgc tccagcggct gtgccacttc tacagcgccg tcatgcccag cgagggcccag
 180
 tgtgtcatct accatgagct ccagctctcc ctggcctgca aggtggccga caagggtgctg
 240
 gagggggcagc tcttgagagc catcagccag ctctacctgt ccctgggcac cgagcggggc
 300
 tacaaatccg cactggacta caccaaacga agtctgggga ttttcattga cctccagaag
 360
 aaagagaagg aggcgcagtc ctggctgcaa gcaggggaaga tctattacat cttgcggcag
 420
 agcgcagctgg tggacctcta catccagggt gcacagaacg tggccctgta cacaggcgac
 480
 cccaacctgg ggctggagct gtttgaggcg gctggagaca tcttctctga cggggcctgg
 540
 gagcgggaga aagctgtgtc cttctaccgg gaccgggccc tgccctggc agtgactacg
 600
 ggcaaccgca aggcggagct gcggctgtgc aacaagctgg tggcactgct ggccaacgctg
 660
 gaggagcccc aggagggctt ggagtttgcc cacatggccc tagcactcag catcactctg
 720
 ggggaccggc tgaacgagcg cgtggcctac caccggctgg ccgcctgca acaccgactg
 780
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 840
 ctggagtttg acgaggagac cctctactac gtgaagggtg acctgggtgct cggtgacatc
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 960
 gccg
 964

<210> 5196
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 5196
 Met Pro Ser Glu Ala Gln Cys Val Ile Tyr His Glu Leu Gln Leu Ser
 1 5 10 15
 Leu Ala Cys Lys Val Ala Asp Lys Val Leu Glu Gly Gln Leu Leu Glu
 20 25 30
 Thr Ile Ser Gln Leu Tyr Leu Ser Leu Gly Thr Glu Arg Ala Tyr Lys
 35 40 45
 Ser Ala Leu Asp Tyr Thr Lys Arg Ser Leu Gly Ile Phe Ile Asp Leu
 50 55 60
 Gln Lys Lys Glu Lys Glu Ala His Ala Trp Leu Gln Ala Gly Lys Ile

```

65          70          75          80
Tyr Tyr Ile Leu Arg Gln Ser Glu Leu Val Asp Leu Tyr Ile Gln Val
85
Ala Gln Asn Val Ala Leu Tyr Thr Gly Asp Pro Asn Leu Gly Leu Glu
100          105          110
Leu Phe Glu Ala Ala Gly Asp Ile Phe Phe Asp Gly Ala Trp Glu Arg
115          120          125
Glu Lys Ala Val Ser Phe Tyr Arg Asp Arg Ala Leu Pro Leu Ala Val
130          135          140
Thr Thr Gly Asn Arg Lys Ala Glu Leu Arg Leu Cys Asn Lys Leu Val
145          150          155          160
Ala Leu Leu Ala Thr Leu Glu Glu Pro Gln Glu Gly Leu Glu Phe Ala
165          170          175
His Met Ala Leu Ala Leu Ser Ile Thr Leu Gly Asp Arg Leu Asn Glu
180          185
Arg Val Ala Tyr His Arg Leu Ala Ala Leu Gln His Arg Leu Gly His
195          200          205
Gly Glu Leu Ala Glu His Phe Tyr Leu Lys Ala Leu Ser Leu Cys Asn
210          215          220
Ser Pro Leu Glu Phe Asp Glu Glu Thr Leu Tyr Tyr Val Lys Val Tyr
225          230          235          240
Leu Val Leu Gly Asp Ile Ile Phe Tyr Asp Leu Lys Asp Pro Phe Asp
245          250          255
Ala Ala Gly Tyr Tyr Gln Leu Ala Leu Ala Ala
260          265

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<210> 5197

<211> 1045

<212> DNA

<213> Homo sapiens

<400> 5197

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natgttggtc aggctgggtc caaactcctg acctcgtgat cgcgccacct cagcctcgca
60
aagtgtctggg attacaggcg tgagccacca tgttggtcag tctggtctca nactcctgtc
120
ctcatgatcc gccacaccca ccctcgcaaa gtgctgggat tacaggcatg agccaccacg
180
tcgggccacc actgaactttt tcattctttc tcattcttcc tgggcccctcc tgctgttgta
240
ggcccccatg aagaagtgga ctattctgag aaactgaagt tcagtgatga tgaagaggag
300
gaagaagtgtg tgaaggacgg caggccaaa tggaacagtt gggaccctag gaggcagcgg
360
cagttgtcaa tgagctctgc agacagtgcg gacgctaagc ggactcgaga ggaagggaag
420
gactgggctg aagcagtggtg tgcgtcccg gtggtccgaa aggcgcgaga ccctcagcca
480
cgcgccagga agcttcatgg ctgggcacca ggccttgact accagaagtc atcaatgggc
540
agcatgttcc ggcaacagtc catcgaggac aaggaggaca agccccacc aaggcagaag
600
ttcattcagt cagagatgtc cgaggcggtg gagcgagccc gaaagcgccg ggaagaagag
660

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gagcgccgag cccgggagga gaggctggcc gcctgtgctg ccaaactcaa gcagctggac
 720
 cagaagtgtg agcaggcacg aaaggcaggt gaggcccgga agcaggcaga gaaggaagtg
 780
 ccctggctct caagtgtctg gaaggcatct cccaggagaa acggccctgc tgtccacaaa
 840
 ggctccccag aattccctgc ccaagagacc cccaccacat tcccagaaga ggcaccaca
 900
 gtgtccccag cagtggcaca gagcaacagc agtgaggaag aggccagaga ggctgggtcc
 960
 cctgcacagg agttcaagta tcagaagtcc cttcctcccc gattccagcg ccagcagcag
 1020
 caacaacagc aggagcagct gtaca
 1045

<210> 5198

<211> 283

<212> PRT

<213> Homo sapiens

<400> 5198

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Thr	Pro	Thr	Thr	Phe	Pro	Glu	Glu	Ala	Pro	Thr	Val	Ser	Pro	Ala	Val	
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Ala	Gln	Ser	Asn	Ser	Ser	Glu	Glu	Glu	Ala	Arg	Glu	Ala	Gly	Ser	Pro	
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<210> 5199
 <211> 1332
 <212> DNA
 <213> Homo sapiens

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1332

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<211> 358

<212> PRT

<213> Homo sapiens

<400> 5200

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Arg Ser Leu Lys Asp Ser Leu Asp His Phe His Val Asn Glu Glu Glu
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Ile Asn Cys Leu Ser Leu Asn Gln Thr Glu Asn Leu Leu Ala Ser Ala
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Val Met Leu Trp Ser Leu Gln Lys Ala Arg Pro Leu Trp Ile Thr Asn
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Leu Gln Glu Asp Glu Thr Glu Glu Met Glu Gly Pro Gln Ser Pro Gly
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Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys
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355

<210> 5201

<211> 6104

<212> DNA

<213> Homo sapiens

<400> 5201

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<211> 108

<212> PRT

<213> Homo sapiens

<400> 5202

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Ser Gln Gly Ser Leu Glu Arg Gly Leu Ala Gly Leu Gly Gly His Arg
      35           40           45
Pro His Ser Gly Leu Pro Ala Gln Gly Arg Arg Pro Glu Pro Val Trp
      50           55           60
Pro Cys Ser Pro Gly Gln Ser Trp Ala Cys Arg Val Phe Leu Pro Gly
65           70           75           80
Arg Cys Arg Cys Trp Pro Ser Ala Gly Gly Arg Arg Trp Glu Ser Trp
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<210> 5203

<211> 1863

<212> DNA

<213> Homo sapiens

<400> 5203

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<210> 5204

<211> 249

<212> PRT

<213> Homo sapiens

<400> 5204

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 Glu Arg Lys His Leu Asp Leu Lys Glu Val Ala Ile Lys Gln Phe Arg
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Asn	Asp	Gly	Lys	Asn	Ile	Phe	Tyr	Ala	Ala	Arg	Thr	Pro	Ala	Thr	Leu
	130		135		140										
Phe	Ala	Val	Met	Phe	Ala	Met	Tyr	Ile	Ile	Ser	Gly	Leu	Thr	Gly	Phe
	145		150		155										160
Ile	Gly	Leu	Asn	Ser	Ile	Ala	Val	Leu	Cys	Asn	Leu	Val	Met	Gly	Leu
			165		170										175
Ala	Leu	Ile	Phe	Leu	Cys	Thr	Trp	Ala	Tyr	Val	Lys	Tyr	Ser	Gly	Glu
			180		185										190
Phe	Arg	Glu	Ile	Gly	Thr	Val	Ile	Asp	Gln	Ile	Ala	Glu	Thr	Leu	Trp
	195		200												205
Glu	Gln	Val	Leu	Lys	Pro	Leu	Gly	Asp	Asn	Leu	Met	Glu	Glu	Asn	Ile
	210		215												220
Arg	Gln	Ser	Val	Thr	Asn	Ser	Ile	Lys	Ala	Gly	Leu	Thr	Asp	Gln	Val
	225		230		235										240
Ser	His	His	Ala	Arg	Leu	Lys	Thr	Asp							
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<210> 5205

<211> 2011

<212> DNA

<213> Homo sapiens

<400> 5205

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 gccaaaggcct ttcgggtcaa gtccaacacg gccatcaagg ggtcggacag gagaagctt
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 420
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 660
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 720
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 780
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 840

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 1860
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 1920
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 1980
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 2011

<210> 5206

<211> 248

<212> PRT

<213> Homo sapiens

<400> 5206

His Ser Leu Ala Ser Val Leu Ser Ser Pro Gly His Pro Ser Arg His
 1 5 10 15
 Val Ala Lys Ala Phe Arg Val Lys Ser Asn Thr Ala Ile Lys Gly Ser
 20 25 30
 Asp Arg Arg Lys Leu Arg Ala Asp Val Thr Thr Ala Phe Pro Thr Leu
 35 40 45
 Gly Thr Asp Gln Val Ser Glu Leu Val Pro Gly Lys Glu Glu Leu Asn

```

      50              55              60
Ile Val Lys Leu Tyr Ala His Lys Gly Asp Ala Val Thr Val Tyr Val
65              70              75              80
Ser Gly Gly Asn Pro Ile Leu Phe Glu Leu Glu Lys Asn Leu Tyr Pro
      85              90              95
Thr Val Tyr Thr Leu Trp Ser Tyr Pro Asp Leu Leu Pro Thr Phe Thr
      100              105              110
Thr Trp Pro Leu Val Leu Glu Lys Leu Val Gly Gly Ala Asp Leu Met
      115              120              125
Leu Pro Gly Leu Val Met Pro Pro Ala Gly Leu Pro Gln Val Gln Lys
      130              135              140
Gly Asp Leu Cys Ala Ile Ser Leu Val Gly Asn Arg Ala Pro Val Ala
145              150              155              160
Ile Gly Val Ala Ala Met Ser Thr Ala Glu Met Leu Thr Ser Gly Leu
      165              170              175
Lys Gly Arg Gly Phe Ser Val Leu His Thr Tyr Gln Asp His Leu Trp
      180              185              190
Arg Ser Gly Asn Lys Ser Ser Pro Pro Ser Ile Ala Pro Leu Ala Leu
      195              200              205
Asp Ser Ala Asp Leu Ser Glu Glu Lys Gly Ser Val Gln Met Asp Ser
      210              215              220
Thr Leu Gln Gly Asp Met Arg His Met Thr Leu Glu Gly Glu Glu Glu
225              230              235              240
Asn Gly Glu Val His Gln Gly Thr
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<210> 5207

<211> 594

<212> DNA

<213> Homo sapiens

<400> 5207

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120
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180
ggaggcatgg tctccacctc cgggttgccc gtgctggggg cgcgaggtgt gggcaagagt
240
gccatgctgc gccagtcttt gtacaacgag ttcagcgagg tctcgctccc caccaccgcc
300
cgccgccttt acctgctctg tctgctcatg aacggccacg tgcacgacct ccagatcctc
360
gactttccac ccatcagcgc ctccctctgc aatacgtccc aggagtgggc agacacctgc
420
tgcaggggac tccggagtgt ccacgcctac atcctggtct acgacatctg ctgctttgac
480
agctttgagt acgtcaagac catccgccag cagatcctgg agacgagggg gatcgggaacc
540
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594

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<210> 5208

<211> 136

<212> PRT

<213> Homo sapiens

<400> 5208

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Met Val Ser Thr Tyr Arg Val Ala Val Leu Gly Ala Arg Gly Val Gly
 1           5           10           15
Lys Ser Ala Ile Val Arg Gln Phe Leu Tyr Asn Glu Phe Ser Glu Val
      20           25           30
Cys Val Pro Thr Thr Ala Arg Arg Leu Tyr Leu Pro Ala Val Val Met
      35           40           45
Asn Gly His Val His Asp Leu Gln Ile Leu Asp Phe Pro Pro Ile Ser
      50           55           60
Ala Phe Pro Val Asn Thr Leu Gln Glu Trp Ala Asp Thr Cys Cys Arg
65           70           75           80
Gly Leu Arg Ser Val His Ala Tyr Ile Leu Val Tyr Asp Ile Cys Cys
      85           90           95
Phe Asp Ser Phe Glu Tyr Val Lys Thr Ile Arg Gln Gln Ile Leu Glu
      100          105          110
Thr Arg Val Ile Gly Thr Ser Glu Thr Pro Ile Ile Val Gly Asn
      115          120          125
Lys Arg Asp Leu Gln Arg Gly Arg
      130          135

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<210> 5209

<211> 1592

<212> DNA

<213> Homo sapiens

<400> 5209

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120
ctgagccggc tcactggctc ccgagcctct ggggcccaac tcgaggccaa ggtgcgaggg
180
ctggaacgcc aggtggagga gctgcgctgg cgccagaggc gagcgcccaa gggggcccgc
240
agtgtggagg aggagtgagc cggatgcccc acacaccgcc agtgtcatac caaagagctg
300
agctgcttgc gggccatgca gccctcctgc cagccccctg cccttttctt gcctgtctc
360
tgaaccttca gaacattgat ccttgccgca gccccactag ccaagagaaa cagagaaaga
420
ccattccccc tgcctgtcct tcgggccctg tcttctgagg ttctctgtct ggggttggtc
480
ctcttaaccc tttctctgct ccagcctgc ctcaccaggg aaggttgagg gggcctccct
540
ctggcttctg catctgcgcc agcaaacatc actgccgttg gtctctcatg acttaactgg
600
cttccctctg ctgctgcctt ggcttctctc taatgctcgt gctctcctgt ccttctgaag
660
ttgctccttg gccaaatctc cagctccctt cttgttttcc tcatcctcct accctgtact
720

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```

cccacaaac catggtcctt taaggcacgc tcctgtcctc ctcattgccc agcagtaggg
780
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840
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900
cagcaggggcc ttctgcttgc ctgctgccat actgtatgta ggaagtgtt ctgtggctgc
960
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1320
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1380
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1440
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1560
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1592

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<210> 5210
<211> 85
<212> PRT
<213> Homo sapiens

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<400> 5210
Ile Leu Trp Gly Leu Lys Leu Val Ile Phe Leu Ala Gly Phe Val Ala
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Leu Met Arg Ser Val Pro Asp Pro Ser Thr Arg Ala Leu Leu Leu
20 25 30
Ala Leu Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser Arg
35 40 45
Ala Ser Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg Gln
50 55 60
Val Glu Glu Leu Arg Trp Arg Gln Arg Arg Ala Lys Gly Ala Arg
65 70 75 80
Ser Val Glu Glu Glu
85

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<210> 5211
<211> 602
<212> DNA
<213> Homo sapiens

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<400> 5211
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120
gcacaggacc agacaacaag tttttaaaaa tgatgccaga gcattagaag cagccagaat
180
aaagataaat gaagaattca aaaataataa aagtgaact tcttctaaga aaatagaaga
240
gctaattgaaa ataggttctg atgttgaatt attactcaga acatctgtta tacaagggtat
300
tcacacagac cacaatacac tgaaactggt ccctaggaaa gaccttcttg tagaaaaatgt
360
gccatattgt gatgcaccaa ctccagaagca atgagtttct tagaatacaa caagtctttg
420
tactttttaa ctttaaaatc tacaactctg gcaaaagtcc tggaaatgca gacattttcc
480
ctgaactggc atattgaaaa tgaatgaatt acagaatagc ttcattattta aatttcctgt
540
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600
ag
602

```

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<210> 5212
<211> 104
<212> PRT
<213> Homo sapiens

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<400> 5212
Met Gly Arg Ala Val Lys Val Leu Gln Leu Phe Lys Thr Leu His Arg
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Thr Arg Gln Gln Val Phe Lys Asn Asp Ala Arg Ala Leu Glu Ala Ala
20 25 30
Arg Ile Lys Ile Asn Glu Glu Phe Lys Asn Asn Lys Ser Glu Thr Ser
35 40 45
Ser Lys Lys Ile Glu Glu Leu Met Lys Ile Gly Ser Asp Val Glu Leu
50 55 60
Leu Leu Arg Thr Ser Val Ile Gln Gly Ile His Thr Asp His Asn Thr
65 70 75 80
Leu Lys Leu Val Pro Arg Lys Asp Leu Leu Val Glu Asn Val Pro Tyr
85 90 95
Cys Asp Ala Pro Thr Gln Lys Gln
100

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<210> 5213
<211> 4387
<212> DNA
<213> Homo sapiens

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<400> 5213
nnccgcggag ctacggtttc ctccagaggt ctccgccctc ctgccctat attcccagaa
60

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cccgagtcgt atccgggcct tgccgggcac cctggaaagg cgggggtgat agtacagatg
120
gagacgcaac tgcagagcat ttctgaagag gtggtgaaaa cggaggttat agaagaggct
180
tttcttgcca tgtttatgga tactcctgaa gatgagaaaa caaaactaat tagctgtttg
240
ggggccttca gacagttttg ggggtggactt tctcaggagt ctcataaaca gtgtatccag
300
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360
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420
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480
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540
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1680

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 4387

<210> 5214

<211> 1364

<212> PRT

<213> Homo sapiens

<400> 5214

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 Val Ile Glu Glu Ala Phe Pro Gly Met Phe Met Asp Thr Pro Glu Asp
 20 25 30
 Glu Lys Thr Lys Leu Ile Ser Cys Leu Gly Ala Phe Arg Gln Phe Trp
 35 40 45
 Gly Gly Leu Ser Gln Glu Ser His Glu Gln Cys Ile Gln Trp Ile Val
 50 55 60
 Lys Phe Ile His Gly Gln His Ser Pro Lys Arg Ile Ser Phe Leu Tyr

```

65          70          75          80
Asp Cys Leu Ala Met Ala Val Glu Thr Gly Leu Pro Pro Arg Leu
      85          90          95
Val Cys Glu Ser Leu Ile Asn Ser Asp Thr Leu Glu Trp Glu Arg Thr
      100          105          110
Gln Leu Trp Ala Leu Thr Phe Lys Leu Val Arg Lys Ile Ile Gly Gly
      115          120          125
Val Asp Tyr Lys Gly Val Arg Asp Leu Leu Lys Val Ile Leu Glu Lys
      130          135          140
Ile Leu Thr Ile Pro Asn Thr Val Ser Ser Ala Val Val Gln Gln Leu
      145          150          155          160
Leu Ala Ala Arg Glu Val Ile Ala Tyr Ile Leu Glu Arg Asn Ala Cys
      165          170          175
Leu Leu Pro Ala Tyr Phe Ala Val Thr Glu Ile Arg Lys Leu Tyr Pro
      180          185          190
Glu Gly Lys Leu Pro His Trp Leu Leu Gly Asn Leu Val Ser Asp Phe
      195          200          205
Val Asp Thr Phe Arg Pro Thr Ala Arg Ile Asn Ser Ile Cys Gly Arg
      210          215          220
Cys Ser Leu Leu Pro Val Val Asn Asn Ser Gly Ala Ile Cys Asn Ser
      225          230          235          240
Trp Lys Leu Asp Pro Ala Thr Leu Arg Phe Pro Leu Lys Gly Leu Leu
      245          250          255
Pro Tyr Asp Lys Asp Leu Phe Glu Pro Gln Thr Ala Leu Leu Arg Tyr
      260          265          270
Val Leu Glu Gln Pro Tyr Ser Arg Asp Met Val Cys Asn Met Leu Gly
      275          280          285
Leu Asn Lys Gln His Lys Gln Arg Cys Pro Val Leu Glu Asp Gln Leu
      290          295          300
Val Asp Leu Val Val Tyr Ala Met Glu Arg Ser Glu Thr Glu Glu Lys
      305          310          315          320
Phe Asp Asp Gly Gly Thr Ser Gln Leu Leu Trp Gln His Leu Ser Ser
      325          330          335
Gln Leu Ile Phe Phe Val Leu Phe Gln Phe Ala Ser Phe Pro His Met
      340          345          350
Val Leu Ser Leu His Gln Lys Leu Ala Gly Arg Gly Leu Ile Lys Gly
      355          360          365
Arg Asp His Leu Met Trp Val Leu Leu Gln Phe Ile Ser Gly Ser Ile
      370          375          380
Gln Lys Asn Ala Leu Ala Asp Phe Leu Pro Val Met Lys Leu Phe Asp
      385          390          395          400
Leu Leu Tyr Pro Glu Lys Glu Tyr Ile Pro Val Pro Asp Ile Asn Lys
      405          410          415
Pro Gln Ser Thr His Ala Phe Ala Met Thr Cys Ile Trp Ile His Leu
      420          425          430
Asn Arg Lys Ala Gln Asn Asp Asn Ser Lys Leu Gln Ile Pro Ile Pro
      435          440          445
His Ser Leu Arg Leu His His Glu Phe Leu Gln Gln Ser Leu Arg His
      450          455          460
Lys Ser Leu Gln Met Asn Asp Tyr Lys Ile Ala Leu Leu Cys Asn Ala
      465          470          475          480
Tyr Ser Thr Asn Ser Glu Cys Val Thr Leu Pro Met Gly Ala Leu Val
      485          490          495
Glu Thr Ile Tyr Gly Asn Gly Ile Met Arg Leu Pro Leu Pro Gly Thr

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 Thr Arg Val Ile Lys Leu Ala His Ala Lys Ser Val Ala Leu Ala
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 Pro Ala Leu Val Glu Thr Tyr Ser Arg Leu Leu Val Tyr Met Glu Ile
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 Glu Ser Leu Gly Ile Lys Gly Phe Ile Ser Gln Leu Leu Pro Thr Val
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 Phe Lys Ser His Ala Trp Gly Ile Leu His Thr Leu Leu Glu Met Phe
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 Ser Tyr Arg Met His His Ile Gln Pro His Tyr Arg Val Gln Leu Leu
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 Ser His Leu His Thr Leu Ala Ala Val Ala Gln Thr Asn Gln Asn Gln
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 Gly Pro Leu Gln Ala Phe Phe Lys Gln Asn Asn Val Pro Gln Glu Ser
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 770 775 780
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 Val Cys Tyr Phe Ile Ile Gln Leu Leu Leu Lys Pro Asn Asp Phe
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 965 970 975
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 Arg Cys Met Ile Glu Ile Gly Val Ala Phe Tyr Asp Met Leu Leu Asn
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 Val Asp Gln Cys Ser Thr His Leu Asn Tyr Met Asp Pro Ile Cys Asp
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<210> 5215
 <211> 548
 <212> DNA
 <213> Homo sapiens

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<210> 5216
 <211> 83
 <212> PRT
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 35 40 45
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<210> 5217
 <211> 4189
 <212> DNA
 <213> Homo sapiens

<400> 5217

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<210> 5218
 <211> 541
 <212> PRT
 <213> Homo sapiens

<400> 5218
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 35 40 45
 Ser Pro Gly Ala Ala Pro Gly Thr Leu Cys Cys Phe Leu Trp Pro Arg
 50 55 60
 Val Gly Thr Gly Leu Cys Pro Gly Leu Ser Leu Pro Gln Pro His Leu
 65 70 75 80
 Pro His Cys Gln Pro Gln Ser Leu Pro Ala Xaa Ala Arg Val Leu Ser
 85 90 95
 Ser Ser Glu Thr Pro Ala Arg Thr Leu Pro Phe Thr Thr Gly Leu Ile
 100 105 110
 Tyr Asp Ser Val Met Leu Lys His Gln Cys Ser Cys Gly Asp Asn Ser

115 120 125
 Arg His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg Leu
 130 135 140
 Gln Glu Arg Gly Leu Arg Ser Gln Cys Glu Cys Leu Arg Gly Arg Lys
 145 150 155 160
 Ala Ser Leu Glu Glu Leu Gln Ser Val His Ser Glu Arg His Val Leu
 165 170 175
 Leu Tyr Gly Thr Asn Pro Leu Ser Arg Leu Lys Leu Asp Asn Gly Lys
 180 185 190
 Leu Ala Gly Leu Leu Ala Gln Arg Met Phe Val Met Leu Pro Cys Gly
 195 200 205
 Gly Val Gly Val Asp Thr Asp Thr Ile Trp Asn Glu Leu His Ser Ser
 210 215 220
 Asn Ala Ala Arg Trp Ala Ala Gly Ser Val Thr Asp Leu Ala Phe Lys
 225 230 235 240
 Val Ala Ser Arg Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
 245 250 255
 Gly His His Ala Asp His Ser Thr Ala Met Gly Phe Cys Phe Phe Asn
 260 265 270
 Ser Val Ala Ile Ala Cys Arg Gln Leu Gln Gln Ser Lys Ala Ser
 275 280 285
 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Ala Thr Gln
 290 295 300
 Gln Thr Phe Tyr Gln Asp Pro Ser Val Leu Tyr Ile Ser Leu His Arg
 305 310 315 320
 His Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Val Asp Glu Val
 325 330 335
 Gly Ala Gly Ser Gly Glu Gly Phe Asn Val Asn Val Ala Trp Ala Gly
 340 345 350
 Gly Leu Asp Pro Pro Met Gly Asp Pro Glu Tyr Leu Ala Ala Phe Arg
 355 360 365
 Ile Val Val Met Pro Ile Ala Arg Glu Phe Ser Pro Asp Leu Val Leu
 370 375 380
 Val Ser Ala Gly Phe Asp Ala Ala Glu Gly His Pro Ala Pro Leu Gly
 385 390 395 400
 Gly Tyr His Val Ser Ala Lys Cys Phe Gly Tyr Met Thr Gln Gln Leu
 405 410 415
 Met Asn Leu Ala Gly Gly Ala Val Val Leu Ala Leu Glu Gly Gly His
 420 425 430
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ala Ala Leu
 435 440 445
 Leu Gly Asn Arg Val Asp Pro Leu Ser Glu Glu Gly Trp Lys Gln Lys
 450 455 460
 Pro Asn Leu Asn Ala Ile Arg Ser Leu Glu Ala Val Ile Arg Val His
 465 470 475 480
 Ser Lys Tyr Trp Gly Cys Met Gln Arg Leu Ala Ser Cys Pro Asp Ser
 485 490 495
 Trp Val Pro Arg Val Pro Gly Ala Asp Lys Glu Glu Val Glu Ala Val
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<210> 5219
<211> 1212
<212> DNA
<213> Homo sapiens

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<210> 5220
<211> 179
<212> PRT
<213> Homo sapiens

<400> 5220

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 35           40           45
Glu Pro Ser Ser Pro Asn Ala Ala Val Pro Glu Ala Ile Pro Thr Pro
 50           55           60
Arg Ala Ala Ala Ser Ala Ala Leu Glu Leu Pro Leu Gly Pro Ala Pro
 65           70           75           80
Val Ser Val Ala Pro Gln Ala Glu Ala Glu Ala Arg Ser Thr Pro Gly
 85           90           95
Pro Ala Gly Ser Arg Leu Gly Pro Glu Thr Phe Arg Gln Arg Phe Arg
100           105           110
Gln Phe Arg Tyr Gln Asp Ala Ala Gly Pro Arg Glu Ala Phe Arg Gln
115           120           125
Leu Arg Glu Leu Ser Arg Gln Trp Leu Arg Pro Asp Ile Arg Thr Lys
130           135           140
Glu Gln Ile Val Glu Met Leu Val Gln Glu Gln Leu Leu Ala Ile Leu
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Pro Glu Ala Ala Arg Ala Arg Arg Ile Arg Arg Arg Thr Asp Val Arg
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<210> 5221

<211> 497

<212> DNA

<213> Homo sapiens

<400> 5221

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<210> 5222

<211> 112

<212> PRT

<213> Homo sapiens

<400> 5222

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 35           40           45
Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu Glu Gln
           50           55           60
Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile Pro
 65           70           75           80
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Thr Lys Asp Asn Leu Met Arg Pro Pro Gly Met Thr Ser Ser Ser Gln
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<210> 5223

<211> 637

<212> DNA

<213> Homo sapiens

<400> 5223

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120
tcagagaaga caggacgggg acagttgagg gaaggctgga gagatagtca tcagcctatc
180
atgtgctcct acaagctggt gactgtgaag tttagggctt gggggcttca gaccagagtg
240
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300
gcatgggttg atgagtggta tgatatgaca atggatgatg ttccgggaata cgagaaaaac
360
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420
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480
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540
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637

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<210> 5224

<211> 148

<212> PRT

<213> Homo sapiens

<400> 5224

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Xaa Thr Ile Phe Asp Asn Glu Ala Lys Asp Val Glu Arg Glu Val Cys

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      1           5           10           15
Phe Ile Asp Ile Ala Cys Asp Glu Ile Pro Glu Arg Tyr Tyr Lys Glu
      20           25           30
Ser Glu Asp Pro Lys His Phe Lys Ser Glu Lys Thr Gly Arg Gly Gln
      35           40           45
Leu Arg Glu Gly Trp Arg Asp Ser His Gln Pro Ile Met Cys Ser Tyr
      50           55           60
Lys Leu Val Thr Val Lys Phe Glu Val Trp Gly Leu Gln Thr Arg Val
      65           70           75           80
Glu Gln Phe Val His Lys Val Val Arg Asp Ile Leu Leu Ile Gly His
      85           90           95
Arg Gln Ala Phe Ala Trp Val Asp Glu Trp Tyr Asp Met Thr Met Asp
      100          105          110
Asp Val Arg Glu Tyr Glu Lys Asn Met His Glu Gln Thr Asn Ile Lys
      115          120          125
Val Cys Asn Gln His Ser Ser Pro Val Asp Asp Ile Glu Ser His Ala
      130          135          140
Gln Thr Ser Thr
145

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<210> 5225

<211> 394

<212> DNA

<213> Homo sapiens

<400> 5225

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120
caggcctggt cagacggaca tgcccaaggg aacagatagt accaggacag gggaccctgg
180
tctgaagggg cgatagcctg gccccagtg gaaacagccc ctcccaacc tggcggcaga
240
cagggagggt cggcaggtat gtgagatgca aacctggggg actgcccac cccagtgga
300
tgtgaggaca cggtaggttc aggaagtgga gtgacaaatg ggctgtgctg gacttgcctt
360
ccccacatga aggttaggaa ccaagagaac ggcc
394

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<210> 5226

<211> 113

<212> PRT

<213> Homo sapiens

<400> 5226

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Met Trp Gly Lys Gln Val Gln His Ser Pro Phe Val Thr Pro Leu Pro
      1           5           10           15
Glu Pro Thr Val Ser Ser His Pro Leu Gly Asp Gly Gln Ser Pro Arg
      20           25           30
Phe Ala Ser His Ile Pro Ala Asp Pro Pro Cys Leu Pro Pro Gly Leu
      35           40           45
Gly Gly Ala Val Ser Thr Gly Gly Gln Ala Ile Ala Pro Ser Asp Gln

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50					55					60				
Gly	Pro	Leu	Ser	Trp	Tyr	Tyr	Leu	Phe	Pro	Trp	Ala	Cys	Pro	Ser
65					70					75			80	
Gln	Ala	Cys	Gln	Asp	Ser	Ala	Tyr	Val	Ser	Pro	Ser	Pro	Ser	Ala
			85					90					95	
Leu	Gly	Pro	Ser	Leu	Pro	Gln	Pro	Gln	Leu	Pro	Pro	Pro	Gly	Ser
			100				105						110	
Pro														

<210> 5227

<211> 2366

<212> DNA

<213> Homo sapiens

<400> 5227

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 120
 ggatgacggt catgccggca ggcaccgtgt agaaggccag tgtgtaacc ttacctgtct
 180
 acctgaactt caccctgca gacctcatct tcaccgtgga ctctgaaatt gctacaaagg
 240
 aggatcctcg cagcttctac gagcgggggtg tcgcagctct gtgcacagag taaacttttc
 300
 tagctgcccc tttctgtaat agtgaaagt ggtatttaac atttattcat ttttaaaata
 360
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 420
 ggaatctgac ggttgaggagt ggtggaatt ggaaggatac caggaggat ttgggaaac
 480
 ctacggagc tgccctcgtc tactggagca gaagaaatag acctaatttt cctcaaggga
 540
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 600
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 660
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 720
 cacttcagct cactgttgga ggcccatgat attgtggcat caaagtgtta tgattcacct
 780
 ccatacgaac cagaaatgaa taattcttct atcaataatc agttattacc agtagatgcc
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 900
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 960
 ctacttcatt tgggagatat aattaagaa gtcaatggcc atgagggttg aataatcca
 1020
 aaggaattac aagaattact gaaaaatatt agtggaagtg tcaccctaaa aatcttacca
 1080
 agttatagag ataccattac tcctcaacag gtatttgtga agtgtcattt tgattataat
 1140

ccatacaatg acaacctaata accttgcaaa gaagcaggat tgaagttttc caaaggagag
 1200
 attcttcaga ttgtaaatag agaagatcca aattggtggc aggctagcca tgtaaaagag
 1260
 ggaggaagcg ctggtctcat tccaagccag ttcttggaag agaagagaaa ggcatttgtt
 1320
 agaagagact gggacaattc aggacctttt tgtggaacta taagtagcaa aaaaaagaaa
 1380
 aagatgatgt atctcacaac cagaaatgca gaatttgatc gtcattgaaat ccagatatat
 1440
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 1500
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 1560
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 1620
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 1680
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 1740
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 1800
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 1920
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 1980
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 2040
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 2100
 aatgaaaatt aaactcttaa aaagtgactg caacaataa accttctact gagaaaatac
 2160
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 2220
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 2340
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 2366

<210> 5228

<211> 550

<212> PRT

<213> Homo sapiens

<400> 5228

Arg Leu Gly Val Val Glu Ile Gly Arg Ile Pro Gly Gly Ile Trp Glu
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 Asn Leu Thr Glu Leu Pro Ser Ser Thr Gly Ala Glu Glu Ile Asp Leu
 20 25 30
 Ile Phe Leu Lys Gly Ile Met Glu Asn Pro Ile Val Lys Ser Leu Ala

```

      35              40              45
Lys Ala Arg Glu Arg Leu Glu Asp Ser Lys Leu Glu Ala Val Ser Asp
  50              55              60
Asn Asn Leu Glu Leu Val Asn Glu Ile Leu Glu Asp Ile Thr Pro Leu
  65              70              75              80
Ile Asn Val Asp Glu Asn Val Ala Glu Leu Val Gly Ile Leu Lys Glu
      85              90              95
Pro His Phe Gln Ser Leu Leu Glu Ala His Asp Ile Val Ala Ser Lys
      100              105              110
Cys Tyr Asp Ser Pro Pro Ser Ser Pro Glu Met Asn Asn Ser Ser Ile
      115              120              125
Asn Asn Gln Leu Leu Pro Val Asp Ala Ile Arg Ile Leu Gly Ile His
      130              135              140
Lys Arg Ala Gly Glu Pro Leu Gly Val Thr Phe Arg Val Glu Asn Asn
      145              150              155              160
Asp Leu Val Ile Ala Arg Ile Leu His Gly Gly Met Ile Asp Arg Gln
      165              170              175
Gly Leu Leu His Val Gly Asp Ile Ile Lys Glu Val Asn Gly His Glu
      180              185              190
Val Gly Asn Asn Pro Lys Glu Leu Gln Glu Leu Leu Lys Asn Ile Ser
      195              200              205
Gly Ser Val Thr Leu Lys Ile Leu Pro Ser Tyr Arg Asp Thr Ile Thr
      210              215              220
Pro Gln Gln Val Phe Val Lys Cys His Phe Asp Tyr Asn Pro Tyr Asn
      225              230              235              240
Asp Asn Leu Ile Pro Cys Lys Glu Ala Gly Leu Lys Phe Ser Lys Gly
      245              250              255
Glu Ile Leu Gln Ile Val Asn Arg Glu Asp Pro Asn Trp Trp Gln Ala
      260              265              270
Ser His Val Lys Glu Gly Gly Ser Ala Gly Leu Ile Pro Ser Gln Phe
      275              280              285
Leu Glu Glu Lys Arg Lys Ala Phe Val Arg Arg Asp Trp Asp Asn Ser
      290              295              300
Gly Pro Phe Cys Gly Thr Ile Ser Ser Lys Lys Lys Lys Met Met
      305              310              315              320
Tyr Leu Thr Thr Arg Asn Ala Glu Phe Asp Arg His Glu Ile Gln Ile
      325              330              335
Tyr Glu Glu Val Ala Lys Met Pro Pro Phe Gln Arg Lys Thr Leu Val
      340              345              350
Leu Ile Gly Ala Gln Gly Val Gly Arg Arg Ser Leu Lys Asn Arg Phe
      355              360              365
Ile Val Leu Asn Pro Thr Arg Phe Gly Thr Thr Val Pro Phe Thr Ser
      370              375              380
Arg Lys Pro Arg Glu Asp Glu Lys Asp Gly Gln Ala Tyr Lys Phe Val
      385              390              395              400
Ser Arg Ser Glu Met Glu Ala Asp Ile Lys Ala Gly Lys Tyr Leu Glu
      405              410              415
His Gly Glu Tyr Glu Gly Asn Leu Tyr Gly Thr Lys Ile Asp Ser Ile
      420              425              430
Leu Glu Val Val Gln Thr Gly Arg Thr Cys Ile Leu Asp Val Asn Pro
      435              440              445
Gln Ala Leu Lys Val Leu Arg Thr Ser Glu Phe Met Pro Tyr Val Val
      450              455              460
Phe Ile Ala Ala Pro Glu Leu Glu Thr Leu Arg Ala Met His Lys Ala

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465		470		475		480
Val Val Asp Ala Gly Ile Thr Thr Lys Leu Leu Thr Asp Ser Asp Leu						
		485		490		495
Lys Lys Thr Val Asp Glu Ser Ala Arg Ile Gln Arg Ala Tyr Asn His						
		500		505		510
Tyr Phe Asp Leu Ile Ile Ile Asn Asp Asn Leu Asp Lys Ala Phe Glu						
		515		520		525
Lys Leu Gln Thr Ala Ile Glu Lys Leu Arg Met Glu Pro Gln Trp Val						
		530		535		540
Pro Ile Ser Trp Val Tyr						
545		550				

<210> 5229

<211> 1031

<212> DNA

<213> Homo sapiens

<400> 5229

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 120
 tctcgcccac attttcccca agcactctca ggaacctggc aacagtgtcc ccttgtggcc
 180
 aagcctggaa catcacatct gtacgttgca atctgtggat cagctacgag actgagagaa
 240
 aggaatgaaa ggatggaaga attacaagat caggcactgc tgtctgtctg ttccacggat
 300
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 360
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 420
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 480
 attgtgcagt gtcatgtcct gtcaccagag cccctcgtg ttgatgttg gccaatgcoy
 540
 ccagcatgat ctagcaggcc aaatcctaata ctaccattct ctgacaccag ctggctccct
 600
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 660
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 720
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 780
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 840
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 900
 aatggggcct tggagacagg aataaaaagga aaatctgga atggaatcac atgacgcaac
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 1020
 gagcatccct g
 1031

<210> 5230
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 5230
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 Val Cys Lys Gln Thr Glu Tyr Arg Lys Ile Ser Arg Ile Thr Lys Phe
 20 25 30
 Leu Val Leu Cys Gly Leu Arg Val Lys Lys Arg Val Thr Arg Ser
 35 40 45
 Glu Lys Asn Glu Glu Glu Lys Gln Leu His Arg Lys Arg Ala Val Ser
 50 55 60
 Gln Val Pro Pro Thr Val Leu Cys Arg Glu Pro Val Gly Glu Ala Lys
 65 70 75 80
 Trp Gly Glu Trp Gly Thr Ser Gly Gly Arg Pro Gln Gly Thr Ser Trp
 85 90 95
 Cys Gln Arg Met Val Asp
 100

<210> 5231
 <211> 845
 <212> DNA
 <213> Homo sapiens

<400> 5231
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 120
 cagctctggcc tgggcgcgcg ggaacgctg tcctggctgc cgccaccga acagcctgtc
 180
 ctggtgcccc ggctccctgc ccgcgcacca gtcattgacc tgcgcccctc actcctcccg
 240
 ctccatctgc tgctgctgct gctgctcagt gcggcggtgt gccgggctga ggctgggctc
 300
 gaaaccgaaa gtcccgctcg gacctccaa gtggagacc tggaggagcc ccagaaacca
 360
 tgtgccgagc ccgctgcttt tggagacacg cttcacatac actacacggg aagcttggtg
 420
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 480
 aagcaggtga ttccaggtct ggagcagagt cttctcgaca tgtgtgtggg agagaagcga
 540
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 660
 ctaaagctgg tgaagggcat ttgcctctg gtagggatgg ccatgggtgc agccctcctg
 720
 ggccctcattg ggtatcacct atacagaaag gccaatagac ccaaagtctc caaaaagaag
 780

ctcaaggaag agaaacgaaa caagagcaaa aagaaataat aaataataaa ttttaaaaaa

840

cttaa

845

<210> 5232

<211> 201

<212> PRT

<213> Homo sapiens

<400> 5232

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Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu
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Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
          20           25           30
Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
 35           40           45
Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
 50           55           60
Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
 65           70           75           80
Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
          85           90           95
Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
          100          105          110
Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
          115          120          125
Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
          130          135          140
Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
          145          150          155          160
Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
          165          170          175
Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
          180          185          190
Glu Lys Arg Asn Lys Ser Lys Lys Lys
          195          200

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<210> 5233

<211> 2801

<212> DNA

<213> Homo sapiens

<400> 5233

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 120
ctgtttccctg gaaaaaatct aatgcaaggaa gggctagttc acagcaaatt cactgcctcc
 180
tcccattgcac gtggtagaga gtaccagtat caacatggcc ctgttttctg ctaaaaccag
 240
attttgagga atcagagacc cccaacacta ctactcagt agctagcagc cccttccttt
 300

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caactgggag tgttattaga atgaaaagta attagttaga agggcataca tctcagtggc
360
atgagcattg tggaatatcc tttcctaggc acatttgtcc actaaggga cagcctcaga
420
aactggtaca gcaatgggtg agatgagatc ctggagagag aacacagcca tccctatag
480
aaaggcagag cttttgggct tctctggcct gaatgccttc tggggtattt ccatatgcaa
540
cagcccagag tcatagcctt gggcaaccac acatagaggt ttccttctca cttcagacac
600
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660
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720
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840
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900
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960
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1020
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1080
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1140
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1200
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1260
ctcctcattc agacatcctc caccatacca gtgtttagaa gcaaacatg aagggtcagc
1320
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1380
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1440
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1740
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1800
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1860
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1920

gaccttggga aaagctggtg ccgagagagg gagaggccag gtgtccccc acccaactgg
 1980
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 2040
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 2280
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 2340
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 2460
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 2520
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 2580
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 2700
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 2760
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 2801

<210> 5234

<211> 57

<212> PRT

<213> Homo sapiens

<400> 5234

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Leu	Asp	Thr	Arg	Ser	Ser	Arg	Pro	Val	Trp	Gln	Arg	Gly	Glu	Thr	Thr
			20				25					30			
Ile	Ile	Ser	Lys	Glu	Thr	Pro	Pro	Pro	Arg	Leu	Ile	Phe	Lys	Lys	
			35				40				45				
Leu	Ala	Val	Pro	Val	Val	Pro	Ala	Thr							
	50					55									

<210> 5235

<211> 3017

<212> DNA

<213> Homo sapiens

<400> 5235

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120
tctcagacta agactgctgt ccctccgttg agtgaaggag atgggtattc tagtgagaat
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240
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360
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420
ctactcccac aacagctgcc tgaatgcaaa gttgatagtg aaaccaacat agaagctagt
480
aagctaccta catctgaacc agaagctgac gctgaaatag agcccaaaga gagcaacggc
540
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<210> 5236

<211> 178

<212> PRT

<213> Homo sapiens

<400> 5236

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		20					25				30			
Pro	Pro	Thr	Trp	Glu	Ser	Pro	Gly	Asp	Asp	Ala	Ser	Leu	Glu	His
		35					40				45			
Ala	Glu	Met	Asp	Leu	Gly	Thr	Pro	Thr	Tyr	Asp	Glu	Asn	Pro	Met
		50					55				60			
Ala	Ser	Lys	Lys	Pro	Lys	Thr	Ala	Glu	Ala	Asp	Thr	Ser	Ser	Glu
		65					70				75			
Ala	Lys	Lys	Ser	Lys	Glu	Val	Phe	Arg	Lys	Glu	Met	Ser	Gln	Phe
			85						90				95	
Val	Gln	Cys	Leu	Asn	Pro	Tyr	Arg	Lys	Pro	Asp	Cys	Lys	Val	Gly
			100						105				110	
Ile	Thr	Thr	Thr	Glu	Asp	Phe	Lys	His	Leu	Ala	Arg	Lys	Leu	Thr
			115					120				125		
Gly	Val	Met	Asn	Lys	Glu	Leu	Lys	Tyr	Cys	Lys	Asn	Pro	Glu	Asp
			130					135				140		
Glu	Cys	Asn	Glu	Asn	Val	Lys	His	Lys	Thr	Lys	Glu	Tyr	Ile	Lys
				150						155			160	
Tyr	Met	Gln	Lys	Phe	Gly	Ala	Val	Tyr	Lys	Pro	Lys	Glu	Asp	Thr
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Leu Glu

<210> 5237

<211> 1238

<212> DNA

<213> Homo sapiens

<400> 5237

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420
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480
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720

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<210> 5238

<211> 212

<212> PRT

<213> Homo sapiens

<400> 5238

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 35 40 45
 Leu Glu Ala Arg Ser His Met His Leu Ala Ser Ala Phe Ala Gly Ile
 50 55 60
 Gly Phe Gly Asn Ala Gly Val His Leu Cys His Gly Met Ser Tyr Pro
 65 70 75 80
 Ile Ser Gly Leu Val Lys Met Tyr Lys Ala Lys Asp Tyr Asn Val Asp
 85 90 95
 His Pro Leu Val Pro His Gly Leu Ser Val Val Leu Thr Ser Pro Ala
 100 105 110
 Val Phe Thr Phe Thr Ala Gln Met Phe Pro Glu Arg His Leu Glu Met
 115 120 125
 Ala Glu Ile Leu Gly Ala Asp Thr Arg Thr Ala Arg Ile Gln Asp Ala
 130 135 140
 Gly Leu Val Leu Ala Asp Thr Leu Arg Lys Phe Leu Phe Asp Leu Asp
 145 150 155 160
 Val Asp Asp Gly Leu Ala Ala Val Gly Tyr Ser Lys Ala Asp Ile Pro
 165 170 175
 Ala Leu Val Lys Gly Thr Leu Pro Gln Glu Arg Val Thr Lys Leu Ala
 180 185 190
 Pro Arg Pro Gln Ser Glu Glu Asp Leu Ala Ala Leu Phe Glu Ala Ser
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 Met Lys Leu Tyr
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<210> 5239

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 5239

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300
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420
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<210> 5240

<211> 226

<212> PRT

<213> Homo sapiens

<400> 5240

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			20					25					30		
Ser	Ala	Gly	Gly	Thr	Pro	Ser	Gly	Cys	Thr	Val	Ala	Gly	Gly	Leu	Gly
	35						40					45			
Ala	Ser	Gly	Gly	Val	Gly	Ser	Thr	Gly	Thr	Gly	Ala	Ser	Pro	Pro	Thr
	50					55					60				
Thr	Val	Ala	Ile	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
65					70				75					80	
Ser	Ser	Glu	Ser	Val	Ser	Leu	Gly	Gly	Ala	Trp	Gly	Gly	Pro	Gly	Gly
			85						90				95		
Gly	Ser	Leu	Ser	Pro	Arg	Ser	Ala	Phe	Phe	Asn	Phe	Arg	Phe	Leu	Leu
			100					105					110		
Phe	Leu	Ile	Arg	Asp	Leu	Phe	Ser	Pro	Ser	Pro	Gly	Val	Gly	Arg	Gly
			115				120					125			
Leu	Arg	Ser	Thr	Pro	Lys	Pro	Ala	Pro	Ala	Pro	Gly	Pro	Asn	Phe	Arg
	130					135					140				
Phe	Phe	Arg	Ser	Phe	Phe	Arg	Gly	Gly	Trp	Glu	Arg	Ser	Pro	Trp	Glu
145					150					155				160	
Arg	Gly	Thr	Gly	Val	Arg	Ala	Ala	Gly	Gly	Arg	Glu	Val	Cys	Val	Arg
				165					170					175	
Asp	Val	Gly	Asp	Lys	Gly	Asp	Ala	Thr	Leu	Gly	Pro	Ser	Arg	Ser	Lys
			180				185						190		
Arg	Glu	Ser	Leu	Ser	Phe	Ile	Phe	Ser	Ser	Lys	Val	Ala	Leu	Ser	Gly

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<210> 5241
<211> 461
<212> DNA
<213> Homo sapiens

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300
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461

<210> 5242
<211> 146
<212> PRT
<213> Homo sapiens

<400> 5242
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20 25 30
Glu Pro Gln Ala Asp Pro Glu Pro Ser Ser Ser Pro Ser Arg Ala Val
35 40 45
Cys Thr Ala Pro Gly Ile Gly Thr Pro Cys Ser Gly Cys Ala Gly Thr
50 55 60
Ala Ala Pro Arg Glu Val Arg Gly Leu Leu Ser His Leu Pro Pro Ser
65 70 75 80
Val Val Ser Trp Arg Phe Gln Trp Phe Gly Ala Ser Leu Leu Thr Trp
85 90 95
Pro Ala Leu Ser Ser Ala Ser Arg Leu Trp Gly Pro Leu His Pro Gly
100 105 110
Gly Arg Arg Arg Arg Lys Lys Pro Pro Glu Val Ala Arg Asn Pro Val
115 120 125
Ala Gly Glu Val Gly Leu Ser Gln Ala Arg Pro Leu Cys Arg Glu Phe
130 135 140
Pro Arg

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145

<210> 5243

<211> 344

<212> DNA

<213> Homo sapiens

<400> 5243

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120
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180
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240
agtttgcgcc gagtcgagat catttccaac aattcaatcc aagcagtctt taacccaact
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<210> 5244

<211> 114

<212> PRT

<213> Homo sapiens

<400> 5244

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20 25 30
Val Thr Val Asp Pro Asp Asn Ser Asn Cys Ser Glu Glu Ser Ala Arg
35 40 45
Leu Ser Leu Lys Leu Gly Asp Ala Gly Asn Pro Arg Ser Leu Ala Ile
50 55 60
Arg Phe Ile Leu Thr Asn Tyr Asn Lys Leu Ser Ile Gln Ser Trp Phe
65 70 75 80
Ser Leu Arg Arg Val Glu Ile Ile Ser Asn Asn Ser Ile Gln Ala Val
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Phe Asn Pro Thr Gly Val Tyr Ala Pro Ser Gly Tyr Ser Tyr Arg Cys
100 105 110
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<210> 5245

<211> 483

<212> DNA

<213> Homo sapiens

<400> 5245

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120

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 240
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 360
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 480
 ttc
 483

<210> 5246

<211> 131

<212> PRT

<213> Homo sapiens

<400> 5246

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			20					25					30		
Ser	Pro	Thr	Gln	Gly	Val	Arg	Phe	Glu	Ser	Cys	Trp	Pro	Ala	Leu	Met
		35					40				45				
Lys	Asp	Ala	His	Gly	Val	Val	Ile	Val	Phe	Asn	Ala	Asp	Ile	Pro	Ser
	50				55					60					
His	Arg	Lys	Glu	Met	Glu	Met	Trp	Tyr	Ser	Cys	Phe	Val	Gln	Gln	Pro
65					70				75						80
Ser	Leu	Gln	Asp	Thr	Gln	Cys	Met	Leu	Ile	Ala	His	His	Lys	Pro	Gly
			85					90					95		
Ser	Gly	Asp	Asp	Lys	Gly	Ser	Leu	Ser	Leu	Ser	Pro	Pro	Leu	Asn	Lys
		100					105				110				
Leu	Lys	Leu	Val	His	Ser	Asn	Leu	Glu	Asp	Asp	Pro	Glu	Glu	Ile	Arg
		115					120				125				
Met	Glu	Phe													
		130													

<210> 5247

<211> 1004

<212> DNA

<213> Homo sapiens

<400> 5247

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 180
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 240

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 360
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 420
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 480
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 720
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 780
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 900
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<210> 5248

<211> 185

<212> PRT

<213> Homo sapiens

<400> 5248

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 20 25 30
 Ser Pro Thr Gln Gly Val Arg Ile Leu Glu Phe Glu Asn Pro His Val
 35 40 45
 Thr Ser Asn Asn Lys Gly Thr Gly Cys Glu Phe Glu Leu Trp Asp Cys
 50 55 60
 Gly Gly Asp Ala Lys Phe Glu Ser Cys Trp Pro Ala Leu Met Lys Asp
 65 70 75 80
 Ala His Gly Val Val Ile Val Phe Asn Ala Asp Ile Pro Ser His Arg
 85 90 95
 Lys Glu Met Glu Met Trp Tyr Ser Cys Phe Val Gln Gln Pro Ser Leu
 100 105 110
 Gln Asp Thr Gln Cys Met Leu Ile Ala His His Lys Pro Gly Ser Gly
 115 120 125
 Asp Asp Lys Gly Ser Leu Ser Leu Ser Pro Pro Leu Asn Lys Leu Lys
 130 135 140
 Leu Val His Ser Asn Leu Glu Asp Asp Pro Glu Glu Ile Arg Met Glu
 145 150 155 160
 Phe Ile Lys Tyr Leu Lys Ser Ile Ile Asn Ser Met Ser Glu Ser Arg

165 170 175
 Asp Arg Glu Glu Met Ser Ile Met Thr
 180 185

<210> 5249
 <211> 653
 <212> DNA
 <213> Homo sapiens

<400> 5249
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 taccggggct ggctagtcac gggggagccc agtagagagg agtataaaat ccagtccttt
 120
 gatgcagaga cccagcagct gctgaagaca gcactcaaag atccgggtgc tgtggacttg
 180
 gagaaagtgg ccaatgtgat tgtggaccat tctctgcagg actgtgtgtt cagcaaggaa
 240
 gcaggacgca tgtgctacgc catcattcag gcagagagta aacaagcagg ccagagtgtc
 300
 ttccgacgtg gactcctcaa ccgggtgcag caggagtacc aggctcggga gcagctgcga
 360
 gcacgctccc tgcagggtgc ggtctgctat gtcaccttta tctgcaacat ctttgactac
 420
 ctgaggggtga acaacatgcc catgatggcc ctggtgaacc ctgtctatga ctgcctcttc
 480
 cggtctggcc agccagacag tttagcaag gaggaggagg tggactgttt ggtgctgcag
 540
 ctgcaccggg ttggggagca gctggagaaa atgaatgggc agcgcatgga tgagctcttt
 600
 gtgctgatcc gggatggctt cctgctccca actggcctca gctccctggc cca
 653

<210> 5250
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 5250
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 1 5 10 15
 Pro Val Lys Ser Tyr Arg Gly Trp Leu Val Met Gly Glu Pro Ser Arg
 20 25 30
 Glu Glu Tyr Lys Ile Gln Ser Phe Asp Ala Glu Thr Gln Gln Leu Leu
 35 40 45
 Lys Thr Ala Leu Lys Asp Pro Gly Ala Val Asp Leu Glu Lys Val Ala
 50 55 60
 Asn Val Ile Val Asp His Ser Leu Gln Asp Cys Val Phe Ser Lys Glu
 65 70 75 80
 Ala Gly Arg Met Cys Tyr Ala Ile Ile Gln Ala Glu Ser Lys Gln Ala
 85 90 95
 Gly Gln Ser Val Phe Arg Arg Gly Leu Leu Asn Arg Leu Gln Gln Glu
 100 105 110
 Tyr Gln Ala Arg Glu Gln Leu Arg Ala Arg Ser Leu Gln Gly Trp Val


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          115              120              125
Cys Tyr Val Thr Phe Ile Cys Asn Ile Phe Asp Tyr Leu Arg Val Asn
      130              135              140
Asn Met Pro Met Met Ala Leu Val Asn Pro Val Tyr Asp Cys Leu Phe
145              150              155              160
Arg Leu Ala Gln Pro Asp Ser Leu Ser Lys Glu Glu Glu Val Asp Cys
      165              170              175
Leu Val Leu Gln Leu His Arg Val Gly Glu Gln Leu Glu Lys Met Asn
      180              185              190
Gly Gln Arg Met Asp Glu Leu Phe Val Leu Ile Arg Asp Gly Phe Leu
      195              200              205
Leu Pro Thr Gly Leu Ser Ser Leu Ala
      210              215

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<210> 5251
 <211> 372
 <212> DNA
 <213> Homo sapiens

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<400> 5251
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120
ccggaagacg gctttcctgc tttctgcagc agaagcttgg gagaagaagg ggcttttgaa
180
aaccagggcc tgtagataaa ctggccgcct ccgcacatct ttgcccgcta ctctcctgct
240
gacagaaagg cctctaggct gtctgctgac aagctgtcct ctaaccatta caaataccct
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360
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372

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<210> 5252
 <211> 124
 <212> PRT
 <213> Homo sapiens

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<400> 5252
Met Asn Arg Arg Val Ile Ser Ala Asn Pro Tyr Leu Gly Gly Thr Ser
1      5      10      15
Asn Gly Tyr Ala His Pro Ser Gly Thr Ala Leu His Tyr Asp Asp Val
      20      25      30
Pro Cys Ile Asn Gly Ser Gly Glu Pro Glu Asp Gly Phe Pro Ala Phe
      35      40      45
Cys Ser Arg Ser Leu Gly Glu Gly Ala Phe Glu Asn Pro Gly Leu
      50      55      60
Tyr Asp Asn Trp Pro Pro His Ile Phe Ala Arg Tyr Ser Pro Ala
65      70      75      80
Asp Arg Lys Ala Ser Arg Leu Ser Ala Asp Lys Leu Ser Ser Asn His
      85      90      95
Tyr Lys Tyr Pro Ala Ser Ala Gln Ser Val Thr Asn Thr Ser Ser Val

```

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100          105          110
Gly Arg Ala Ser Leu Gly Leu Asn Ser Gln Pro Gln
115          120

<210> 5253
<211> 898
<212> DNA
<213> Homo sapiens

<400> 5253
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120
tcattctcaat gccatccttg tggagagcca cagtgtagtg caagggtcca tccaattcac
180
tgtggacaag gtcttgagc aacatcacca ggctgccaag gctcagcaga aactacaggc
240
ctcactctca gtggctgtga actccatcat gagtattctg actggaagca ctaggagcag
300
cttcgaaaag atgtgtctcc agacccttca agcagctgac acacaagagt tcaggaccaa
360
actgcacaaa gtatttctg agatcaccca acaccaattt cttcaccact gctcatgtga
420
gggtgaagcag cagctaacc tagaaaaaaa ggactcagcc cagggcactg aggagcacc
480
tgataacagc agcctggagc tcctagcaga taccagcggg caagcagaaa acaagaggct
540
caagaggggc agcccccgca tagaggagat gcgagctctg cgctctgcc aggccccgag
600
cccgtcagag gccgccccg gccgccccga agccaccgcg gccccctca ctctagagg
660
aaggggagcac cgcgaggctc acggcagggc cctggcgccg ggcagggcga gcctcgaa
720
ccgcctggag gacgtgctgt ggctgcagga ggtctccaac ctgtcagagt ggctgagtc
780
cagccctggg ccttgagccg ggtcccttc cgcaagcgc caccgatccg gaggtgcgg
840
gcagccgtta tcccgtggtt taataaagct gccgcgcgct caaaaaaaaa aaaaaaaaa
898

<210> 5254
<211> 56
<212> PRT
<213> Homo sapiens

<400> 5254
Gln Gln Pro Gly Ala Pro Ser Arg Tyr Gln Arg Ala Ser Arg Lys Gln
1          5          10          15
Glu Ala Gln Glu Gly Gln Pro Pro His Arg Gly Asp Ala Ser Ser Ala
20          25          30
Leu Cys Gln Gly Pro Glu Pro Val Arg Gly Arg Pro Ala Pro Pro Gly
35          40          45
Ser His Arg Gly Pro Pro His Ser

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50

55

<210> 5255
 <211> 1410
 <212> DNA
 <213> Homo sapiens

<400> 5255
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 caaccccaga tccccatgcc tcgagccctg gatctccaag ctcagctgct ggattctgga
 120
 tgtcaacaaa cctcaccact ggatcctgac aaccacaatg cctggatcct ggggccccca
 180
 tcaactggatc ccagatcccc tcaactccacc cactggatc ctgcattgggt ttttggtttt
 240
 ttgttttttt ttaacctcga cactgggtct cagatccttc tgctgactgc cagatccctg
 300
 catttcaagc actacgcctt ccaccccag gcaactggatc ccagattccc aagccttcac
 360
 ccaccagatt ctggctccta aaacaagtgc gggggcccca gtggcacagc aagtggatcc
 420
 tggcaactgc agctgctgga ttccagatc tgggtcccca atccctctgc ccagtccttc
 480
 aatgttgaaa cctcatctct tgaaggcaga tcctgatatt ccaaggcact gaatcccaag
 540
 cctgtaatcc ccggtttctg atctgaatct tccaggcgcc ggggtccaaa tgttcaggcc
 600
 ccaagtctag atcctggcag cccagtcaca gagtatccca cacacactgg tgcccagagc
 660
 cggtctctca tgacatgaaa ttgcatggtc gagggagtct gtggggaagg aagcccagggt
 720
 cctggctgca acctgcacgg atgctggatt cccctcacc ccacctctgc atggccaccc
 780
 cctcccagcc ctgtggggaa actgttcctt ggaaccactc cactccctgc atcccacac
 840
 ttcacagcat ctccatcccc cctcccacct tctaggcgaa tagtcccag agctgtgttc
 900
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 960
 agggacacat gaagggatgt cccacccca gcactatcag ggctcccca ggctccaga
 1020
 gttgaaagcc aggagaaaat cggcaagac cacccttccc taaacccaag cacccaatga
 1080
 tgcaaaaaaa aaaaacaaaa aaaccacca aatccccaaa ttcattccag atctattttt
 1140
 ctaccagaga gaggagcaaa gtcctcctcc cctgcgcctt tacattctgc acttcatagt
 1200
 tggattctga gcttaggac atctggagac cccatggagg gacttggaag ggggaactgg
 1260
 gatttgggga ggggctggag gacttccgca cgcttcacac tccttegacc tccactgcgc
 1320
 cccacctccc tgctgtgtg tgttatttca aaggaaaaga aaaaaggaa taaattttct
 1380

aagctctttaa aaaaaaaaaa aaaaaaaaaa
1410

<210> 5256

<211> 95

<212> PRT

<213> Homo sapiens

<400> 5256

Met	Val	Glu	Gly	Val	Cys	Gly	Glu	Gly	Ser	Pro	Gly	Pro	Gly	Cys	Asn
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Leu	His	Gly	Cys	Trp	Ile	Pro	Pro	His	Pro	Thr	Ser	Ala	Trp	Pro	Pro
		20						25					30		
Pro	Pro	Ser	Pro	Val	Gly	Lys	Leu	Phe	Pro	Gly	Thr	Thr	Pro	Leu	Pro
		35					40					45			
Ala	Ser	Pro	His	Phe	Thr	Ala	Ser	Ser	Ile	Pro	Leu	Pro	Pro	Ser	Arg
	50					55					60				
Arg	Ile	Val	Pro	Arg	Ala	Val	Phe	Leu	Gln	Gly	Val	Arg	Gly	Ile	Thr
65				70					75					80	
His	Ser	Trp	Arg	Leu	Ala	Arg	Arg	Gln	Ser	Glu	Ala	Arg	Asp	Thr	
			85					90						95	

<210> 5257

<211> 1366

<212> DNA

<213> Homo sapiens

<400> 5257

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120
tcctectact ccgcatccgc cgagcctgcc cgggtccgcg gccttgtcta tgggcaccac
180
ggggatccag ccaaggtcgt cgaactcaag aacctggagc tagctgctgt gagaggatca
240
gatgtccgtg tgaagatgct ggcggccctc atcaatccat ctgacataaa tatgatccaa
300
ggaaactacg gactccttcc tgaactgcct gctgttgagg ggaacgaagg tgtgtcacag
360
gtggtagcgg tgggcagcaa tgtgaccggg ctgaagccag gagactgggt gattccagca
420
aatgctgtgt tagactcagg aacctggcgg accgaggctg tgttcacgga ggaagcactg
480
atccaagtgc cgagtgcacat ccctcttccag agcgctgcca ccctgggtgt caatccctgc
540
acagcctaca ggatgttgat ggacttcgag caactgcagc cagggggattc tgtcatccag
600
aatgcatcca acagcggagt ggggcaagca gtcattccaga tcgccgcagc cctggggccta
660
agaacctatca atgtggtccg agacagacct gatattccaga agctgagtga cagactgaag
720
agtctggggg ctgagcatgt catcacagaa gaggagctaa gaaggccca aatgaaaaac
780

ttctttaagg acatgcccc gccacggctt gctctcaact gtgttggtgg gaaaagctcc
 840
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 900
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 960
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 1020
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 1080
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 1200
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 1260
 cactgectct tcctattagg aggatggtga agccagccac gggtttcccc agggccagcc
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 1366

<210> 5258

<211> 375

<212> PRT

<213> Homo sapiens

<400> 5258

Met	Trp	Val	Cys	Ser	Thr	Leu	Trp	Arg	Val	Arg	Thr	Pro	Pro	Gly	Ser
1				5				10						15	
Gly	Gly	Gly	Leu	Pro	Ala	Ser	Gly	Cys	His	Gly	Pro	Ala	Ala	Ser	
			20				25				30				
Ser	Tyr	Ser	Ala	Ser	Ala	Glu	Pro	Ala	Arg	Val	Arg	Gly	Leu	Val	Tyr
		35				40					45				
Gly	His	His	Gly	Asp	Pro	Ala	Lys	Val	Val	Glu	Leu	Lys	Asn	Leu	Glu
	50				55					60					
Leu	Ala	Ala	Val	Arg	Gly	Ser	Asp	Val	Arg	Val	Lys	Met	Leu	Ala	Ala
65				70				75					80		
Pro	Ile	Asn	Pro	Ser	Asp	Ile	Asn	Met	Ile	Gln	Gly	Asn	Tyr	Gly	Leu
			85					90					95		
Leu	Pro	Glu	Leu	Pro	Ala	Val	Gly	Gly	Asn	Glu	Gly	Val	Ala	Gln	Val
		100					105						110		
Val	Ala	Val	Gly	Ser	Asn	Val	Thr	Gly	Leu	Lys	Pro	Gly	Asp	Trp	Val
		115				120						125			
Ile	Pro	Ala	Asn	Ala	Gly	Leu	Asp	Ser	Gly	Thr	Trp	Arg	Thr	Glu	Ala
	130			135						140					
Val	Phe	Ser	Glu	Glu	Ala	Leu	Ile	Gln	Val	Pro	Ser	Asp	Ile	Pro	Leu
145				150					155				160		
Gln	Ser	Ala	Ala	Thr	Leu	Gly	Val	Asn	Pro	Cys	Thr	Ala	Tyr	Arg	Met
			165					170					175		
Leu	Met	Asp	Phe	Glu	Gln	Leu	Gln	Pro	Gly	Asp	Ser	Val	Ile	Gln	Asn
		180					185					190			
Ala	Ser	Asn	Ser	Gly	Val	Gly	Gln	Ala	Val	Ile	Gln	Ile	Ala	Ala	Ala
		195				200					205				
Leu	Gly	Leu	Arg	Thr	Ile	Asn	Val	Val	Arg	Asp	Arg	Pro	Asp	Ile	Gln

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      210              215              220
Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile Thr
225              230              235              240
Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp Met
      245              250              255
Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser Thr
      260              265              270
Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr Gly
      275              280              285
Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile Phe
      290              295              300
Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys Asp
305              310              315              320
His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp Leu
      325              330              335
Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro Leu
      340              345              350
Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile Ser
      355              360              365
Ser Lys Gln Ile Leu Thr Met
      370              375

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<210> 5259

<211> 306

<212> DNA

<213> Homo sapiens

<400> 5259

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ctgaattgct gtgagggcag aacacccaag gagacaatag aaaatttggt gcacagaatg
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actgaagaga agacgctgac tgctgagggg ttggtaaaac tcctccaggc tgtgaagacg
120
actttcccaa acctgggcct tctgctagag aagttgcaga aatcagccac ttgccaagc
180
accacagatcc aaccaagccc tgaatgattat gggactgagc tattgagacg ctatcatgaa
240
aacctctctg agattttcac agacaaccag attttattaa agatgatctc acacatgaca
300
agttta
306

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<210> 5260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 5260

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Met Thr Glu Glu Lys Thr Leu Thr Ala Glu Gly Leu Val Lys Leu Leu
1      5      10      15
Gln Ala Val Lys Thr Thr Phe Pro Asn Leu Gly Leu Leu Leu Glu Lys
      20      25      30
Leu Gln Lys Ser Ala Thr Leu Pro Ser Thr Thr Val Gln Pro Ser Pro
      35      40      45
Asp Asp Tyr Gly Thr Glu Leu Leu Arg Arg Tyr His Glu Asn Leu Ser

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50	55	60
Glu Ile Phe Thr Asp Asn Gln Ile Leu Leu Lys Met Ile Ser His Met		
65	70	75
Thr Ser Leu		80

<210> 5261
 <211> 2394
 <212> DNA
 <213> Homo sapiens

<400> 5261
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 180
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 300
 tacgaggaga agcggggagca ggaggactgc tgggagaact ttgtggtgct gggcgggagc
 360
 aagttccagct tgaagacgct cttcatcctc ttccggaacg agacggtgga cgtggaggac
 420
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 480
 aggttttgga tctggaccgg ggagtacaaa tgcgagatcg agctgcgcca gggggagggc
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 aaggggcagc ccaagacatg ctttaaagt ggttcccgga ccacatgag cggcagctgc
 660
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 720
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 780
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 840
 ctgccagggt gaacacacag ccagcttatc cctcttaagt gccaaaactt ttttttaaac
 900
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 1020
 aacgactcgc gagaactgta gcgtgcagat gtgttgcccc tcccttttaa aattttattt
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 1260

gtgtttgctg aattgaaaac attgttgact gtggcttcta tcagagtgtc taccttttgc
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 agctcttccc ctccctcatt taatttgctg cttttaatct acgtggctg agaatttggtg
 1380
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 1500
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 1620
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 1680
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 1860
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 1920
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 1980
 agaaatgggg gtgccctgt gtaaaagaac ctaccaagg tttacatttg caccttagcc
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 2100
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 2160
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 2220
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 2340
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 2394

<210> 5262

<211> 275

<212> PRT

<213> Homo sapiens

<400> 5262

Xaa	Ala	Ala	Met	Ala	Thr	Pro	Ala	Arg	Pro	Gly	Glu	Ala	Glu	Asp	Ala
1				5					10				15		
Ala	Glu	Arg	Pro	Leu	Gln	Asp	Glu	Pro	Ala	Ala	Ala	Ala	Ala	Gly	Pro
			20					25					30		
Gly	Lys	Gly	Arg	Phe	Leu	Val	Arg	Ile	Cys	Phe	Gln	Gly	Asp	Glu	Gly
			35				40				45				
Ala	Cys	Pro	Thr	Arg	Asp	Phe	Val	Val	Gly	Ala	Leu	Ile	Leu	Arg	Ser
	50						55				60				


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Ile Gly Met Asp Pro Ser Asp Ile Tyr Ala Val Ile Gln Ile Pro Gly
70                      75                      80
Ser Arg Glu Phe Asp Val Ser Phe Arg Ser Ala Glu Lys Leu Ala Leu
85                      90                      95
Phe Leu Arg Val Tyr Glu Glu Lys Arg Glu Gln Glu Asp Cys Trp Glu
100                     105                     110
Asn Phe Val Val Leu Gly Arg Ser Lys Ser Ser Leu Lys Thr Leu Phe
115                     120                     125
Ile Leu Phe Arg Asn Glu Thr Val Asp Val Glu Asp Ile Val Thr Trp
130                     135                     140
Leu Lys Arg His Cys Asp Val Leu Ala Val Pro Val Lys Val Thr Asp
145                     150                     155
Arg Phe Gly Ile Trp Thr Gly Glu Tyr Lys Cys Glu Ile Glu Leu Arg
165                     170                     175
Gln Gly Glu Gly Val Arg His Leu Pro Gly Ala Phe Phe Leu Gly
180                     185                     190
Ala Glu Arg Gly Tyr Ser Trp Tyr Lys Gly Gln Pro Lys Thr Cys Phe
195                     200                     205
Lys Cys Gly Ser Arg Thr His Met Ser Gly Ser Cys Thr Gln Asp Arg
210                     215                     220
Cys Phe Arg Cys Gly Glu Glu Gly His Leu Ser Pro Tyr Cys Arg Lys
225                     230                     235
Gly Ile Val Cys Asn Leu Cys Gly Lys Arg Gly His Ala Phe Ala Gln
245                     250                     255
Cys Pro Lys Ala Val His Asn Ser Val Ala Gln Leu Thr Gly Val
260                     265                     270
Ala Gly His
275

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<210> 5263

<211> 319

<212> DNA

<213> Homo sapiens

<400> 5263

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120
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<210> 5264

<211> 105

<212> PRT

<213> Homo sapiens

<400> 5264

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Cys Phe Leu Leu Ile Leu Pro Pro Cys Gln Lys Ile Met Cys Ile Tyr
 50           55           60
Phe Gln Leu Leu Leu Met Glu Thr Thr Ala Met Leu Asp Leu Leu Val
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<210> 5265

<211> 3203

<212> DNA

<213> Homo sapiens

<400> 5265

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<210> 5266

<211> 853

<212> PRT

<213> Homo sapiens

<400> 5266

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 Val Thr Ser Pro Val Leu Cys Asn Asn Ile Ser Glu Gly Glu Gly
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Leu	Gly	Ser	Ser	Ile	Leu	Thr	Cys	Gln	Trp	Asp	Leu	Ser	Trp	Ser	Ala	
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<211> 885
<212> DNA
<213> Homo sapiens
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<211> 279

<212> PRT

<213> Homo sapiens

<400> 5268

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Ala	Thr	Ala	Phe	Pro	Gly	Tyr	Ala	Val	Pro	Asn	Ala	Thr	Ala	Pro	Val
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Ser	Ala	Ala	Gln	Leu	Lys	Gln	Ala	Val	Thr	Leu	Gly	Gln	Asp	Leu	Ala
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Ala	Tyr	Thr	Thr	Tyr	Glu	Val	Tyr	Pro	Thr	Phe	Ala	Val	Thr	Ala	Arg
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<211> 1177

<212> DNA

<213> Homo sapiens

<400> 5269

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<210> 5270

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<212> PRT

<213> Homo sapiens

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Gln Pro Ile Ser Glu Glu Glu Ala Ile Gln Ile Ile Ala Asp Pro Pro
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Leu Pro Pro Ala Ser Phe Thr Leu Arg Asp Tyr Val Asp His Ser Glu
 50          55          60
Thr Leu Gln Lys Leu Val Leu Leu Gly Val Asp Leu Ser Lys Ile Glu
 65          70          75          80
Lys His Pro Glu Ala Ala Asn Leu Leu Leu Arg Leu Asp Phe Glu Lys
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Asp Ile Lys Gln Met Leu Leu Phe Leu Lys Asp Val Gly Ile Glu Asp
100          105          110
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115          120          125
Asp Leu Glu Asn Leu Lys Thr Arg Val Ala Tyr Leu His Ser Lys Asn
130          135          140
Phe Ser Lys Ala Asp Val Ala Gln Met Val Arg Lys Ala Pro Phe Leu
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165          170          175
Lys Glu Leu Glu Leu Ser Val Lys Lys Thr Arg Asp Leu Val Val Arg
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Lys Val Tyr Arg Leu Glu Leu Gly Phe Lys His Asn Glu Ile Gln His
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Pro Ala Lys Pro Asn Tyr Ile Ser Leu Asp Lys Leu Val Ser Ile Pro
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<211> 1185

<212> DNA

<213> Homo sapiens

<400> 5271

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<210> 5272

<211> 385

<212> PRT

<213> Homo sapiens

<400> 5272

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 Lys Asp Val Asp Tyr Val Cys Ile Ser Asp Asn Tyr Trp Leu Gly Lys
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 Lys Lys Pro Cys Ile Thr Tyr Gly Leu Arg Gly Ile Cys Tyr Phe Phe
 245 250 255
 Ile Glu Val Glu Cys Ser Asn Lys Asp Leu His Ser Gly Val Tyr Gly
 260 265 270
 Gly Ser Val His Glu Ala Met Thr Asp Leu Ile Leu Met Gly Ser
 275 280 285
 Leu Val Asp Lys Arg Gly Asn Ile Leu Ile Pro Gly Ile Asn Glu Ala
 290 295 300
 Val Ala Ala Val Thr Glu Glu Glu His Lys Leu Tyr Asp Asp Ile Asp
 305 310 315 320
 Phe Asp Ile Glu Glu Phe Ala Lys Asp Val Gly Ala Gln Ile Leu Leu
 325 330 335
 His Ser His Lys Lys Asp Ile Leu Met His Arg Trp Arg Tyr Pro Ser
 340 345 350
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 Pro
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<210> 5273

<211> 4580

<212> DNA

<213> Homo sapiens

<400> 5273

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3480

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<210> 5274

<211> 185

<212> PRT

<213> Homo sapiens

<400> 5274

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Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
                20            25            30
Val Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
                35            40            45
Pro Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
                50            55            60
Gly Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp

```

65					70					75					80
Ser	Gly	Ile	Thr	Tyr	Leu	Gly	Ile	Lys	Ala	Asn	Asp	Thr	Gln	Glu	Phe
				85					90					95	
Asn	Leu	Ser	Ala	Tyr	Phe	Glu	Arg	Ala	Ala	Asp	Phe	Ile	Asp	Gln	Ala
			100					105					110		
Leu	Ala	Gln	Lys	Asn	Gly	Arg	Val	Leu	Val	His	Cys	Arg	Glu	Gly	Tyr
		115					120					125			
Ser	Arg	Ser	Pro	Thr	Leu	Val	Ile	Ala	Tyr	Leu	Met	Met	Arg	Gln	Lys
	130					135					140				
Met	Asp	Val	Lys	Ser	Ala	Leu	Ser	Ile	Val	Arg	Gln	Asn	Arg	Glu	Ile
	145				150					155				160	
Gly	Pro	Asn	Asp	Gly	Phe	Leu	Ala	Gln	Leu	Cys	Gln	Leu	Asn	Asp	Arg
			165						170					175	
Leu	Ala	Lys	Glu	Gly	Lys	Leu	Lys	Pro							
			180					185							

<210> 5275

<211> 810

<212> DNA

<213> Homo sapiens

<400> 5275

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120
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tatctgttac ggtaacttca tcagcccgcc aagatggcga tgcaagcggc caagagggcg
240
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360
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420
gccaagaatg catgtgatca cctatcgagg ttaaatgttt gtaacagata ccttgtggtt
480
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540
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600
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660
taatactaaa tatttgtatt tcttatttga ggttcaaaat gacctgcttg aaactttgat
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<210> 5276

<211> 125

<212> PRT

<213> Homo sapiens

<400> 5276

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Val Asn Arg Ile Leu Tyr Ile Arg Asn Leu Pro Tyr Lys Ile Thr Ala
      20              25              30
Glu Glu Met Tyr Asp Ile Phe Gly Lys Tyr Gly Pro Ile Arg Gln Ile
      35              40              45
Arg Val Gly Asn Thr Pro Glu Thr Arg Gly Thr Ala Tyr Val Val Tyr
      50              55              60
Glu Asp Ile Phe Asp Ala Lys Asn Ala Cys Asp His Leu Ser Gly Phe
      65              70              75              80
Asn Val Cys Asn Arg Tyr Leu Val Val Leu Tyr Tyr Asn Ala Asn Arg
      85              90              95
Ala Phe Gln Lys Met Asp Thr Lys Lys Lys Glu Glu Gln Leu Lys Leu
      100             105             110
Leu Lys Glu Lys Tyr Gly Ile Asn Thr Asp Pro Pro Lys
      115             120             125

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<210> 5277

<211> 612

<212> DNA

<213> Homo sapiens

<400> 5277

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120
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acctggacgg cctggcgctt ctctctgcgg gacatcacat tgagggtacaa ggagaccggg
240
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420
gcctcctcct gtgtgagtcc caccaggagc cactgtgccg gccttgccct caagggtttt
480
tgctttttct ctgtgcacct ggcgaggctg aaggcgaggg gtggaggagg cccacgcaca
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612

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<210> 5278

<211> 123

<212> PRT

<213> Homo sapiens

<400> 5278
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 20 25 30
 Val Lys Tyr Asp Pro His Thr Leu Thr Leu Ser Leu Pro Phe Tyr Ile
 35 40 45
 Ser Gln Cys Trp Thr Leu Gly Ser Val Leu Ala Leu Thr Trp Thr Val
 50 55 60
 Trp Arg Phe Phe Leu Arg Asp Ile Thr Leu Arg Tyr Lys Glu Thr Arg
 65 70 75 80
 Trp Gln Lys Trp Gln Asn Lys Asp Asp Gln Gly Ser Thr Val Gly Asn
 85 90 95
 Gly Asp Gln His Pro Leu Gly Leu Asp Glu Asp Leu Leu Gly Pro Gly
 100 105 110
 Val Ala Glu Gly Glu Gly Ala Pro Thr Pro Asn
 115 120

<210> 5279
 <211> 1225
 <212> DNA
 <213> Homo sapiens

<400> 5279
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 120
 ctactcccta agctgattgc aggtggccac aaagtactca tcttctccca gatggtgcgc
 180
 tgcttcgaca tcctagaaga ttatttaac cagagaagat acacctatga acgtattgat
 240
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 300
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 480
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 660
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 780
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 840
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 900

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 960
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 1020
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 1080
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<210> 5280

<211> 408

<212> PRT

<213> Homo sapiens

<400> 5280

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		20					25						30		
Gly	Lys	Leu	Val	Leu	Ile	Asp	Lys	Leu	Leu	Pro	Lys	Leu	Ile	Ala	Gly
		35				40						45			
Gly	His	Lys	Val	Leu	Ile	Phe	Ser	Gln	Met	Val	Arg	Cys	Leu	Asp	Ile
	50					55				60					
Leu	Glu	Asp	Tyr	Leu	Ile	Gln	Arg	Arg	Tyr	Thr	Tyr	Glu	Arg	Ile	Asp
65				70					75					80	
Gly	Arg	Val	Arg	Gly	Asn	Leu	Arg	Gln	Ala	Ala	Ile	Asp	Arg	Phe	Ser
			85					90						95	
Lys	Pro	Asp	Ser	Asp	Arg	Phe	Val	Phe	Leu	Leu	Cys	Thr	Arg	Ala	Gly
			100					105						110	
Gly	Leu	Gly	Ile	Asn	Leu	Thr	Ala	Ala	Asp	Thr	Cys	Ile	Ile	Phe	Asp
		115					120					125			
Ser	Asp	Trp	Asn	Pro	Gln	Asn	Asp	Leu	Gln	Ala	Gln	Ala	Arg	Cys	His
		130				135					140				
Arg	Ile	Gly	Gln	Ser	Lys	Ala	Val	Lys	Val	Tyr	Arg	Leu	Ile	Thr	Arg
145					150					155				160	
Asn	Ser	Tyr	Glu	Arg	Glu	Met	Phe	Asp	Lys	Ala	Ser	Leu	Lys	Leu	Gly
			165					170						175	
Leu	Asp	Lys	Ala	Val	Leu	Gln	Thr	Ser	Thr	Glu	Arg	Ala	Ala	Pro	Met
			180					185					190		
Gly	Thr	Ala	Leu	Ser	Lys	Met	Glu	Val	Glu	Asp	Leu	Leu	Arg	Lys	Gly
		195				200						205			
Ala	Tyr	Gly	Ala	Leu	Met	Asp	Glu	Glu	Asp	Glu	Gly	Ser	Lys	Phe	Cys
		210				215					220				
Glu	Glu	Asp	Ile	Asp	Gln	Ile	Leu	Gln	Arg	Arg	Thr	His	Thr	Ile	Thr
225					230					235				240	
Ile	Gln	Ser	Glu	Gly	Lys	Gly	Ser	Thr	Phe	Ala	Lys	Ala	Ser	Phe	Val
				245				250						255	
Ala	Ser	Gly	Asn	Arg	Thr	Asp	Ile	Ser	Leu	Asp	Asp	Pro	Asn	Phe	Trp
			260					265				270			
Gln	Lys	Trp	Ala	Lys	Ile	Ala	Glu	Leu	Asp	Thr	Glu	Ala	Lys	Asn	Glu

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      275              280              285
Lys Glu Ser Leu Val Ile Asp Arg Pro Arg Val Arg Lys Gln Thr Lys
  290              295              300
His Tyr Asn Ser Phe Glu Glu Asp Glu Leu Met Glu Phe Ser Glu Leu
  305              310              315              320
Asp Ser Asp Ser Asp Glu Arg Pro Thr Arg Ser Arg Arg Leu Asn Asp
      325              330              335
Lys Ala Arg Arg Tyr Leu Arg Ala Glu Cys Phe Arg Val Glu Lys Asn
      340              345              350
Leu Leu Ile Phe Gly Trp Gly Arg Trp Lys Asp Ile Leu Thr His Gly
      355              360              365
Arg Phe Lys Trp His Leu Asn Glu Lys Asp Met Glu Met Ile Cys Arg
      370              375              380
Ala Leu Leu Val Tyr Cys Val Lys His Tyr Lys Gly Asp Glu Lys Ile
  385              390              395              400
Lys Ser Phe Ile Trp Glu Leu Ile
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<210> 5281

<211> 336

<212> DNA

<213> Homo sapiens

<400> 5281

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aagagaaaaa acaacgcatg tcattaatga gacatcacat gggacaatca ttgtccaaaag
240
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300
acttgagatt gctcattaat ggggattatg aagaag
336

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<210> 5282

<211> 91

<212> PRT

<213> Homo sapiens

<400> 5282

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Tyr Arg Ala Gln Ala Phe Leu Val Leu Thr Gly Leu Thr Ala Thr Val
      20              25              30
Gly Asp Thr Ala Ile Ser Ser Glu Glu Lys Thr Gln Arg Met Ser Leu
      35              40              45
Met Arg His His Met Gly Gln Ser Leu Ser Lys Glu Val Ala His Val
      50              55              60
Leu Thr Lys Pro Gly Ala Asp His Asp Trp Glu Asn Leu Glu Lys Asp
      65              70              75              80
Leu Arg Leu Leu Ile Asn Gly Asp Tyr Glu Glu

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85

90

<210> 5283
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 5283
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 120
 atggatggca tcattgaaca gaagagcatg ctgggtgcaca gtaaaatcag tgatgctggc
 180
 aagaggaatg gtttaattaa caccagaaac ttgatggcgg agagcagaga tggctctggtg
 240
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 300
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 420
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 480
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 1980
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 1989

<210> 5284

<211> 258

<212> PRT

<213> Homo sapiens

<400> 5284

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 Ala Glu Ser Arg Asp Gly Leu Val Ser Val Tyr Pro Ala Pro Gln Tyr
 35 40 45
 Gln Ser His Arg Val Gly Ala Ser Thr Val Pro Ala Ser Leu Asp Ser
 50 55 60
 Ser Arg Ser Glu Pro Met Gln Gln Leu Leu Asp Pro Asn Thr Leu Gln
 65 70 75 80
 Gln Ser Val Glu Ser Arg Tyr Arg Pro Asn Ile Ile Leu Tyr Ser Glu
 85 90 95
 Gly Val Leu Arg Ser Trp Gly Asp Gly Val Ala Ala Asp Cys Cys Glu
 100 105 110
 Thr Thr Phe Ile Glu Asp Arg Ser Pro Thr Lys Asp Ser Leu Glu Tyr
 115 120 125
 Pro Asp Gly Lys Phe Ile Asp Leu Ser Ala Asp Asp Ile Lys Ile His
 130 135 140
 Thr Leu Ser Tyr Asp Val Glu Glu Glu Glu Phe Gln Glu Leu Glu
 145 150 155 160
 Ser Asp Tyr Ser Ser Asp Thr Glu Ser Glu Asp Asn Phe Leu Met Met
 165 170 175
 Pro Pro Arg Asp His Leu Gly Leu Ser Val Phe Ser Met Leu Cys Cys
 180 185 190
 Phe Trp Pro Leu Gly Ile Ala Ala Phe Tyr Leu Ser His Glu Thr Asn

	195				200					205				
Lys	Ala	Val	Ala	Lys	Gly	Asp	Leu	His	Gln	Ala	Ser	Thr	Ser	Arg
	210					215					220			
Arg	Ala	Leu	Phe	Leu	Ala	Val	Leu	Ser	Ile	Thr	Ile	Gly	Thr	Gly
225					230					235				240
Tyr	Val	Gly	Val	Ala	Val	Ala	Leu	Ile	Tyr	Leu	Ser	Lys	Asn	Asn
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His Leu

<210> 5285

<211> 2155

<212> DNA

<213> Homo sapiens

<400> 5285

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 180
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 360
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 420
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 480
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 540
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 600
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 660
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 1860
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 1920
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 1980
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<210> 5286

<211> 628

<212> PRT

<213> Homo sapiens

<400> 5286

Xaa	Arg	Val	Gln	Gln	Arg	Met	Glu	Glu	Ser	Glu	Pro	Glu	Arg	Lys	Arg
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Ala	Arg	Thr	Asp	Glu	Val	Pro	Ala	Gly	Gly	Ser	Arg	Ser	Glu	Ala	Glu
		20						25					30		
Asp	Glu	Asp	Asp	Glu	Asp	Tyr	Val	Pro	Tyr	Val	Pro	Leu	Arg	Gln	Arg
		35				40					45				
Arg	Gln	Leu	Leu	Leu	Gln	Lys	Leu	Leu	Gln	Arg	Arg	Arg	Lys	Gly	Ala
		50			55					60					
Ala	Glu	Glu	Glu	Gln	Gln	Asp	Ser	Gly	Ser	Glu	Pro	Arg	Gly	Asp	Glu
		65			70				75					80	
Asp	Asp	Ile	Pro	Leu	Gly	Pro	Gln	Ser	Asn	Val	Ser	Leu	Leu	Asp	Gln
			85					90					95		
His	Gln	His	Leu	Lys	Glu	Lys	Ala	Glu	Ala	Arg	Lys	Glu	Ser	Ala	Lys

100 105 110
 Glu Lys Gln Leu Lys Glu Glu Glu Lys Ile Leu Glu Ser Val Ala Glu
 115 120 125
 Gly Arg Ala Leu Met Ser Val Lys Glu Met Ala Lys Gly Ile Thr Tyr
 130 135 140
 Asp Asp Pro Ile Lys Thr Ser Trp Thr Pro Pro Arg Tyr Val Leu Ser
 145 150 155 160
 Met Ser Glu Glu Arg His Glu Arg Val Arg Lys Lys Tyr His Ile Leu
 165 170 175
 Val Glu Gly Asp Gly Ile Pro Pro Pro Ile Lys Ser Phe Lys Glu Met
 180 185 190
 Lys Phe Pro Ala Ala Ile Leu Arg Gly Leu Lys Lys Lys Gly Ile His
 195 200 205
 His Pro Thr Pro Ile Gln Ile Gln Gly Ile Pro Thr Ile Leu Ser Gly
 210 215 220
 Arg Asp Met Ile Gly Ile Ala Phe Thr Gly Ser Gly Lys Thr Leu Val
 225 230 235 240
 Phe Thr Leu Pro Val Ile Met Phe Cys Leu Glu Gln Glu Lys Arg Leu
 245 250 255
 Pro Phe Ser Lys Arg Glu Gly Pro Tyr Gly Leu Ile Ile Cys Pro Ser
 260 265 270
 Arg Glu Leu Ala Arg Gln Thr His Gly Ile Leu Glu Tyr Tyr Cys Arg
 275 280 285
 Leu Leu Gln Glu Asp Ser Ser Pro Leu Leu Arg Cys Ala Leu Cys Ile
 290 295 300
 Gly Gly Met Ser Val Lys Glu Gln Met Glu Thr Ile Arg His Gly Val
 305 310 315 320
 His Met Met Val Ala Thr Pro Gly Arg Leu Met Asp Leu Leu Gln Lys
 325 330 335
 Lys Met Val Ser Leu Asp Ile Cys Arg Tyr Leu Ala Leu Asp Glu Ala
 340 345 350
 Asp Arg Met Ile Asp Met Gly Phe Glu Gly Asp Ile Arg Thr Ile Phe
 355 360 365
 Ser Tyr Phe Lys Gly Gln Arg Gln Thr Leu Leu Phe Ser Ala Thr Met
 370 375 380
 Pro Lys Lys Ile Gln Asn Phe Ala Lys Ser Ala Leu Val Lys Pro Val
 385 390 395 400
 Thr Ile Asn Val Gly Arg Ala Gly Ala Ala Ser Leu Asp Val Ile Gln
 405 410 415
 Glu Val Glu Tyr Val Lys Glu Glu Ala Lys Met Val Tyr Leu Leu Glu
 420 425 430
 Cys Leu Gln Lys Thr Pro Pro Pro Val Leu Ile Phe Ala Glu Lys Lys
 435 440 445
 Ala Asp Val Asp Ala Ile His Glu Tyr Leu Leu Leu Lys Gly Val Glu
 450 455 460
 Ala Val Ala Ile His Gly Gly Lys Asp Gln Glu Glu Arg Thr Lys Ala
 465 470 475 480
 Ile Glu Ala Phe Arg Glu Gly Lys Lys Asp Val Leu Val Ala Thr Asp
 485 490 495
 Val Ala Ser Lys Gly Leu Asp Phe Pro Ala Ile Gln His Val Ile Asn
 500 505 510
 Tyr Asp Met Pro Glu Glu Ile Glu Asn Tyr Val His Arg Ile Gly Arg
 515 520 525
 Thr Gly Arg Ser Gly Asn Thr Gly Ile Ala Thr Thr Phe Ile Asn Lys


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      530                      535                      540
Ala Cys Asp Glu Ser Val Leu Met Asp Leu Lys Ala Leu Leu Leu Glu
545                      550                      555                      560
Ala Lys Gln Lys Val Pro Pro Val Leu Gln Val Leu His Cys Gly Asp
      565                      570                      575
Glu Ser Met Leu Asp Ile Gly Gly Glu Arg Gly Cys Ala Phe Cys Gly
      580                      585                      590
Gly Leu Gly His Arg Ile Thr Asp Cys Pro Lys Leu Glu Ala Met Gln
      595                      600                      605
Thr Lys Gln Val Ser Asn Ile Gly Arg Lys Asp Tyr Leu Ala His Ser
      610                      615                      620
Ser Met Asp Phe
625

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<210> 5287

<211> 581

<212> DNA

<213> Homo sapiens

<400> 5287

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300
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420
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480
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581

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<210> 5288

<211> 193

<212> PRT

<213> Homo sapiens

<400> 5288

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Xaa Glu Pro Pro Glu Pro Pro Gly Leu Gly Gly Ala Ser Ala Pro Pro
1          5          10          15
Glu Pro Pro Ala Ser Pro Ala Pro His Ser Ile Pro Thr Gly Trp Gly
20          25          30
Arg Ala Arg Cys Gly Cys Val Gly Ser Gly Ala Glu Leu Gln Asn Pro
35          40          45
Arg Thr His Phe Val Leu Ser Pro His Cys Phe Met Gly Gly Ile Met

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      50              55              60
Ala Pro Lys Asp Ile Met Thr Asn Thr His Ala Lys Ser Ile Leu Asn
65              70              75              80
Ser Met Asn Ser Leu Arg Lys Ser Asn Thr Leu Cys Asp Val Thr Leu
      85              90              95
Arg Val Glu Gln Lys Asp Phe Pro Ala His Arg Ile Val Leu Ala Ala
      100              105              110
Cys Ser Asp Tyr Phe Cys Ala Met Phe Thr Ser Glu Leu Ser Glu Lys
      115              120              125
Gly Lys Pro Tyr Val Asp Ile Gln Gly Leu Thr Ala Ser Thr Met Glu
      130              135              140
Ile Leu Leu Asp Phe Val Tyr Thr Glu Thr Val His Val Thr Val Glu
145              150              155              160
Asn Val Gln Glu Leu Leu Pro Ala Ala Cys Leu Leu Gln Leu Lys Gly
      165              170              175
Val Lys Gln Ala Cys Cys Glu Phe Leu Glu Ser Gln Leu Asp Pro Ser
      180              185              190
Arg

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<210> 5289
<211> 361
<212> DNA
<213> Homo sapiens

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120
caatgaggat actgcttcag cttctgaagg ggaagtatat gataggggtc tgaagaaact
180
tattttgatc ggggctacat taaaaaagaa attagaacat ggacttacac gaatatggca
240
ggatgttcag ctaaaaagtaa aaacctactt gcttggaact gatttgtcta tattcaaata
300
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360
c
361

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<210> 5290
<211> 95
<212> PRT
<213> Homo sapiens

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<400> 5290
Met Leu Ser Tyr Arg Thr Met Glu Trp His Glu Lys His Asp Asn
1      5      10      15
Glu Asp Thr Ala Ser Ala Ser Glu Gly Glu Val Tyr Asp Arg Val Leu
      20      25      30
Lys Lys Leu Ile Leu Ile Gly Ala Thr Leu Lys Lys Lys Leu Glu His
      35      40      45
Gly Leu Thr Arg Ile Trp Gln Asp Val Gln Leu Lys Val Lys Thr Tyr

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65					70					75					80
Arg	Gly	Gln	Arg	His	Thr	Val	Ala	Ala	Pro	Ala	Xaa	Arg	Ala	Arg	Ala
				85					90					95	
Gly	Ala	Glu	Pro	His	Ala	Ala	Ala	Ala	Pro	Arg	Arg	Leu	Pro	His	Ser
			100					105					110		
Pro	Pro	Pro	Arg	Ala	Gly	His	Pro	Ala	Pro	Gln	Leu	Ala	Gly	Trp	His
			115				120					125			
Gln	Ala	Pro	Arg	Leu	Lys	Arg	Thr	Val	Pro	Val	Arg	Arg	Ser		
	130					135					140				

<210> 5293

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 5293

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 120
 gcttactgt tgctcttggc aacatccact tccgggagcg agtgccgttt cccccgtca
 180
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 240
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 300
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 360
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 420
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 960
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aaactgctt tgaagaagaca ttttcattgga gtgaaagaca taaagtggag accaagatga
 1200
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 1320
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 1380
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 1428

<210> 5294

<211> 290

<212> PRT

<213> Homo sapiens

<400> 5294

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 Arg Val Tyr Asn Gly Arg Leu Lys Val Gln Arg Leu Cys Ser Glu Met
 35 40 45
 Glu Glu Leu Ala Glu His Gly Ile Phe Leu Pro Pro Asn Met Gln Gly
 50 55 60
 Leu Thr Asp Asp Gln Ile Glu Glu Leu Lys Leu Lys Asp Glu Trp Gly
 65 70 75 80
 Glu Lys Cys Val Pro Ser Gly Gly Ala Val Phe Lys Lys Asp Asp Ile
 85 90 95
 Gly Arg Arg Asn Gly Gln Ala Pro Asn Glu Lys Met Lys Gln Val Leu
 100 105 110
 Lys Lys Thr Ile Glu Glu Ala Lys Ala Ile Ile Ser Lys Lys Gln Val
 115 120 125
 Glu Ala Gly Val Cys Val Thr Met Glu Met Val Lys Asp Ala Leu Asp
 130 135 140
 Gln Leu Arg Gly Ala Val Met Ile Val Tyr Pro Met Gly Leu Pro Pro
 145 150 155 160
 Tyr Asp Pro Ile Arg Met Glu Phe Glu Asn Lys Glu Asp Leu Ser Gly
 165 170 175
 Thr Gln Ala Gly Leu Asn Val Ile Lys Glu Ala Glu Ala Gln Leu Trp
 180 185 190
 Trp Ala Ala Lys Glu Leu Arg Arg Thr Lys Lys Leu Ser Asp Tyr Val
 195 200 205
 Gly Lys Asn Glu Lys Thr Lys Ile Ile Ala Lys Ile Gln Gln Arg Gly
 210 215 220
 Gln Gly Ala Pro Ala Arg Glu Pro Ile Ile Ser Ser Glu Glu Gln Lys
 225 230 235 240
 Gln Leu Met Leu Tyr Tyr His Arg Arg Gln Glu Glu Leu Lys Arg Leu
 245 250 255
 Glu Glu Asn Asp Asp Ala Tyr Leu Asn Ser Pro Trp Ala Asp Asn
 260 265 270
 Thr Ala Leu Lys Arg His Phe His Gly Val Lys Asp Ile Lys Trp Arg
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290

<210> 5295

<211> 1451

<212> DNA

<213> Homo sapiens

<400> 5295

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180
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240
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300
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360
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480
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600
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780
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960
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1320
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1380

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 1440
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 1451

<210> 5296
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 5296
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 20 25 30
 Leu Asp Thr Lys Arg Asn Gln Asn Arg Glu Gly Leu Arg Ala Leu Gln
 35 40 45
 Lys Asp Leu Ser Leu Ser Glu Asp Val Met Val Cys Phe Gly Asn Met
 50 55 60
 Phe Ile Lys Met Pro His Pro Glu Thr Lys Glu Met Ile Glu Lys Asp
 65 70 75 80
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<211> 1339

<212> PRT

<213> Homo sapiens

<400> 5302

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 35 40 45
 Ser Gly Leu Pro His Val Ala Phe Ser Ser Ser Ser Ser Ile Ser Gly

50
 Ser Tyr Ser Pro Gly Tyr 55
 65 70
 Gly Trp Ser Pro Ser Asp Ser Asp His Tyr Gln Trp Leu Gln Val Asp
 85 90 95
 Phe Gly Asn Arg Lys Gln Ile Ser Ala Ile Ala Thr Gln Gly Arg Tyr
 100 105 110
 Ser Ser Ser Asp Trp Val Thr Gln Tyr Arg Met Leu Tyr Ser Asp Thr
 115 120 125
 Gly Arg Asn Trp Lys Pro Tyr His Gln Asp Gly Asn Ile Trp Ala Phe
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 Pro Gly Asn Ile Asn Ser Asp Gly Val Val Arg His Glu Leu Gln His
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 Pro Ile Ile Ala Arg Tyr Val Arg Ile Val Pro Leu Asp Trp Asn Gly
 165 170 175
 Glu Gly Arg Ile Gly Leu Arg Ile Glu Val Tyr Gly Cys Ser Tyr Trp
 180 185 190
 Ala Asp Val Ile Asn Phe Asp Gly His Val Val Leu Pro Tyr Arg Phe
 195 200 205
 Arg Asn Lys Lys Met Lys Thr Leu Lys Asp Val Ile Ala Leu Asn Phe
 210 215 220
 Lys Thr Ser Glu Ser Glu Gly Val Ile Leu His Gly Glu Gly Gln Gln
 225 230 235 240
 Gly Asp Tyr Ile Thr Leu Glu Leu Lys Lys Ala Lys Leu Val Leu Ser
 245 250 255
 Leu Asn Leu Gly Ser Asn Gln Leu Gly Pro Ile Tyr Gly His Thr Ser
 260 265 270
 Val Met Thr Gly Ser Leu Leu Asp Asp His His Trp His Ser Val Val
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 Ile Glu Arg Gln Gly Arg Ser Ile Asn Leu Thr Leu Asp Arg Ser Met
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 Gln His Phe Arg Thr Asn Gly Glu Phe Asp Tyr Leu Asp Leu Asp Tyr
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 Glu Ile Thr Phe Gly Gly Ile Pro Phe Ser Gly Lys Pro Ser Ser Ser
 325 330 335
 Ser Arg Lys Asn Phe Lys Gly Cys Met Glu Ser Ile Asn Tyr Asn Gly
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 Val Asn Ile Thr Asp Leu Ala Arg Arg Lys Lys Leu Glu Pro Ser Asn
 355 360 365
 Val Gly Asn Leu Ser Phe Ser Cys Val Glu Pro Tyr Thr Val Pro Val
 370 375 380
 Phe Phe Asn Ala Thr Ser Tyr Leu Glu Val Pro Gly Arg Leu Asn Gln
 385 390 395 400
 Asp Leu Phe Ser Val Ser Phe Gln Phe Arg Thr Trp Asn Pro Asn Gly
 405 410 415
 Leu Leu Val Phe Ser His Phe Ala Asp Asn Leu Gly Asn Val Glu Ile
 420 425 430
 Asp Leu Thr Glu Ser Lys Val Gly Val His Ile Asn Ile Thr Gln Thr
 435 440 445
 Lys Met Ser Gln Ile Asp Ile Ser Ser Gly Ser Gly Leu Asn Asp Gly
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 Gln Trp His Glu Val Arg Phe Leu Ala Lys Glu Asn Phe Ala Ile Leu
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 Thr Ile Asp Gly Asp Glu Ala Ser Ala Val Arg Thr Asn Ser Pro Leu

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Ser	Pro	Thr	Pro	Leu	Asn	Asp	Asp	Gln	Trp	His	Arg	Val	Thr	Ala	Glu						
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Arg	Asn	Val	Lys	Gln	Ala	Ser	Leu	Gln	Val	Asp	Arg	Leu	Pro	Gln	Gln						
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His	Gly	Tyr	Ser	Cys	Asp	Cys	Ser	Asn	Thr	Ala	Tyr	Asp	Gly	Thr	Phe			
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Cys	Asn	Lys	Asp	Val	Gly	Ala	Phe	Phe	Glu	Glu	Gly	Met	Trp	Leu	Arg			
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His	Ser	Val	Asn	Ile	Thr	Arg	His	Glu	Lys	Thr	Ile	Phe	Leu	Lys	Leu			
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			1205					1210					1215					
Leu	Val	Glu	Ser	Asn	Cys	Gly	Ala	Ser	Pro	Leu	Thr	Leu	Ser	Pro	Met			
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Ser	Ser	Ala	Thr	Asp	Pro	Trp	His	Leu	Asp	His	Leu	Asp	Ser	Ala	Ser			
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<211> 334

<212> DNA

<213> Homo sapiens

<400> 5303

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 240
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<210> 5304

<211> 95

<212> PRT

<213> Homo sapiens

<400> 5304

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Arg	Gly	Ala	Arg	Leu	Gly	Ser	Arg	Asp	Gly	Cys	Met	Lys	Glu	Ser	Gln
			20					25					30		
Arg	Arg	Gly	Tyr	Cys	Ser	Arg	His	Leu	Ser	Met	Arg	Thr	Lys	Glu	Met
			35				40					45			
Glu	Gly	Leu	Ala	Asp	Ser	Gly	Pro	Gly	Gly	Ala	Gly	Arg	Pro	Ala	Ala
		50				55				60					
Val	Ala	Ala	Arg	Glu	Gly	Ser	Thr	Glu	Phe	Asp	Trp	Gly	Asp	Glu	Thr
65				70					75				80		
Ser	Arg	Asp	Ser	Gly	Gly	Gln	Gln	Cys	Gly	Asp	Ser	Trp	Arg	Leu	
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<210> 5305

<211> 582

<212> DNA

<213> Homo sapiens

<400> 5305

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 300

cggggtcttt gttctcggt cccacagcag agccaggtag gggggggcct gccaggacta
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 420
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<210> 5306

<211> 62

<212> PRT

<213> Homo sapiens

<400> 5306

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Gln	Leu	Ala	Gly	Pro	Ser	Leu	Trp	Leu	Glu	Leu	Val	Cys	Val	Tyr	Leu
			20					25					30		
Ile	Lys	Ser	His	Arg	Cys	Leu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
			35				40					45			
Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
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<210> 5307

<211> 1551

<212> DNA

<213> Homo sapiens

<400> 5307

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 120
 cattctgtct cccagccttt ctctctctct tgtgtgtctc cagcacttcc tttctttcta
 180
 acatggcctg gagagagtct ctctctctct gtctctgtct cttaataata gtttttaacg
 240
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 360
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 480
 tggaaatttt tttttaagaa acttttttgt gtttttttta atttttaggtc acttattagt
 540
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 1440
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<210> 5308

<211> 112

<212> PRT

<213> Homo sapiens

<400> 5308

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Leu	Leu	Ile	Asp	Leu	Thr	Trp	Thr	His	Arg	Gly	Gly	Lys	Thr	Cys	Gly
			20					25					30		
Asp	His	His	Arg	Gly	His	Gly	Pro	Thr	Ser	Val	Ile	Trp	Glu	Thr	Gly
		35					40					45			
Leu	Gly	Arg	Gly	Gly	Asp	Phe	Pro	Lys	Ser	Pro	Ser	Ile	His	Asp	Arg
		50			55					60					
Gly	Arg	Ala	Trp	Glu	Leu	Gly	Thr	Gln	Gly	Ser	Ser	Lys	Arg	Ser	Arg
65				70					75				80		
Ser	Leu	Cys	Tyr	Pro	Gln	Ile	His	Lys	Leu	Arg	Ile	Thr	Cys	Ile	His
			85					90					95		
Phe	Pro	Pro	Pro	Trp	Thr	Leu	Cys	Phe	Glu	Leu	Phe	Cys	Leu	Pro	Asp
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<210> 5309

<211> 2078

<212> DNA

<213> Homo sapiens

<400> 5309

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240
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300
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360
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420
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480
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540
gatttccctg acaagccaac cttgttgtca ccagaagaac tcaaggcagc aagtagagga
600
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660
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720
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780
ggacgtcgca ggaagattaa gcgagatata atagatatac caaagaaggg agtagctgga
840
cttaggctag actgtgatgc taataccgta aacctagcaa gagagagctc tgcgtacgga
900
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960
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<210> 5310

<211> 359

<212> PRT

<213> Homo sapiens

<400> 5310

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Thr	Asn	Arg	Lys	Ala	Asn	Glu	Ser	Cys	Ser	Asn	Thr	Ala	Pro	Ser	Leu
			20					25					30		
Thr	Val	Pro	Glu	Cys	Ala	Ile	Cys	Leu	Gln	Thr	Cys	Val	His	Pro	Val
			35				40					45			
Ser	Leu	Pro	Cys	Lys	His	Val	Phe	Cys	Tyr	Leu	Cys	Val	Lys	Gly	Ala
			50				55				60				
Ser	Trp	Leu	Gly	Lys	Arg	Cys	Ala	Leu	Cys	Arg	Gln	Glu	Ile	Pro	Glu
					70					75				80	
Asp	Phe	Leu	Asp	Lys	Pro	Thr	Leu	Leu	Ser	Pro	Glu	Glu	Leu	Lys	Ala
				85					90					95	
Ala	Ser	Arg	Gly	Asn	Gly	Glu	Tyr	Ala	Trp	Tyr	Tyr	Glu	Gly	Arg	Asn
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Gly	Trp	Trp	Gln	Tyr	Asp	Glu	Arg	Thr	Ser	Arg	Glu	Leu	Glu	Asp	Ala
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Tyr	Val	Ala	Asp	Leu	Glu	Asn	Met	Val	Gln	Tyr	Arg	Arg	Asn	Glu	His
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Gly	Arg	Arg	Arg	Lys	Ile	Lys	Arg	Asp	Ile	Asp	Ile	Pro	Lys	Lys	
				165				170					175		
Gly	Val	Ala	Gly	Leu	Arg	Leu	Asp	Cys	Asp	Ala	Asn	Thr	Val	Asn	Leu
			180					185					190		
Ala	Arg	Glu	Ser	Ser	Ala	Asp	Gly	Ala	Asp	Ser	Val	Ser	Ala	Gln	Ser
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Val Asp Gly Gln Leu Thr Ser Pro Ala Thr Pro Ser Pro Asp Ala Ser
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Thr Ser Leu Glu Asp Ser Phe Ala His Leu Gln Leu Ser Gly Asp Asn
      245              250              255
Thr Ala Glu Arg Ser His Arg Gly Glu Gly Glu Glu Asp His Glu Ser
      260              265              270
Pro Ser Ser Gly Arg Val Pro Ala Pro Asp Thr Ser Ile Glu Glu Thr
      275              280              285
Glu Ser Asp Ala Ser Ser Asp Ser Glu Asp Val Ser Ala Val Val Ala
      290              295              300
Gln His Ser Leu Thr Gln Gln Arg Leu Leu Val Ser Asn Ala Asn Gln
305              310              315              320
Thr Val Pro Asp Arg Ser Asp Arg Ser Gly Thr Asp Arg Ser Val Ala
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Gly Gly Gly Thr Val Ser Val Ser Val Arg Ser Arg Arg Pro Asp Gly
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Gln Cys Thr Val Thr Glu Val
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<211> 572
<212> DNA
<213> Homo sapiens

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180
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572

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<210> 5312
<211> 190
<212> PRT
<213> Homo sapiens

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<400> 5312
Cys His Cys Glu Gly Asp Asp Glu Ser Pro Leu Ile Thr Pro Cys His

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Cys Thr Gly Ser Leu His Phe Val His Gln Ala Tyr Leu Gln Gln Trp
      20           25           30
Ile Lys Ser Ser Asp Thr Arg Cys Cys Glu Leu Cys Lys Tyr Glu Phe
      35           40           45
Ile Met Glu Thr Lys Leu Lys Pro Leu Arg Lys Trp Glu Lys Leu Gln
      50           55           60
Met Thr Ser Ser Glu Arg Arg Lys Ile Met Cys Ser Val Thr Phe His
      65           70           75           80
Val Ile Ala Ile Thr Cys Val Val Trp Ser Leu Tyr Val Leu Ile Asp
      85           90           95
Arg Pro Ala Glu Glu Ile Lys Gln Gly Gln Ala Thr Gly Ile Leu Glu
      100          105          110
Trp Pro Phe Trp Thr Lys Leu Val Val Ala Ile Gly Phe Thr Arg
      115          120          125
Gly Leu Leu Phe Met Tyr Val Gln Cys Lys Val Tyr Val Gln Leu Trp
      130          135          140
Lys Arg Leu Lys Ala Tyr Asn Arg Val Ile Tyr Val Gln Asn Cys Pro
      145          150          155          160
Glu Thr Ser Lys Lys Asn Ile Phe Glu Lys Ser Pro Leu Thr Glu Pro
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Asn Phe Glu Asn Lys His Gly Tyr Gly Ile Cys His Ser Asp
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<210> 5313

<211> 322

<212> DNA

<213> Homo sapiens

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<210> 5314

<211> 107

<212> PRT

<213> Homo sapiens

<400> 5314

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Thr Arg Val Leu Lys Gly Val Met Arg Val Gly Ile Leu Ala Lys Gly
      20           25           30
Leu Leu Leu Arg Gly Asp Arg Asn Val Arg Leu Ala Leu Leu Cys Ser

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	35					40						45			
Glu	Lys	Pro	Thr	His	Ser	Leu	Leu	Arg	Arg	Ile	Ala	Gln	Gln	Leu	Pro
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Arg	Gln	His	Arg	Gln	Phe	His	Val	Val	Cys	Asp	Trp	Pro	Val	His	Met
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Glu	Val	Phe	Ser	Asp	Leu	Ala	Leu	Asp	Thr	Pro	Ala	Asn	Arg	Thr	His
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Thr	Tyr	Ser	Leu	Thr	His	Ile	His	Val	His	Thr					
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<210> 5315

<211> 2298

<212> DNA

<213> Homo sapiens

<400> 5315

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 120
 gcatgtcccc gggcctccgt gaagggggag cgcgcggcta tggagatcgc gcccgaggag
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<211> 544

<212> PRT

<213> Homo sapiens

<400> 5316

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 35 40 45
 Glu Lys Leu Asp Tyr Lys Thr Cys Glu Ala Leu Glu Glu Val Phe Lys

50 55 60
 Arg Leu Gln Phe Lys Val Val Asp Leu Glu Gln Thr Asn Leu Asp Glu
 65 70 75 80
 Asp Gly Ala Ser Ala Leu Phe Asp Met Ile Glu Tyr Tyr Glu Ser Ala
 85 90 95
 Thr His Leu Asn Ile Ser Phe Asn Lys His Ile Gly Thr Arg Gly Trp
 100 105 110
 Gln Ala Ala Ala His Met Met Arg Lys Thr Ser Cys Leu Gln Tyr Leu
 115 120 125
 Asp Ala Arg Asn Thr Pro Leu Leu Asp His Ser Ala Pro Phe Val Ala
 130 135 140
 Arg Ala Leu Arg Ile Arg Ser Ser Leu Ala Val Leu His Leu Glu Asn
 145 150 155 160
 Ala Ser Leu Ser Gly Arg Pro Leu Met Leu Leu Ala Thr Ala Leu Lys
 165 170 175
 Met Asn Met Asn Leu Arg Glu Leu Tyr Leu Ala Asp Asn Lys Leu Asn
 180 185 190
 Gly Leu Gln Asp Ser Ala Gln Leu Gly Asn Leu Leu Lys Phe Asn Cys
 195 200 205
 Ser Leu Gln Ile Leu Asp Leu Arg Asn Asn His Val Leu Asp Ser Gly
 210 215 220
 Leu Ala Tyr Ile Cys Glu Gly Leu Lys Glu Gln Arg Lys Gly Leu Val
 225 230 235 240
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 245 250 255
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 260 265 270
 Gly His Asn Pro Ile Gly Asn Glu Gly Val Arg His Leu Lys Asn Gly
 275 280 285
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 290 295 300
 Leu Thr Cys Glu Gly Ala Val Ala Val Ala Glu Phe Ile Ala Glu Ser
 305 310 315 320
 Pro Arg Leu Leu Arg Leu Asp Leu Arg Glu Asn Glu Ile Lys Thr Gly
 325 330 335
 Gly Leu Met Ala Leu Ser Leu Ala Leu Lys Val Asn His Ser Leu Leu
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 Arg Leu Asp Leu Asp Arg Glu Pro Lys Lys Glu Ala Val Lys Ser Phe
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 Ile Glu Thr Gln Lys Ala Leu Leu Ala Glu Ile Gln Asn Gly Cys Lys
 370 375 380
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 385 390 395 400
 Gln Leu Ser Ala Ser Met Pro Glu Thr Thr Ala Thr Glu Pro Gln Pro
 405 410 415
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Pro	Ser	Trp	Ala	Ser	Ser	Ser	Thr	Arg	Ala	Ser	Thr	Gly	Thr	Arg	Ser		
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Pro	Ala	Ala	Ala	Ser	Arg	Arg	Pro	Cys	Gly	Ser	Pro	Ala	Arg	Gly	Arg		
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Thr	Ser	Trp	Ser	Ala	Arg	Tyr	Thr	Ser	Pro	Arg	Met	Trp	Thr	Lys	Met		
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Thr	Cys	Arg	Arg	Cys	Arg	Thr	Ser	Ala	Trp	Trp	Trp	Ala	Trp	Ser	Ser		
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<211> 4231

<212> DNA

<213> Homo sapiens

<400> 5319

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<211> 96

<212> PRT

<213> Homo sapiens

<400> 5320

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<212> DNA

<213> Homo sapiens

<400> 5321

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<210> 5322

<211> 209

<212> PRT

<213> Homo sapiens

<400> 5322

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 35 40 45
 Glu Arg Leu Thr Glu Leu Glu Arg Lys Leu Thr Phe Glu Gln Gln Arg
 50 55 60
 Ser Asp Leu Trp Glu Arg Leu Tyr Val Glu Ala Lys Asp Gln Asn Gly
 65 70 75 80
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 85 90 95
 Ala Lys Asn Lys Ser Lys Glu Thr Phe Leu Gly Ser Val Lys Glu Thr
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 Phe Asp Ala Met Lys Asn Ser Thr Lys Glu Phe Val Arg His His Lys
 115 120 125
 Glu Lys Ile Lys Gln Ala Lys Glu Ala Val Lys Glu Asn Leu Lys Lys
 130 135 140
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 145 150 155 160
 Lys Asn Ile Phe Asp Glu Lys Gly Asn Lys Arg Phe Gly Ala Thr Lys
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<210> 5323
 <211> 475
 <212> DNA
 <213> Homo sapiens

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<400> 5324
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 Gly Arg Arg Pro Tyr Lys Trp Arg Gly Val Gly Arg Lys Ala Trp Gln
 50 55 60
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<210> 5325
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 <212> DNA
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<210> 5326
 <211> 234
 <212> PRT
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<400> 5326
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 35 40 45
 Gly Ser Ala Gly Cys Val Leu Ala Gly Arg Leu Thr Glu Asp Pro Ala
 50 55 60
 Glu Arg Val Leu Leu Leu Glu Ala Gly Pro Lys Asp Val Arg Ala Gly
 65 70 75 80
 Ser Lys Arg Leu Ser Trp Lys Ile His Met Pro Ala Ala Leu Val Ala
 85 90 95
 Asn Leu Cys Asp Asp Arg Tyr Asn Trp Cys Tyr His Thr Glu Val Gln

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<210> 5328

<211> 694

<212> PRT

<213> Homo sapiens

<400> 5328

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 Arg Cys Val Val Ala Ala Phe Trp Ala Asp Val Asp Asn Arg Arg Ala
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 Gly Asp Val Tyr Tyr Arg Glu Ala Thr Asp Pro Ala Met Leu Arg Arg

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Ala Thr Trp Val Phe Val Ala Thr Trp Tyr Arg Val Thr Phe Phe Gly		80
	85	90
Gly Ser Ser Ser Pro Val Asn Thr Phe Gln Thr Val Leu Ile Thr		95
	100	105
Asp Gly Lys Leu Ser Phe Thr Ile Phe Asn Tyr Glu Ser Ile Val Trp		110
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Thr Thr Gly Thr His Ala Ser Ser Gly Gly Asn Ala Thr Gly Leu Gly		125
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	145	150
Phe Ser Ile Pro Gly Ser Arg Thr Ala Asp Met Ala Glu Val Glu Thr		155
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Thr Thr Asn Val Gly Val Pro Gly Arg Trp Ala Phe Arg Ile Asp Asp		175
	180	185
Ala Gln Val Arg Val Gly Gly Cys Gly His Thr Thr Ser Val Cys Leu		190
	195	200
Ala Leu Arg Pro Cys Leu Asn Gly Gly Lys Cys Ile Asp Asp Cys Val		205
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Thr Gly Asn Pro Ser Tyr Thr Cys Ser Cys Leu Ser Gly Phe Thr Gly		220
	225	230
Arg Arg Cys His Leu Asp Val Asn Glu Cys Ala Ser Gln Pro Cys Gln		235
	245	250
Asn Gly Gly Thr Cys Thr His Gly Ile Asn Ser Phe Arg Cys Gln Cys		255
	260	265
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	275	280
Asp Thr Lys Glu Cys Gln His Gly Gly Gln Cys Gln Val Glu Asn Gly		285
	290	295
Ser Ala Val Cys Val Cys Gln Ala Gly Tyr Thr Gly Ala Ala Cys Glu		300
	305	310
Met Asp Val Asp Asp Cys Ser Pro Asp Pro Cys Leu Asn Gly Gly Ser		315
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	340	345
Lys Gly Leu Arg Cys Glu Thr Gly Asp His Pro Val Pro His Ala Cys		350
	355	360
Leu Ser Ala Pro Cys His Asn Gly Gly Thr Cys Val Asp Ala Asp Gln		365
	370	375
Gly Tyr Val Cys Glu Cys Pro Glu Gly Phe Met Gly Leu Asp Cys Arg		380
	385	390
Glu Arg Val Xaa Pro Met Thr Val Ser Ala Ala Thr Glu Ala Asp Ala		395
	405	410
Trp Ala Pro Thr Pro Pro Ser Ala His Ala Pro Cys Gly Xaa Ser Leu		415
	420	425
Gly Phe Ser Val Asn Leu Lys Ser Gln Pro Xaa Pro Cys Asn Met Asn		430
	435	440
Thr Gln Cys Pro Asp Gly Gly Tyr Cys Met Glu His Gly Gly Ser Tyr		445
	450	455
Leu Cys Val Cys His Thr Asp His Asn Ala Ser His Ser Leu Pro Ser		460
	465	470
Pro Cys Asp Ser Asp Pro Cys Phe Asn Gly Gly Ser Cys Asp Ala His		475
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                485                490                495
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Gly Gly Thr Cys Lys Glu Ala Gly Gly Glu Tyr His Cys Ser Cys Pro
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Tyr Arg Phe Thr Gly Arg His Cys Glu Ile Gly Lys Pro Asp Ser Cys
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Ala Ser Gly Pro Cys His Asn Gly Gly Thr Cys Phe His Tyr Ile Gly
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Lys Tyr Lys Cys Asp Cys Pro Pro Gly Phe Ser Gly Arg His Cys Glu
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Ile Ala Pro Ser Pro Cys Phe Arg Ser Pro Cys Val Asn Gly Gly Thr
      595
Cys Glu Asp Arg Asp Thr Asp Phe Phe Cys His Cys Gln Ala Gly Tyr
      610
Met Gly Arg Arg Cys Gln Ala Glu Val Asp Cys Gly Pro Pro Glu Glu
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Val Lys His Ala Thr Leu Arg Phe Asn Gly Thr Arg Leu Gly Ala Val
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Ala Leu Tyr Ala Cys Asp Arg Gly Tyr Ser Leu Ser Ala Pro Ser Arg
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Leu Gly Asp Ser Val Gly
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<210> 5329

<211> 2582

<212> DNA

<213> Homo sapiens

<400> 5329

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<210> 5330

<211> 308

<212> PRT

<213> Homo sapiens

<400> 5330

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		20					25						30		
Ala	Leu	Arg	Lys	Lys	Glu	Leu	Asp	Glu	Glu	Glu	Ser	Ile	Arg	Lys	Lys
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Ala	Val	Gln	Phe	Gly	Thr	Gly	Glu	Leu	Cys	Asp	Ala	Ile	Ser	Ala	Val
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Glu	Glu	Lys	Val	Ser	Tyr	Leu	Arg	Pro	Leu	Asp	Phe	Glu	Glu	Ala	Arg
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Glu	Leu	Phe	Leu	Leu	Gly	Gln	His	Tyr	Val	Phe	Glu	Ala	Lys	Glu	Phe
			85						90					95	
Phe	Gln	Ile	Asp	Gly	Tyr	Val	Thr	Asp	His	Ile	Glu	Val	Val	Gln	Asp
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His	Ser	Ala	Leu	Phe	Lys	Val	Leu	Ala	Phe	Phe	Glu	Thr	Asp	Met	Glu
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				130		135					140				
Thr	Val	Asp	Leu	Asn	Pro	Gln	Tyr	Tyr	Leu	Leu	Val	Asn	Arg	Gln	Ile
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Gln	Phe	Glu	Ile	Ala	His	Ala	Tyr	Tyr	Asp	Met	Met	Asp	Leu	Lys	Val
			165						170					175	
Ala	Ile	Ala	Asp	Arg	Leu	Arg	Asp	Pro	Asp	Ser	His	Ile	Val	Lys	Lys
			180					185					190		
Ile	Asn	Asn	Leu	Asn	Lys	Ser	Ala	Leu	Lys	Tyr	Tyr	Gln	Leu	Phe	Leu
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Asp	Ser	Leu	Arg	Asp	Pro	Asn	Lys	Val	Phe	Pro	Glu	His	Ile	Gly	Glu
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Asp	Val	Leu	Arg	Pro	Ala	Met	Leu	Ala	Lys	Phe	Arg	Val	Ala	Arg	Leu
225					230					235					240
Tyr	Gly	Lys	Ile	Ile	Thr	Ala	Asp	Pro	Lys	Lys	Glu	Leu	Glu	Asn	Leu
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<213> Homo sapiens

<400> 5332

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Ser Gln Pro Gln Gly Leu Ser Tyr Ala Xaa Gly Arg Gly
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<210> 5333

<211> 883

<212> DNA

<213> Homo sapiens

<400> 5333

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<210> 5334

<211> 269

<212> PRT

<213> Homo sapiens

<400> 5334

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 35 40 45
 Ile Gln Ala Arg Met Gly Val Phe Ala Gln Ala Asp Gly Ser Ala Tyr
 50 55 60
 Ile Glu Gln Gly Asn Thr Lys Ala Leu Ala Val Val Tyr Gly Pro His
 65 70 75 80
 Glu Ile Arg Gly Ser Arg Ala Arg Ala Leu Pro Asp Arg Ala Leu Val
 85 90 95
 Asn Cys Gln Tyr Ser Ser Ala Thr Phe Ser Thr Gly Glu Arg Lys Arg
 100 105 110
 Arg Pro His Gly Asp Arg Lys Ser Cys Glu Met Gly Leu Gln Leu Arg
 115 120 125
 Gln Thr Phe Glu Ala Ala Ile Leu Thr Gln Leu His Pro Arg Ser Gln
 130 135 140
 Ile Asp Ile Tyr Val Gln Val Leu Gln Ala Asp Gly Gly Thr Tyr Ala
 145 150 155 160
 Ala Cys Val Asn Ala Ala Thr Leu Ala Val Leu Asp Ala Gly Ile Pro
 165 170 175
 Met Arg Asp Phe Val Cys Ala Cys Ser Ala Gly Phe Val Asp Gly Thr
 180 185 190
 Ala Leu Ala Asp Leu Ser His Val Glu Glu Ala Ala Gly Gly Pro Gln
 195 200 205
 Leu Ala Leu Ala Leu Leu Pro Ala Ser Gly Gln Ile Ala Leu Leu Glu
 210 215 220
 Met Asp Ala Arg Leu His Glu Asp His Leu Glu Arg Val Leu Glu Ala
 225 230 235 240
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<210> 5335

<211> 4282

<212> DNA

<213> Homo sapiens

<400> 5335

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<211> 766

<212> PRT

<213> Homo sapiens

<400> 5336

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 Arg Leu Val Asn Glu Tyr Val Glu Leu Val Asn Ala Ala Cys Asn Phe
 50 55 60
 Glu Pro His Glu Ser Phe Phe Ser Leu Phe Ser Asp Pro Arg Ser Thr
 65 70 75 80
 Arg Leu Thr Arg Ile His Leu Arg Glu Asp Leu Val Gln Asp Gln Asp
 85 90 95
 Leu Glu Ala Ile Arg Lys Gln Asp Leu Val Glu Leu Tyr Leu Thr Asn
 100 105 110
 Cys Glu Lys Leu Ser Ala Lys Ser Leu Gln Thr Leu Arg Ser Phe Ser
 115 120 125
 His Thr Leu Val Ser Leu Ser Leu Phe Gly Cys Thr Asn Ile Phe Tyr
 130 135 140
 Glu Glu Glu Asn Pro Gly Gly Cys Glu Asp Glu Tyr Leu Val Asn Pro
 145 150 155 160
 Thr Cys Gln Val Leu Val Lys Asp Phe Thr Phe Glu Gly Phe Ser Arg
 165 170 175
 Leu Arg Phe Leu Asn Leu Gly Arg Met Ile Asp Trp Val Pro Val Glu

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Ser	Leu	Leu	Arg	Pro	Leu	Asn	Ser	Leu	Ala	Ala	Leu	Asp	Leu	Ser	Gly
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Ile	Gln	Thr	Ser	Asp	Ala	Ala	Phe	Leu	Thr	Gln	Trp	Lys	Asp	Ser	Leu
210					215					220					
Val	Ser	Leu	Val	Leu	Tyr	Asn	Met	Asp	Leu	Ser	Asp	Asp	His	Ile	Arg
225					230					235					
Val	Ile	Val	Gln	Leu	His	Lys	Leu	Arg	His	Leu	Asp	Ile	Ser	Arg	Asp
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Arg	Leu	Ser	Ser	Tyr	Tyr	Lys	Phe	Lys	Leu	Thr	Arg	Glu	Val	Leu	Ser
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Glu	Arg	Cys	Asn	Gln	Leu	Leu	Arg	Ala	Leu	Lys	Leu	Val	Ile	Thr	Ala
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Lys	Leu	Arg	Arg	Gln	Val	Ile	Gln	Val	Val	Leu	Asn	Gly	Met	Glu	Ser
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Asn	Cys	Glu	Met	Phe	Leu	Asn	Phe	Asn	Gly	Met	Lys	Leu	Phe	Leu	Asp
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Cys	Leu	Lys	Glu	Phe	Pro	Glu	Lys	Gln	Glu	Leu	His	Arg	Asn	Met	Leu
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Gly	Leu	Leu	Gly	Asn	Val	Ala	Glu	Val	Lys	Glu	Leu	Arg	Pro	Gln	Leu
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Ile Met Phe Asp Gly Pro Glu Ala Trp Gly Val Cys Glu Pro Gln Arg					
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Glu Glu Val Glu Glu Arg Met Trp Ala Ala Ile Gln Ser Trp Asp Ile					
	660		665		670
Asn Ser Arg Arg Asn Ile Asn Tyr Arg Ser Phe Glu Pro Ile Leu Arg					
	675		680		685
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	690		695		700
Ala Leu Tyr Asn Leu Val Ser Val Tyr Pro Asp Lys Tyr Cys Pro Leu					
705		710		715	720
Leu Ile Lys Glu Gly Gly Met Pro Leu Leu Arg Asp Ile Ile Lys Met					
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<210> 5337

<211> 2742

<212> DNA

<213> Homo sapiens

<400> 5337

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<210> 5338

<211> 139

<212> PRT

<213> Homo sapiens

<400> 5338

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Val	Ser	Lys	Asn	Gln	Gln	Gln	Leu	Asn	Arg	Gln	Lys	Thr	Lys	Glu	Gln
			20				25					30			
Asn	Ser	Gln	Met	Lys	Ile	Val	His	Lys	Lys	Lys	Glu	Arg	Gly	His	Gly
		35					40				45				
Tyr	Asn	Ser	Ser	Ala	Ala	Ala	Trp	Gln	Ala	Met	Gln	Asn	Gly	Gly	Lys
	50					55				60					
Asn	Lys	Asn	Phe	Pro	Asn	Asn	Gln	Ser	Trp	Asn	Ser	Ser	Leu	Ser	Gly
65			70						75				80		
Pro	Arg	Leu	Leu	Phe	Lys	Ser	Gln	Ala	Asn	Gln	Asn	Tyr	Ala	Gly	Ala
			85					90					95		
Lys	Phe	Ser	Glu	Pro	Pro	Ser	Pro	Ser	Val	Leu	Pro	Lys	Pro	Pro	Ser
		100					105					110			
His	Trp	Val	Pro	Val	Ser	Phe	Asn	Pro	Ser	Asp	Lys	Glu	Ile	Met	Thr
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Phe	Gln	Leu	Lys	Thr	Leu	Leu	Lys	Val	Gln	Val					
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<210> 5339

<211> 847

<212> DNA

<213> Homo sapiens

<400> 5339

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 180
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 720
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<211> 217

<212> PRT

<213> Homo sapiens

<400> 5340

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			20					25					30		
Leu	Leu	Ser	Gly	Asp	Glu	Tyr	Asn	Gln	Asp	Phe	Asp	Ser	Thr	Asn	Phe
			35				40					45			
Glu	Glu	Ser	Gln	Asp	Glu	Asp	Asp	Ala	Leu	Asn	Glu	Ile	Val	Arg	Cys
			50			55					60				
Ile	Cys	Glu	Met	Asp	Glu	Glu	Asn	Gly	Phe	Met	Ile	Gln	Cys	Glu	Glu
65					70				75					80	
Cys	Leu	Cys	Trp	Gln	His	Ser	Val	Cys	Met	Gly	Leu	Leu	Glu	Glu	Ser
			85						90					95	
Ile	Pro	Glu	Gln	Tyr	Ile	Cys	Tyr	Ile	Cys	Arg	Asp	Pro	Pro	Gly	Gln
			100					105					110		
Arg	Trp	Ser	Ala	Lys	Tyr	Arg	Tyr	Asp	Lys	Glu	Trp	Leu	Asn	Asn	Gly
			115				120					125			
Arg	Met	Cys	Gly	Leu	Ser	Phe	Phe	Lys	Glu	Asn	Tyr	Ser	His	Leu	Asn
			130			135					140				
Ala	Lys	Lys	Ile	Val	Ser	Thr	His	His	Leu	Leu	Ala	Asp	Val	Tyr	Gly
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Val	Thr	Glu	Val	Leu	His	Gly	Leu	Gln	Leu	Lys	Ile	Gly	Ile	Leu	Lys
			165						170					175	
Asn	Lys	His	His	Pro	Asp	Leu	His	Leu	Trp	Ala	Cys	Ser	Gly	Lys	Arg
			180				185						190		
Lys	Asp	Gln	Asp	Gln	Ile	Ile	Ala	Gly	Val	Glu	Lys	Lys	Ile	Ala	Gln
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<210> 5341

<211> 2455

<212> DNA

<213> Homo sapiens

<400> 5341

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1440

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<211> 690

<212> PRT

<213> Homo sapiens

<400> 5342

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 Ala Met Leu Ala Arg Pro Trp Leu Gly Pro Trp Val Pro His Gly Leu
 50 55 60
 Ser Leu Ala Ala Ala Leu Ala Leu Thr Leu Leu Pro Ala Arg Leu
 65 70 75 80
 Pro Pro Gly Leu Arg Trp Leu Pro Ala Asp Val Ile Phe Leu Ala Lys
 85 90 95
 Ile Leu His Leu Gly Leu Lys Ile Arg Gly Cys Leu Ser Arg Gln Pro

100 105 110
 Pro Asp Thr Phe Val Asp Ala Phe Glu Arg Arg Ala Arg Ala Gln Pro
 115 120 125
 Gly Arg Ala Leu Leu Val Trp Thr Gly Pro Gly Ala Gly Ser Val Thr
 130 135 140
 Phe Gly Glu Leu Asp Ala Arg Ala Cys Gln Ala Ala Trp Ala Leu Lys
 145 150 155 160
 Ala Glu Leu Gly Asp Pro Ala Ser Leu Cys Ala Gly Glu Pro Thr Ala
 165 170 175
 Leu Leu Val Leu Ala Ser Gln Ala Val Pro Ala Leu Cys Met Trp Leu
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 Gly Leu Ala Lys Leu Gly Cys Pro Thr Ala Trp Ile Asn Pro His Gly
 195 200 205
 Arg Gly Met Pro Leu Ala His Ser Val Leu Ser Ser Gly Ala Arg Val
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 Pro Thr Pro Gly Val Gly Ala Leu Gly Ala Ala Leu Asp Ala Ala Pro
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 Ser His Pro Val Pro Ala Asp Leu Arg Ala Gly Ile Thr Trp Arg Ser
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 Pro Ala Leu Phe Ile Tyr Thr Ser Gly Thr Thr Gly Leu Pro Lys Pro
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 Gly Ala Thr Cys Val Leu Ala Pro Lys Phe Ser Thr Ser Cys Phe Trp
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 Asp Asp Cys Arg Gln His Gly Val Thr Val Ile Leu Tyr Val Gly Glu
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 Leu Leu Arg Tyr Leu Cys Asn Ile Pro Gln Gln Pro Glu Asp Arg Thr
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 His Thr Val Arg Leu Ala Met Gly Asn Gly Leu Arg Ala Asp Val Trp
 405 410 415
 Glu Thr Phe Gln Gln Arg Phe Gly Pro Ile Arg Ile Trp Glu Val Tyr
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 Gln Gly Phe Cys Ile Pro Val Gly Leu Gly Glu Pro Gly Leu Leu Leu
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 Glu Leu Ser Glu Arg Lys Leu Val Arg Asn Val Arg Gln Ser Gly Asp
 515 520 525
 Val Tyr Tyr Asn Thr Gly Asp Val Leu Ala Met Asp Arg Glu Gly Phe

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      565              570              575
Leu Gln Gln Val Asn Val Tyr Gly Val Cys Val Pro Gly Cys Glu Gly
      580              585              590
Lys Val Gly Met Ala Ala Val Gln Leu Ala Pro Gly Gln Thr Phe Asp
      595              600              605
Gly Glu Lys Leu Tyr Gln His Val Arg Ala Trp Leu Pro Ala Tyr Ala
      610              615              620
Thr Pro His Phe Ile Arg Ile Gln Asp Ala Met Glu Val Thr Ser Thr
      625              630              635
Phe Lys Leu Met Lys Thr Arg Leu Val Arg Glu Gly Phe Asn Val Gly
      645              650              655
Ile Val Val Asp Pro Leu Phe Val Leu Asp Asn Arg Ala Gln Ser Phe
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Lys Leu
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<210> 5343
<211> 752
<212> DNA
<213> Homo sapiens

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<210> 5344

<211> 124

<212> PRT

<213> Homo sapiens

<400> 5344

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Glu Arg Ser Phe Phe Leu Lys Lys Arg Arg Ala Asp Phe Val Ala Gly
      35           40           45
Ser Leu Ser Gly Arg Val Ile Val Ala Gly Gly Leu Gly Asn Gln Pro
      50           55           60
Thr Val Leu Glu Thr Ala Glu Ala Phe His Pro Gly Lys Asn Lys Trp
      65           70           75           80
Glu Ile Leu Pro Ala Met Pro Thr Pro Arg Cys Ala Cys Ser Ser Ile
      85           90           95
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<210> 5345

<211> 1912

<212> DNA

<213> Homo sapiens

<400> 5345

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120
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<210> 5346

<211> 534

<212> PRT

<213> Homo sapiens

<400> 5346

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Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu	Leu	Lys	Val	Gln	Phe
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<212> DNA

<213> Homo sapiens

<400> 5347

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<211> 694

<212> PRT

<213> Homo sapiens

<400> 5348

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Tyr	Leu	Leu	Leu	Pro	Pro	Pro	Thr	Leu	Leu	Gln	Asp	Glu	Leu	Leu	Phe
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			100					105					110		
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Gly	Ala	Ala	Ala	Ala	Ser	Ser	Thr	Gly	Gly	Ala	Gly	Ala	Ser	Val	Asp
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Gly	Gly	Ser	Gln	Ala	Val	Gln	Gly	Gly	Cys	Gly	Asp	Ser	Arg	Ala	Ala
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		210				215					220				
Gln	Asn	Asp	Asp	Asp	Asp	Asn	Lys	Ile	Ala	Glu	Lys	Pro	Asp	Trp	Glu
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Pro	Glu	Asn	Ser	Leu	Glu	Gly	Ile	Ser	Leu	Gly	Asp	Ile	Pro	Leu	Pro
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Phe	Ser	Gln	Ala	Ile	Ser	Gln	Asp	Val	Asn	Leu	His	Glu	Ala	Ile	Leu
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Asp Ile Asn Ile Phe Asp Glu Ile Asn Leu Met Ser Leu Ala Thr Glu
          385          390          395
Asp Asn Phe Asp Pro Ile Asp Val Ser Gln Leu Phe Asp Glu Ser Asp
          405          410          415
Ser Asp Ser Gly Leu Ser Leu Asp Ser Ser His Asn Asn Thr Ser Val
          420          425          430
Ile Lys Ser Asn Ser Ser His Ser Val Cys Asp Glu Gly Ala Ile Gly
          435          440          445
Tyr Cys Thr Asp His Glu Ser Ser Ser His His Asp Leu Glu Gly Ala
          450          455          460
Val Gly Gly Tyr Tyr Pro Glu Pro Ser Lys Leu Cys His Leu Asp Gln
          465          470          475
Ser Asp Ser Asp Phe His Gly Asp Leu Thr Phe Gln His Val Phe His
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Asn His Thr Tyr His Leu Gln Pro Thr Ala Pro Glu Ser Thr Ser Glu
          500          505          510
Pro Phe Pro Trp Pro Gly Lys Ser Gln Lys Ile Arg Ser Arg Tyr Leu
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Glu Asp Thr Asp Arg Asn Leu Ser Arg Asp Glu Gln Arg Ala Lys Ala
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Leu His Ile Pro Phe Ser Val Asp Glu Ile Val Gly Met Pro Val Asp
          545          550          555
Ser Phe Asn Ser Met Leu Ser Arg Tyr Tyr Leu Thr Asp Leu Gln Val
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Asp Ile Arg Arg Arg Gly Lys Asn Lys Val Ala Ala
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Gln Asn Cys Arg Lys Arg Lys Leu Asp Ile Ile Leu Asn Leu Glu Asp
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Asp Val Cys Asn Leu Gln Ala Lys Lys Glu Thr Leu Lys Arg Glu Gln
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Ala Gln Cys Asn Lys Ala Ile Asn Ile Met Lys Gln Lys Leu His Asp
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Val Asn Pro Asn His Tyr Ala Leu Gln Cys Thr His Asp Gly Ser Ile
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<211> 425

<212> DNA

<213> Homo sapiens

<400> 5349

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<211> 134

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Leu	Gly	Lys	His	His	Thr	Ser	Arg	Glu	Pro	Gln	Ala	Gln	Pro	Lys	Pro
		35					40				45				
His	Lys	Val	Ser	Ser	Gln	Glu	Gly	Glu	Arg	Ile	Pro	Leu	Pro	Gly	
	50				55				60						
Lys	Ala	Glu	Val	Arg	Glu	Ala	Gly	Gln	Pro	Ile	Pro	Val	Ser	Leu	Leu
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Leu	Leu	Ser	Pro	Lys	Lys	Ala	Leu	Thr	Leu	Ala	Thr	Ala	Gln	Gly	
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 Val Ser Lys Pro Ser Leu Phe Ser Ser Val Gln Leu Tyr Arg Gln Ser
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<213> Homo sapiens

<400> 5354

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Pro Ile Ala Thr Pro Asp Tyr Ile Gln Asn Ala Pro Gly Leu Pro Lys
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<212> PRT

<213> Homo sapiens

<400> 5360

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 Ser Leu Glu Ser Ala Ala Ser Ser Ala Ile Pro Pro Lys Tyr Val Asn
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 Lys Ser His Leu Trp Arg Ser Ala Ser Leu Glu Ser Val Glu Ser Pro
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 Ser Pro Gln Lys Ser Cys Ser Pro Ser Phe Asp Thr Pro Glu Ser Gln
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<211> 1080

<212> DNA

<213> Homo sapiens

<400> 5361

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<212> PRT

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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 1620
 agggttctct ggcatcacgc tggcagccat tagacacaca ggggggtttc tcaaatctca
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<210> 5366

<211> 477

<212> PRT

<213> Homo sapiens

<400> 5366

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Ser	Ile	Cys	Leu	Asp	Tyr	Phe	Thr	Asp	Pro	Val	Met	Thr	Thr	Cys	Gly
			20					25					30		
His	Asn	Phe	Cys	Arg	Ala	Cys	Ile	Gln	Leu	Ser	Trp	Glu	Lys	Ala	Arg
			35				40					45			
Gly	Lys	Lys	Gly	Arg	Arg	Lys	Arg	Lys	Gly	Ser	Phe	Pro	Cys	Pro	Glu
	50					55					60				
Cys	Arg	Glu	Met	Ser	Pro	Gln	Arg	Asn	Leu	Leu	Pro	Asn	Arg	Leu	Leu
65					70				75					80	
Thr	Lys	Val	Ala	Glu	Met	Ala	Gln	Gln	His	Pro	Gly	Leu	Gln	Lys	Gln
				85				90					95		
Asp	Leu	Cys	Gln	Glu	His	His	Glu	Pro	Leu	Lys	Leu	Phe	Cys	Gln	Lys
			100					105					110		
Asp	Gln	Ser	Pro	Ile	Cys	Val	Val	Cys	Arg	Glu	Ser	Arg	Glu	His	Arg
			115				120					125			
Leu	His	Arg	Val	Leu	Pro	Ala	Glu	Glu	Ala	Val	Gln	Gly	Tyr	Lys	Leu
	130					135				140					
Lys	Leu	Glu	Glu	Asp	Met	Glu	Tyr	Leu	Arg	Glu	Gln	Ile	Thr	Arg	Thr
145					150					155				160	
Gly	Asn	Leu	Gln	Ala	Arg	Glu	Glu	Gln	Ser	Leu	Ala	Glu	Trp	Gln	Gly
			165					170						175	
Lys	Val	Lys	Glu	Arg	Arg	Glu	Arg	Ile	Val	Leu	Glu	Phe	Glu	Lys	Met
			180					185					190		
Asn	Leu	Tyr	Leu	Val	Glu	Glu	Glu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu
	195						200					205			
Thr	Glu	Glu	Glu	Glu	Thr	Ala	Ser	Arg	Leu	Arg	Glu	Ser	Val	Ala	Cys
	210					215					220				
Leu	Asp	Arg	Gln	Gly	His	Ser	Leu	Glu	Leu	Leu	Leu	Gln	Leu	Glu	
225					230					235				240	
Glu	Arg	Ser	Thr	Gln	Gly	Pro	Leu	Gln	Met	Leu	Gln	Asp	Met	Lys	Glu
			245					250					255		
Pro	Leu	Ser	Arg	Lys	Asn	Asn	Val	Ser	Val	Gln	Cys	Pro	Glu	Val	Ala
			260					265					270		
Pro	Pro	Thr	Arg	Pro	Arg	Thr	Val	Cys	Arg	Val	Pro	Gly	Gln	Ile	Glu

275	280	285
Val Leu Arg Gly Phe Leu Glu Asp Val Val Pro Asp Ala Thr Ser Ala		
290	295	300
Tyr Pro Tyr Leu Leu Leu Tyr Glu Ser Arg Gln Arg Arg Tyr Leu Gly		
305	310	315
Ser Ser Pro Glu Gly Ser Gly Phe Cys Ser Lys Asp Arg Phe Val Ala		
	325	330
Tyr Pro Cys Ala Val Gly Gln Thr Ala Phe Ser Ser Gly Arg His Tyr		
	340	345
Trp Glu Val Gly Met Asn Ile Thr Gly Asp Ala Leu Trp Ala Leu Gly		
	355	360
Val Cys Arg Asp Asn Val Ser Arg Lys Asp Arg Val Leu Lys Cys Pro		
	370	375
Glu Asn Gly Phe Trp Val Val Gln Leu Ser Lys Gly Thr Lys Tyr Leu		
	385	390
Ser Thr Phe Ser Ala Leu Thr Pro Val Met Leu Met Glu Pro Pro Ser		
		405
His Met Gly Ile Phe Leu Asp Phe Glu Ala Gly Glu Val Ser Phe Tyr		
	420	425
Ser Val Ser Asp Gly Ser His Leu His Thr Tyr Ser Gln Ala Thr Phe		
	435	440
Pro Gly Pro Leu Gln Pro Phe Phe Cys Leu Gly Ala Pro Lys Ser Gly		
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Gln Met Val Ile Ser Thr Val Thr Met Trp Val Lys Gly		
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<210> 5367

<211> 549

<212> DNA

<213> Homo sapiens

<400> 5367

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120
gagtctcagg ggctggggat gctgcccccg aagcccccta cttttgggga gttcctgtcc
180
cagcacaaag ctgaggccag cagccgcaga aggagaaaga gcagtcggcc ccaggccaag
240
gcagcgccca gggcctacag tgaccatgat gaccgctggg agacaaaaga aggggcagca
300
tccccagccc ctgagactcc acagcctact tcccccgaga cttcccccaa ggagacaccc
360
atgcagccac ccgagatccc agctcctgcc caccggcctc ctgaagacga gggggaagag
420
aatgaggggg aagaggatga agaatgggag gacataagtg aggatgagga agaggaggag
480
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540
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549

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<210> 5368

<211> 137

<212> PRT

<213> Homo sapiens

<400> 5368

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20          25          30
Ala Lys Ala Ala Pro Arg Ala Tyr Ser Asp His Asp Asp Arg Trp Glu
35          40          45
Thr Lys Glu Gly Ala Ala Ser Pro Ala Pro Glu Thr Pro Gln Pro Thr
50          55          60
Ser Pro Glu Thr Ser Pro Lys Glu Thr Pro Met Gln Pro Pro Glu Ile
65          70          75          80
Pro Ala Pro Ala His Arg Pro Pro Glu Asp Glu Gly Glu Glu Asn Glu
85          90          95
Gly Glu Glu Asp Glu Glu Trp Glu Asp Ile Ser Glu Asp Glu Glu Glu
100         105         110
Glu Glu Ile Glu Val Glu Glu Gly Asp Glu Glu Glu Pro Ala Gln Asp
115         120         125
His Gln Ala Pro Glu Ala Ala Pro Thr
130         135

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<210> 5369

<211> 646

<212> DNA

<213> Homo sapiens

<400> 5369

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cgcccgccgc tcggtcccg ccccgccatg gcccgccctga cgagagcgga ggcgcgccgg
120
cagcagcagc agctcctgca gcccgggccc tcgcccgtgg gcagcagcgg gcccgagccc
180
cccggggggc agcccgacgg catgaaggac ctggagcgcca tcaaactctt cgtggggccag
240
atcccgcgcg acctggacga gaaggacctc aagccgctct tcgagcagtt cgcccgcatc
300
tacgagctca cggtgctcaa agaccctac acgggggatgc aaaaaggtag gcggcgccgc
360
ccctcccccc tctcccccct cctccgcctc ccacccccc ttccggcatc ttctctcccc
420
catcaccatc cctctctctg tcacctccct cctctgcctg cctctgccgg agcatcggtt
480
cttaccacct ccctccccc caccctctct ccctctctg ggggtgcagc tgacagatcc
540
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<210> 5370

<211> 148

<212> PRT

<213> Homo sapiens

<400> 5370

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Met Lys Asp Leu Asp Ala Ile Lys Leu Phe Val Gly Gln Ile Pro Arg
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His Leu Asp Glu Lys Asp Leu Lys Pro Leu Phe Glu Gln Phe Gly Arg
      20           25           30
Ile Tyr Glu Leu Thr Val Leu Lys Asp Pro Tyr Thr Gly Met His Lys
      35           40           45
Gly Gly Arg Pro Ala Pro Ser Pro Leu Ser Pro Ser Leu Arg Leu Pro
      50           55           60
Pro His Leu Pro Ala Ser Ser Leu Pro His His His Pro Ser Ser Ala
65           70           75           80
His Leu Pro Pro Leu Pro Ala Ser Ala Gly Ala Ser Val Leu Thr Pro
      85           90           95
Ser Leu Pro Pro Thr Pro Pro Pro Leu Ser Gly Gly Ala Ala Asp Arg
      100          105          110
Ser Glu Arg Ala Pro Ser Pro Pro Pro Pro Leu Pro Pro Ser Pro
      115          120          125
Pro Ser Gly Ile Ser Ser Leu Ser Pro Ser Leu Ser Pro Ser Leu Ser
      130          135          140
Pro Phe Leu Phe
145

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<210> 5371

<211> 1177

<212> DNA

<213> Homo sapiens

<400> 5371

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120
tccacgcctt ccactgtcct cagcgaccag gccaaagtatc taaaccctt actgggagag
180
tggaagcact tcactgcctt cctggccccc cgcattgcca accagggcat cgcgggtgctc
240
aacaacttcg tatacttgat tggaggggac aacaatgtcc aaggatttcg agcagagtcc
300
cgatgctgga ggtatgacc acggcacaac cgctggnttc cagatccagt cctgcagca
360
ggagcacgcc gacctgtcnn cgtgtgtgtt gtaggcaggt acatctacgc tgtggcgggc
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gcatacgtgg cccactcaa gagggagggtg tatgcccacg caggcgcgac gctggagggg
540
aagatgtata tcacctcggg ccgcagaggg gaggattacc tgaagagac aactgctac
600
gatccaggca gcaaaccttg gcacacactg gctgatgggc ctgtgcggcg cgctggcac
660

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 720
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 780
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 900
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 1177

<210> 5372

<211> 368

<212> PRT

<213> Homo sapiens

<400> 5372

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Pro	Ser	Leu	Gln	Ser	Pro	Gln	Thr	Glu	Leu	Arg	Ser	Asp	Phe	Gln	Cys
		20						25					30		
Val	Val	Gly	Phe	Gly	Gly	Ile	His	Ser	Thr	Pro	Ser	Thr	Val	Leu	Ser
		35				40					45				
Asp	Gln	Ala	Lys	Tyr	Leu	Asn	Pro	Leu	Leu	Gly	Glu	Trp	Lys	His	Phe
50					55					60					
Thr	Ala	Ser	Leu	Ala	Pro	Arg	Met	Ser	Asn	Gln	Gly	Ile	Ala	Val	Leu
65				70					75				80		
Asn	Asn	Phe	Val	Tyr	Leu	Ile	Gly	Gly	Asp	Asn	Asn	Val	Gln	Gly	Phe
			85						90				95		
Arg	Ala	Glu	Ser	Arg	Cys	Trp	Arg	Tyr	Asp	Pro	Arg	His	Asn	Arg	Trp
		100						105					110		
Xaa	Pro	Asp	Pro	Val	Pro	Ala	Ala	Gly	Ala	Arg	Arg	Pro	Val	Xaa	Val
		115					120					125			
Cys	Val	Val	Gly	Arg	Tyr	Ile	Tyr	Ala	Val	Ala	Gly	Arg	Asp	Tyr	His
		130				135					140				
Asn	Asp	Leu	Asn	Ala	Val	Glu	Arg	Tyr	Asp	Pro	Ala	Thr	Asn	Ser	Trp
145				150					155					160	
Ala	Tyr	Val	Ala	Pro	Leu	Lys	Arg	Glu	Val	Tyr	Ala	His	Ala	Gly	Ala
			165					170					175		
Thr	Leu	Glu	Gly	Lys	Met	Tyr	Ile	Thr	Cys	Gly	Arg	Arg	Gly	Glu	Asp
		180					185						190		
Tyr	Leu	Lys	Glu	Thr	His	Cys	Tyr	Asp	Pro	Gly	Ser	Asn	Thr	Trp	His
		195				200					205				
Thr	Leu	Ala	Asp	Gly	Pro	Val	Arg	Arg	Ala	Trp	His	Gly	Met	Ala	Thr
	210					215					220				
Leu	Leu	Asn	Lys	Leu	Tyr	Val	Ile	Gly	Gly	Ser	Asn	Asn	Asp	Ala	Gly

225		230		235		240									
Tyr	Arg	Arg	Asp	Val	His	Gln	Val	Ala	Cys	Tyr	Ser	Cys	Thr	Ser	Gly
			245					250						255	
Gln	Trp	Ser	Ser	Val	Cys	Pro	Leu	Pro	Ala	Gly	His	Gly	Glu	Pro	Gly
			260					265					270		
Ile	Ala	Val	Leu	Asp	Asn	Arg	Ile	Tyr	Val	Leu	Gly	Gly	Arg	Ser	His
		275					280								
Asn	Arg	Gly	Ser	Arg	Thr	Gly	Tyr	Val	His	Ile	Tyr	Asp	Val	Glu	Lys
		290				295					300				
Asp	Cys	Trp	Glu	Glu	Gly	Pro	Gln	Leu	Asp	Asn	Ser	Ile	Ser	Gly	Leu
305					310						315				320
Ala	Ala	Cys	Val	Leu	Thr	Leu	Pro	Arg	Ser	Leu	Leu	Leu	Glu	Pro	Pro
			325						330					335	
Arg	Gly	Thr	Pro	Asp	Arg	Ser	Gln	Ala	Asp	Pro	Asp	Phe	Ala	Ser	Glu
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<210> 5373

<211> 4221

<212> DNA

<213> Homo sapiens

<400> 5373

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 120
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 180
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 240
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 300
 aatgaaggag aaacatcaga tggagtggag aagtcagttc acaagggtctt tgcttccatg
 360
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 420
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 480
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 720
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 900

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<210> 5374

<211> 886

<212> PRT

<213> Homo sapiens

<400> 5374

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			20				25						30		
Lys	Lys	Ser	Leu	Gln	Glu	Lys	Gly	Lys	Leu	Ser	Ala	Glu	Glu	Asn	Pro
		35					40				45				
Asp	Asp	Ser	Glu	Val	Pro	Ser	Ser	Ser	Gly	Ile	Asn	Ser	Thr	Lys	Ser
	50					55					60				
Gln	Asp	Lys	Asp	Val	Asn	Glu	Gly	Glu	Thr	Ser	Asp	Gly	Val	Arg	Lys
65				70					75					80	
Ser	Val	His	Lys	Val	Phe	Ala	Ser	Met	Leu	Gly	Glu	Asn	Glu	Asp	Asp
			85						90					95	
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr
			100					105					110		
Pro	Glu	Gln	Pro	Thr	Ala	Gly	Asp	Val	Phe	Val	Leu	Glu	Met	Val	Leu
			115				120					125			
Asn	Arg	Glu	Thr	Lys	Lys	Met	Met	Lys	Glu	Lys	Arg	Pro	Arg	Ser	Lys
			130			135					140				
Leu	Pro	Arg	Ala	Leu	Arg	Gly	Leu	Met	Gly	Glu	Ala	Asn	Ile	Arg	Phe
145				150					155					160	
Ala	Arg	Gly	Glu	Arg	Glu	Glu	Ala	Ile	Leu	Met	Cys	Met	Glu	Ile	Ile
			165						170					175	
Arg	Gln	Ala	Pro	Leu	Ala	Tyr	Glu	Pro	Phe	Ser	Thr	Leu	Ala	Met	Ile
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Tyr	Glu	Asp	Gln	Gly	Asp	Met	Glu	Lys	Ser	Leu	Gln	Phe	Glu	Leu	Ile
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Ala	Ala	His	Leu	Asn	Pro	Ser	Asp	Thr	Glu	Glu	Trp	Val	Arg	Leu	Ala
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Glu	Met	Ser	Leu	Glu	Gln	Asp	Asn	Ile	Lys	Gln	Ala	Ile	Phe	Cys	Tyr
225					230					235				240	
Thr	Lys	Ala	Leu	Lys	Tyr	Glu	Pro	Thr	Asn	Val	Arg	Tyr	Leu	Trp	Glu
			245					250					255		
Arg	Ser	Ser	Leu	Tyr	Glu	Gln	Met	Gly	Asp	His	Lys	Met	Ala	Met	Asp
		260					265						270		
Gly	Tyr	Arg	Arg	Ile	Leu	Asn	Leu	Leu	Ser	Pro	Ser	Asp	Gly	Glu	Arg
	275					280						285			
Phe	Met	Gln	Leu	Ala	Arg	Asp	Met	Ala	Lys	Ser	Tyr	Tyr	Glu	Ala	Asn
	290					295					300				
Asp	Val	Thr	Ser	Ala	Ile	Asn	Ile	Ile	Asp	Glu	Ala	Phe	Ser	Lys	His
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Gln	Gly	Leu	Val	Ser	Met	Glu	Asp	Val	Asn	Ile	Ala	Ala	Glu	Leu	Tyr
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Pro	Glu	Asp	Met	Gly	Asp	Leu	Tyr	Leu	Asp	Val	Ala	Glu	Ala	Phe	Leu														
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Asp	Val	Gly	Glu	Tyr	Asn	Ser	Ala	Leu	Pro	Leu	Leu	Ser	Ala	Leu	Val														
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Cys	Ser	Glu	Arg	Tyr	Asn	Leu	Ala	Val	Val	Trp	Leu	Arg	His	Ala	Glu														
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Phe	Cys	Leu	Arg	Leu	Met	Leu	Lys	Asn	Pro	Glu	Asn	His	Ala	Leu	Cys														
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Val	Leu	Asn	Gly	His	Asn	Ala	Phe	Val	Ser	Gly	Ser	Phe	Lys	His	Ala														
740										745										750									
Leu	Gly	Gln	Tyr	Val	Gln	Ala	Phe	Arg	Thr	His	Pro	Asp	Glu	Pro	Leu														
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Tyr	Ser	Phe	Cys	Ile	Gly	Leu	Thr	Phe	Ile	His	Met	Al																	

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Tyr Val Leu Arg Arg His Ala Leu Ile Val Gln Gly Phe Ser Phe Leu
785              790              795              800
Asn Arg Tyr Leu Ser Ser Leu Arg Gly Pro Cys Gln Glu Ser Phe Tyr Asn
      805              810              815
Leu Gly Arg Gly Leu His Gln Leu Gly Leu Ile His Leu Ala Ile His
      820              825              830
Tyr Tyr Gln Lys Ala Leu Glu Leu Pro Pro Leu Val Val Glu Gly Ile
      835              840              845
Glu Leu Asp Gln Leu Asp Leu Arg Arg Asp Ile Ala Tyr Asn Leu Ser
      850              855              860
Leu Ile Tyr Gln Ser Ser Gly Asn Thr Gly Met Ala Gln Thr Leu Leu
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Tyr Thr Tyr Cys Ser Ile
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<210> 5375

<211> 526

<212> DNA

<213> Homo sapiens

<400> 5375

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120
tggttaacgat ctgtcttctg caaatggggt acagcgtgct gctgccagtt ctgaatcccc
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240
cccctctcc ttattaaaga agaatacatg tcgctgccat ttgccacgta ttgccatag
300
accaggact attagcatct ttaaccacac taaccacact ggggatggct ggggaatggt
360
catgtcccca ttttacagga gtggtgatta aggctcaaag tagggagggt atggatcaaa
420
gtcgtctgcc aagtgggtgc agcattgggt ctcagaccga ggcccgctcta cacagtgtgt
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<210> 5376

<211> 112

<212> PRT

<213> Homo sapiens

<400> 5376

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Arg Ala Ser Arg Val Leu Ser Gly Asn Asp Leu Ser Ser Ala Asn Gly
20          25          30
Leu Gln Arg Ala Ala Ser Ser Glu Ser Pro Val Ala Arg Thr Trp
35          40          45
Val Gln Leu Lys Ser Ile Ser Leu Phe Ala Phe Ser Glu Ala Ser Pro

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50		55		60
Ser Ser Leu Leu Lys Lys Asn Thr Cys Arg Cys His Leu Pro Arg Ile				
65	70		75	80
Cys His Arg Pro Arg Thr Ile Ser Ile Phe Asn Pro Arg Asn His Thr				
	85	90	95	
Gly Asp Gly Trp Gly Met Phe Met Ser Pro Phe Tyr Arg Ser Gly Asp				
100	105	110		

<210> 5377

<211> 1452

<212> DNA

<213> Homo sapiens

<400> 5377

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120
cggggactgt gcacgaggtt ggcgacgcgc ccccgccggg cccagatca ggcgcgagag
180
atcgggagcc gcgggagcac taaggcgcaa gggccacagc agcagccggg ctcagagggg
240
cccagctatg ccaaaaaagt tgcgctctgg cttgctgggc tgcttgagc tgggtgggact
300
gtgagcgctg tctatatctt tggaaacaac ccgggtggagc aaaatggtgc caagattcct
360
gatgagttcg acaatgatcc aattctggta cagcagttgc gccggacata caaatatttc
420
aaagattata gacagatgat catcgagccc accagccctt gccttctccc agaccctctg
480
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720
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960
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1200

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 1320
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 1452

<210> 5378

<211> 374

<212> PRT

<213> Homo sapiens

<400> 5378

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			20					25					30		
Arg	Ser	Gly	Leu	Arg	Leu	Gly	Ser	Arg	Gly	Leu	Cys	Thr	Arg	Leu	Ala
		35					40					45			
Thr	Pro	Pro	Arg	Arg	Ala	Pro	Asp	Gln	Ala	Ala	Glu	Ile	Gly	Ser	Arg
		50				55					60				
Gly	Ser	Thr	Lys	Ala	Gln	Gly	Pro	Gln	Gln	Gln	Pro	Gly	Ser	Glu	Gly
65					70					75				80	
Pro	Ser	Tyr	Ala	Lys	Lys	Val	Ala	Leu	Trp	Leu	Ala	Gly	Leu	Leu	Gly
			85						90					95	
Ala	Gly	Gly	Thr	Val	Ser	Val	Val	Tyr	Ile	Phe	Gly	Asn	Asn	Pro	Val
			100					105					110		
Asp	Glu	Asn	Gly	Ala	Lys	Ile	Pro	Asp	Glu	Phe	Asp	Asn	Asp	Pro	Ile
		115				120					125				
Leu	Val	Gln	Gln	Leu	Arg	Arg	Thr	Tyr	Lys	Tyr	Phe	Lys	Asp	Tyr	Arg
		130				135					140				
Gln	Met	Ile	Ile	Glu	Pro	Thr	Ser	Pro	Cys	Leu	Leu	Pro	Asp	Pro	Leu
145					150					155				160	
Gln	Glu	Pro	Tyr	Tyr	Gln	Pro	Pro	Tyr	Thr	Leu	Val	Leu	Glu	Leu	Thr
			165					170						175	
Gly	Val	Leu	Leu	His	Pro	Glu	Trp	Ser	Leu	Ala	Thr	Gly	Trp	Arg	Phe
		180						185					190		
Lys	Lys	Arg	Pro	Gly	Ile	Glu	Thr	Leu	Phe	Gln	Gln	Leu	Ala	Pro	Leu
		195					200					205			
Tyr	Glu	Ile	Val	Ile	Phe	Thr	Ser	Glu	Thr	Gly	Met	Thr	Ala	Phe	Pro
		210				215					220				
Leu	Ile	Asp	Ser	Val	Asp	Pro	His	Gly	Phe	Ile	Ser	Tyr	Arg	Leu	Phe
225					230					235				240	
Arg	Asp	Ala	Thr	Arg	Tyr	Met	Asp	Gly	His	His	Val	Lys	Asp	Ile	Ser
				245					250					255	
Cys	Leu	Asn	Arg	Asp	Pro	Ala	Arg	Val	Val	Val	Val	Asp	Cys	Lys	Lys
		260					265						270		
Glu	Ala	Phe	Arg	Leu	Gln	Pro	Tyr	Asn	Gly	Val	Ala	Leu	Arg	Pro	Trp
		275					280					285			
Asp	Gly	Asn	Ser	Asp	Asp	Arg	Val	Leu	Leu	Asp	Leu	Ser	Ala	Phe	Leu

290		295		300
Lys Thr Ile Ala Leu Asn Gly Val Glu Asp Val Arg Thr Val Leu Glu				
305		310		315
His Tyr Ala Leu Glu Asp Asp Pro Leu Ala Ala Phe Lys Gln Arg Gln				
	325		330	335
Ser Arg Leu Glu Gln Glu Glu Gln Gln Arg Leu Ala Glu Leu Ser Lys				
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Ser Asn Lys Gln Asn Leu Phe Leu Gly Ser Leu Thr Ser Arg Leu Trp				
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<210> 5379

<211> 3213

<212> DNA

<213> Homo sapiens

<400> 5379

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<210> 5380

<211> 903

<212> PRT

<213> Homo sapiens

<400> 5380

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 35 40 45
 Cys Asp Arg Gly Cys Leu Ala Ala Ile Leu Ala Ser Thr Ser Ala Thr
 50 55 60
 Gln Ala Arg Met Val Leu Arg Cys Cys Ser Glu Phe Ile Glu Ala His
 65 70 75 80
 Gly Val Val Asp Gly Ile Tyr Arg Leu Ser Gly Val Ser Ser Asn Ile
 85 90 95
 Gln Arg Leu Arg His Glu Phe Asp Ser Glu Arg Ile Pro Glu Leu Ser
 100 105 110
 Gly Pro Ala Phe Leu Gln Asp Ile His Ser Val Ser Ser Leu Cys Lys
 115 120 125
 Leu Tyr Phe Arg Glu Leu Pro Asn Pro Leu Leu Thr Tyr Gln Leu Tyr
 130 135 140
 Gly Lys Phe Ser Glu Ala Met Ser Val Pro Gly Glu Glu Glu Arg Leu
 145 150 155 160
 Val Arg Val His Asp Val Ile Gln Gln Leu Pro Pro Pro His Tyr Arg
 165 170 175
 Thr Leu Glu Tyr Leu Leu Arg His Leu Ala Arg Met Ala Arg His Ser
 180 185 190
 Ala Asn Thr Ser Met His Ala Arg Asn Leu Ala Ile Val Trp Ala Pro
 195 200 205
 Asn Leu Leu Arg Ser Met Glu Leu Glu Ser Val Gly Met Gly Gly Ala
 210 215 220
 Ala Ala Phe Arg Glu Val Arg Val Gln Ser Val Val Val Glu Phe Leu

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225                230                235                240
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Gly Ser Cys Pro Ser Thr Arg Leu Leu Thr Leu Glu Glu Ala Gln Ala
                275                280                285
Arg Thr Gln Gly Arg Leu Gly Thr Pro Thr Glu Pro Thr Thr Pro Lys
                290                295                300
Ala Pro Ala Ser Pro Ala Glu Arg Arg Lys Gly Glu Arg Gly Glu Lys
305                310                315
Gln Arg Lys Pro Gly Gly Ser Ser Trp Lys Thr Phe Phe Ala Leu Gly
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Arg Gly Pro Ser Val Pro Arg Lys Lys Pro Leu Pro Trp Leu Gly Gly
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Thr Arg Ala Pro Pro Gln Pro Ser Ala Trp Leu Asp Asp Gly Asp Glu
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Leu Asp Phe Ser Pro Pro Arg Cys Leu Glu Gly Leu Arg Gly Leu Asp
370                375                380
Phe Asp Pro Leu Thr Phe Arg Cys Ser Ser Pro Thr Pro Gly Asp Pro
385                390                395
Ala Pro Pro Ala Ser Pro Ala Pro Pro Ala Pro Ala Ser Ala Phe Pro
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Pro Arg Val Thr Pro Gln Ala Ile Ser Pro Arg Gly Pro Thr Ser Pro
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Ala Ser Pro Ala Ala Leu Asp Ile Ser Glu Pro Leu Ala Val Ser Val
                435                440                445
Pro Pro Ala Val Leu Glu Leu Leu Gly Ala Gly Gly Ala Pro Ala Ser
450                455                460
Ala Thr Pro Thr Pro Ala Leu Ser Pro Gly Arg Ser Leu Arg Pro His
465                470                475
Leu Ile Pro Leu Leu Leu Arg Gly Ala Glu Ala Pro Leu Thr Asp Ala
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Cys Gln Gln Glu Met Cys Ser Lys Leu Arg Gly Ala Gln Gly Pro Leu
500                505
Ala Arg Leu Met Ala Leu Ala Leu Ala Glu Arg Ala Gln Gln Val Ala
515                520                525
Glu Gln Gln Ser Gln Gln Glu Cys Gly Gly Thr Pro Pro Ala Ser Gln
530                535                540
Ser Pro Phe His Arg Ser Leu Ser Leu Glu Val Gly Gly Glu Pro Leu
545                550                555
Gly Thr Ser Gly Ser Gly Pro Pro Pro Asn Ser Leu Ala His Pro Gly
565                570                575
Ala Trp Val Pro Gly Pro Pro Pro Tyr Leu Pro Arg Gln Gln Ser Asp
580                585                590
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595                600                605
Leu Arg Gly Pro Ala Gln Val Ser Ala Gln Leu Arg Ala Gly Gly Gly
610                615                620
Gly Arg Asp Ala Pro Glu Ala Ala Ala Gln Ser Pro Cys Ser Val Pro
625                630                635
Ser Gln Val Pro Thr Pro Gly Phe Phe Ser Pro Ala Pro Arg Glu Cys
645                650                655
Leu Pro Pro Phe Leu Gly Val Pro Lys Pro Gly Leu Tyr Pro Leu Gly

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 690 695 700
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 Ser Pro Phe Arg Ser Met Pro Pro Asp Arg Leu Asn Ala Ser Tyr Gly
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 Met Leu Gly Gln Ser Pro Pro Leu His Arg Ser Pro Asp Phe Leu Leu
 740 745 750
 Ser Tyr Pro Pro Ala Pro Ser Cys Phe Pro Pro Asp His Leu Gly Tyr
 755 760 765
 Ser Ala Pro Gln His Pro Ala Arg Arg Pro Thr Pro Pro Glu Pro Leu
 770 775 780
 Tyr Val Asn Leu Ala Leu Gly Pro Arg Gly Pro Ser Pro Ala Ser Ser
 785 790 795 800
 Ser Ser Ser Ser Pro Pro Ala His Pro Arg Ser Arg Ser Asp Pro Gly
 805 810 815
 Pro Pro Val Pro Arg Leu Pro Gln Lys Gln Arg Ala Pro Trp Gly Pro
 820 825 830
 Arg Thr Pro Pro His Arg Val Pro Gly Pro Trp Gly Pro Pro Glu Pro Leu
 835 840 845
 Leu Leu Tyr Arg Ala Ala Pro Pro Ala Tyr Gly Arg Gly Gly Glu Leu
 850 855 860
 His Arg Gly Ser Leu Tyr Arg Asn Gly Gly Gln Arg Gly Glu Gly Ala
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<210> 5381

<211> 1576

<212> DNA

<213> Homo sapiens

<400> 5381

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<210> 5382

<211> 223

<212> PRT

<213> Homo sapiens

<400> 5382

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 35 40 45
 Gln Arg Phe Val Asp Ala Tyr Phe Lys Ala Tyr Pro Gly Tyr Tyr Phe
 50 55 60
 Thr Gly Asp Gly Ala Tyr Arg Thr Glu Gly Gly Tyr Tyr Gln Ile Thr

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			100					105					110		
Ala	Val	Ile	Gly	Tyr	Pro	His	Asp	Ile	Lys	Gly	Glu	Ala	Ala	Phe	Ala
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Phe	Ile	Val	Val	Lys	Asp	Ser	Ala	Gly	Asp	Ser	Asp	Val	Val	Val	Gln
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Glu	Leu	Lys	Ser	Met	Val	Ala	Thr	Lys	Ile	Ala	Lys	Tyr	Ala	Val	Pro
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Asp	Glu	Ile	Leu	Val	Val	Lys	Arg	Leu	Pro	Lys	Thr	Arg	Ser	Gly	Lys
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Val	Met	Arg	Arg	Leu	Leu	Arg	Lys	Ile	Ile	Thr	Ser	Glu	Ala	Gln	Glu
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<210> 5383

<211> 2027

<212> DNA

<213> Homo sapiens

<400> 5383

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<210> 5384

<211> 508

<212> PRT

<213> Homo sapiens

<400> 5384

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 Leu Asp Arg Pro Gln Gln Trp Leu Gln Leu Val Leu Leu Pro Pro Ala
 35 40 45
 Leu Phe Ile Pro Ser Thr Glu Asn Glu Glu Gln Arg Leu Ala Ser Ala

50					55					60				
Arg Val Ala Pro	Arg Asn Val	Gln Pro Tyr	Val Val Tyr	Glu Glu Val	80									
65	Thr Asn Val	Trp Ile Asn	Val His Asp	Ile Phe Tyr	Pro Phe Pro	85								
70														
75	Ser Glu Gly	Glu Asp Glu	Leu Cys Phe	Leu Arg Ala	Asn Glu Cys	90								
80	Thr Gly Phe	Cys His Leu	Tyr Lys Val	Thr Ala Val	Leu Lys Ser	95								
85														
90	Gly Tyr Asp	Trp Ser Glu	Pro Phe Ser	Pro Gly Glu	Gly Glu Gln	100								
95	Leu Thr Asn	Ala Ile Trp	Val Asn Glu	Glu Thr Lys	Leu Val Tyr	105								
100														
105	Gln Gly Thr	Lys Asp Thr	Pro Leu Glu	His His Leu	Tyr Val Val	110								
110	Tyr Glu Ala	Ala Gly Glu	Ile Glu Ile	Val Arg Leu	Thr Thr Pro	115								
115	His Ser Cys	Ser Met Ser	Gln Asn Phe	Asp Met Phe	Val Ser His	120								
120														
125	Ser Ser Val	Ser Thr Pro	Pro Cys Val	His Val Tyr	Lys Leu Ser	130								
130	Pro Asp Asp	Asp Pro Leu	His Lys Gln	Pro Arg Phe	Trp Ala Ser	135								
135	Met Glu Ala	Ala Lys Ile	Phe His Phe	His Thr Arg	Ser Asp Val	140								
140	Leu Tyr Gly	Met Ile Tyr	Lys Pro His	Ala Leu Gln	Pro Gly Lys	145								
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150	His Pro Thr	Val Leu Phe	Val Tyr Gly	Gly Gly Pro	Gln Val Gln	155								
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160	Asn Asn Ser	Phe Lys Gly	Ile Lys Tyr	Leu Arg Leu	Asn Thr Leu	165								
165	Ser Leu Gly	Tyr Ala Val	Val Val Ile	Asp Gly Arg	Gly Ser Cys	170								
170	Arg Gly Leu	Arg Phe Glu	Gly Ala Val	Gln Lys Asn	Gln Val Tyr	175								
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180	Glu Ile Glu	Asp Gln Val	Glu Gly Leu	Phe Val Ala	Glu Lys Tyr	185								
185	Gly Phe Ile	Asp Leu Ser	Arg Val Ala	Ile His Gly	Trp Ser Tyr	190								
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195	Val Ala Ile	Ala Gly Ala	Pro Val Thr	Val Trp Met	Ala Tyr Asp	195								
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205	Gly Tyr Thr	Glu Ser Leu	Val Tyr Gly	Gly Gly Pro	Gln Val Gln	210								
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215	Val Ala Ile	Asp Gly Arg	Gly Ala Val	Gln Lys Asn	Thr Leu Ala	220								
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225	Ser Leu Gly	Tyr Ala Val	Val Val Ile	Asp Gly Arg	Gly Ser Cys	225								
230	Arg Gly Leu	Arg Phe Glu	Gly Ala Val	Lys Asn Gln	Met Gly Gln	230								
235														
240	Glu Ile Glu	Asp Gln Val	Glu Gly Leu	Phe Val Ala	Glu Lys Tyr	240								
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250	Gly Phe Ile	Asp Leu Ser	Arg Val Ala	Ile His Gly	Trp Ser Tyr	250								
255														
260	Gly Phe Leu	Ser Leu Met	Gly Leu Ile	His Lys Pro	Gln Val Phe	260								
265														
270	Val Ala Ile	Ala Gly Ala	Pro Val Thr	Val Trp Met	Ala Tyr Asp	270								
275														
280	Asn Asn Ser	Phe Lys Gly	Ile Lys Tyr	Leu Arg Leu	Asn Thr Leu	280								
285														
290	Ser Leu Gly	Tyr Ala Val	Val Val Ile	Asp Gly Arg	Gly Ser Cys	290								
295	Arg Gly Leu	Arg Phe Glu	Gly Ala Val	Lys Asn Gln	Met Gly Gln	300								
300														
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<210> 5388
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 5388
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 Phe Thr Trp Cys Phe Cys Phe Ser Met Thr Leu Ile Ile Leu Ile Val
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 Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe
 50 55 60
 Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser
 65 70 75 80
 Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser
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<210> 5389
 <211> 1711
 <212> DNA
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<400> 5389
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<210> 5390

<211> 118

<212> PRT

<213> Homo sapiens

<400> 5390

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Thr Asn Ala Gln Thr Lys Glu Glu Tyr Thr Asp Asp Asn Ala Leu Ile					
	50		55		60
Pro Lys Asn Ser Ser Val Ile Val Arg Arg Ile Pro Ile Gly Gly Val					
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Lys Ser Thr Ser Lys Thr Tyr Val Ile Ser Arg Thr Glu Pro Ala Met					
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<210> 5391

<211> 797

<212> DNA

<213> Homo sapiens

<400> 5391

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<210> 5392

<211> 55

<212> PRT

<213> Homo sapiens

<400> 5392

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<210> 5393

<211> 4837

<212> DNA

<213> Homo sapiens

<400> 5393

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 5394

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<211> 3711

<212> DNA

<213> Homo sapiens

<400> 5395

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<212> PRT

<213> Homo sapiens

<400> 5396

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Leu	Glu	Met	Glu	Asn	Glu	Asn	Leu	Val	Glu	Asn	Gly	Ala	Asp	Ser	Asp	Leu	Glu	Met	Glu	Asn	Glu	Asn	Leu	Val	Glu	Asn	Gly	Ala	Asp	Ser	Asp	Leu	Glu	Met	Glu	Asn	Glu	Asn	Leu	Val	Glu	Asn	Gly	Ala	Asp	Ser	Asp	
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		690																																														
Ser	Leu	Asn	Trp	Ser	Ser	Phe	Val	Asp	Asn	Thr	Phe	Ala	Glu	Glu	Phe	Ser	Leu	Asn	Trp	Ser	Ser	Phe	Val	Asp	Asn	Thr	Phe	Ala	Glu	Glu	Phe	Ser	Leu	Asn	Trp	Ser	Ser	Phe	Val	Asp	Asn	Thr	Phe	Ala	Glu	Glu	Phe	
705						710																																										
Thr	Thr	Gln	Asn	Gln	Lys	Ser	Gln	Asp	Val	Glu	Leu	Trp	Glu	Gly	Glu	Thr	Thr	Gln	Asn	Gln	Lys	Ser	Gln	Asp	Val	Glu	Leu	Trp	Glu	Gly	Glu	Thr	Thr	Gln	Asn	Gln	Lys	Ser	Gln	Asp	Val	Glu	Leu	Trp	Glu	Gly	Glu	
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Val	Val	Lys	Glu	Leu	Ser	Val	Glu	Gln	Ile	Lys	Arg	Asn	Arg	Tyr	Val	Val	Lys	Glu	Leu	Ser	Val	Glu	Gln	Ile	Lys	Arg	Asn	Arg	Tyr	Val	Val	Lys	Glu	Leu	Ser	Val	Glu	Gln	Ile	Lys	Arg	Asn	Arg	Tyr				
		740																																														
Tyr	Asp	Glu	Asp	Glu	Asp	Glu	Glu								Tyr	Asp	Glu	Asp	Glu	Asp	Glu	Glu							Tyr	Asp	Glu	Asp	Glu	Asp	Glu	Glu												
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<210> 5397

<211> 561

<212> DNA

<213> Homo sapiens

<400> 5397

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 240
 aagctcaggg ctggcgga gctggcaggg ctgtccacag ggaggacccc cgtgtgtctc
 300
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 360
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 420

ggtttgaaga ggagagcaga ccaccagag tagtgggaga aagcaccggc agaaaagctg
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<210> 5398

<211> 154

<212> PRT

<213> Homo sapiens

<400> 5398

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 35 40 45
 Ala Gln Gly Trp Ala Glu Ala Gly Arg Ala Val His Arg Glu Asp Pro
 50 55 60
 Arg Val Ser Leu Gly Leu Pro Arg Trp Leu Cys Pro Pro Phe Cys Leu
 65 70 75 80
 Gly Gly Ser Leu Arg Leu Gly Arg Ala Gln Arg Glu Gly Asp Pro Glu
 85 90 95
 Gly Leu Ala Asp Ser Gly Pro Pro Cys Glu Leu Arg Phe Glu Glu Glu
 100 105 110
 Ser Arg Pro Pro Arg Val Val Gly Glu Ser Thr Gly Arg Lys Ala Gly
 115 120 125
 Ile Ser Thr Glu Gly Leu Ser Ala Ser Phe Asp Leu Phe Gln Ser Phe
 130 135 140
 Arg Val Met Asn Gln Ile Ala Phe Met Arg
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<210> 5399

<211> 835

<212> DNA

<213> Homo sapiens

<400> 5399

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 120
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 180
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 240
 gccggaatgc agtaccctca gcagcagatg ccacctcagt atggacagca aggtgtgagt
 300
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 420

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 480
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<210> 5400
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 5400
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 Met Lys Arg Pro Gln Leu Tyr Gly Met Gly Ser Asn Pro His Ser Gln
 35 40 45
 Pro Gln Gln Ser Ser Pro Tyr Pro Gly Gly Ser Tyr Gly Pro Pro Gly
 50 55 60
 Pro Gln Arg Tyr Pro Ile Gly Ile Gln Gly Arg Thr Pro Gly Ala Met
 65 70 75 80
 Ala Gly Met Gln Tyr Pro Gln Gln Gln Met Pro Pro Gln Tyr Gly Gln
 85 90 95
 Gln Gly Val Ser Gly Tyr Cys Gln Gln Gly Gln Gln Pro Tyr Tyr Ser
 100 105 110
 Gln Gln Pro Gln Pro Pro His Leu Pro Pro Gln Ala Gln Tyr Leu Pro
 115 120 125
 Ser Gln Ser Gln Gln Arg Tyr Gln Pro Gln Gln Asp Met Ser Gln Glu
 130 135 140
 Gly Tyr Gly Thr Arg Ser Gln Pro Pro Leu Ala Pro Gly Lys Pro Asn
 145 150 155 160
 His Glu Asp Leu Asn Leu Ile Gln Gln Glu Arg Pro Ser Ser Leu Pro
 165 170 175
 Val Arg His Tyr Cys Ala Asp Leu Glu Met
 180 185

<210> 5401
 <211> 2674
 <212> DNA
 <213> Homo sapiens

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120
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180
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240
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360
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420
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480
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1320
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1380
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1440
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1560
tataaatttg tgaataaga atcagtttaa tttttcacat taaatcctgg ttctagtttg
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accattttaa ttatgacctt tttcaaaggt tgtaaatact gcacggagaa tgtattttta
1680

gacgttcctt taataactta aaagacaaag catcacacaac cagcatatta taggcattgta
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 1980
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 2520
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 2580
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<210> 5402

<211> 507

<212> PRT

<213> Homo sapiens

<400> 5402

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 35 40 45
 Phe Arg Ile Arg Gly Gly Leu Asp Leu Ala Phe Gln Leu Ala Thr Pro
 50 55 60
 Asn Glu Ile Phe Leu Lys Lys Ala Leu Lys His Val Leu Ser Asp Leu
 65 70 75 80
 Ser Thr Lys Leu Ser Ser Asn Ala Leu Val Phe Arg Ile Cys His Ser
 85 90 95
 Ser Val Tyr Ile Trp Pro Ser Ser Asp Ile Asn Thr Ile Pro Gly Glu


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Leu Thr Asp Ala Ser Ala Cys Lys Asn Ile Leu Arg Phe Ile Gln Phe
      115      120      125
Glu Pro Glu Glu Asp Ile Lys Arg Lys Phe Met Arg Lys Lys Asp Lys
      130      135      140
Lys Leu Ser Asp Met His Gln Ile Val Asn Ile Asp Leu Met Leu Glu
145      150      155      160
Met Ser Thr Ser Leu Ala Ala Val Thr Pro Ile Ile Glu Arg Glu Ser
      165      170      175
Gly Gly His His Tyr Val Asn Met Thr Leu Pro Val Asp Ala Val Ile
      180      185      190
Ser Val Ala Pro Glu Glu Thr Trp Gly Lys Val Arg Lys Leu Leu Val
      195      200      205
Asp Ala Ile His Asn Gln Leu Thr Asp Met Glu Lys Cys Ile Leu Lys
      210      215      220
Tyr Met Lys Arg Thr Ser Ile Val Val Pro Glu Pro Leu His Phe Leu
225      230      235      240
Leu Pro Gly Lys Lys Asn Leu Val Thr Ile Ser Tyr Pro Ser Gly Ile
      245      250      255
Pro Asp Gly Gln Leu Gln Ala Tyr Arg Lys Glu Leu His Asp Leu Phe
      260      265      270
Asn Leu Pro His Asp Arg Pro Tyr Phe Lys Arg Ser Asn Ala Tyr His
      275      280      285
Phe Pro Asp Glu Pro Tyr Lys Asp Gly Tyr Ile Arg Asn Pro His Thr
290      295      300
Tyr Leu Asn Pro Pro Asn Met Glu Thr Gly Met Ile Tyr Val Val Gln
305      310      315      320
Gly Ile Tyr Gly Tyr His His Tyr Met Gln Asp Arg Ile Asp Asp Asn
      325      330      335
Gly Trp Gly Cys Ala Tyr Arg Ser Leu Gln Thr Ile Cys Ser Trp Phe
      340      345      350
Lys His Gln Gly Tyr Thr Glu Arg Ser Ile Pro Thr His Arg Glu Ile
      355      360      365
Gln Gln Ala Leu Val Asp Ala Gly Asp Lys Pro Ala Thr Phe Val Gly
370      375      380
Ser Arg Gln Trp Ile Gly Ser Ile Glu Val Gln Leu Val Leu Asn Gln
385      390      395      400
Leu Ile Gly Ile Thr Ser Lys Ile Leu Phe Val Ser Gln Gly Ser Glu
      405      410      415
Ile Ala Ser Gln Gly Arg Glu Leu Ala Asn His Phe Gln Ser Glu Gly
      420      425      430
Thr Pro Val Met Ile Gly Gly Gly Val Leu Ala His Thr Ile Leu Gly
      435      440      445
Val Ala Trp Asn Glu Ile Thr Gly Gln Ile Lys Phe Leu Ile Leu Asp
      450      455      460
Pro His Tyr Thr Gly Ala Glu Asp Leu Gln Val Ile Leu Glu Lys Gly
465      470      475      480
Trp Cys Gly Trp Lys Gly Pro Asp Phe Trp Asn Lys Asp Ala Tyr Tyr
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<210> 5403

<211> 451

<212> DNA

<213> Homo sapiens

<400> 5403

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 180
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 240
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 300
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<210> 5404

<211> 150

<212> PRT

<213> Homo sapiens

<400> 5404

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			20					25				30			
Ser	Pro	Ala	Leu	Thr	Met	Ala	Pro	Ser	Ser	Leu	Gly	Ala	Leu	Gly	Pro
			35				40				45				
Trp	Val	Gly	Ala	Leu	Glu	Leu	Pro	Arg	Leu	Gln	Ala	Pro	Leu	Ser	Gln
	50					55					60				
Pro	Gly	Thr	His	Ala	Gly	Ala	Xaa	Asp	Pro	Arg	Pro	Ser	Leu	Arg	Lys
65					70				75					80	
Ala	Ser	Leu	Arg	Ala	Ala	Ser	Pro	Ala	Ala	Ser	Ser	Ser	Pro	Trp	Ala
				85					90				95		
Arg	Val	Pro	Cys	Ser	Arg	Ala	Arg	Pro	Lys	Ser	Ala	Glu	Leu	Leu	
			100					105				110			
Arg	ile	Pro	Gly	Thr	Ser	Thr	Arg	Pro	Lys	Lys	Glu	Arg	Gly	Cys	Pro
		115					120					125			
Ser	Pro	Gly	Leu	Pro	Ala	Ala	Gly	Pro	Gly	Pro	Ser	Pro	Ala	Gly	Arg
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<210> 5405

<211> 1609

<212> DNA

<213> Homo sapiens

<400> 5405

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180
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240
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300
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<210> 5406
 <211> 291
 <212> PRT
 <213> Homo sapiens

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 Ala Gln Cys Leu Arg Asn Gly Gln Val Ile Glu Pro Asp Lys Asn Arg
 35 40 45
 Lys Tyr Cys Ser Ala Lys Ala Arg His Ser Trp Thr Lys Asp Arg Arg
 50 55 60
 Ala Met Arg Val Met Ser Ile Glu Arg Lys Lys Trp Met Asn Ile Arg
 65 70 75 80
 Pro Leu Pro Thr Lys Lys Gln Met Pro Leu Gln Phe Asp Leu Cys Asn
 85 90 95
 His Ile Ala Ser Gly Lys Lys Cys Gln Tyr Val Gly Asn Cys Ser Phe
 100 105 110
 Ala His Ser Pro Glu Glu Arg Glu Val Trp Thr Tyr Met Lys Glu Asn
 115 120 125
 Gly Ile Gln Asp Met Glu Gln Phe Tyr Glu Leu Trp Leu Lys Ser Gln
 130 135 140
 Lys Asn Glu Lys Ser Glu Asp Ile Ala Ser Gln Ser Asn Lys Glu Asn
 145 150 155 160
 Gly Lys Gln Ile His Met Pro Thr Asp Tyr Ala Glu Val Thr Val Asp
 165 170 175
 Phe His Cys Trp Met Cys Gly Lys Asn Cys Asn Ser Glu Lys Gln Trp
 180 185 190
 Gln Gly His Ile Ser Ser Glu Lys His Lys Glu Lys Val Phe His Thr
 195 200 205
 Glu Asp Asp Gln Tyr Cys Trp Gln His Arg Phe Pro Thr Gly Tyr Phe
 210 215 220
 Ser Ile Cys Asp Arg Tyr Met Asn Gly Thr Cys Pro Glu Gly Asn Ser
 225 230 235 240
 Cys Lys Phe Ala His Gly Asn Ala Glu Leu His Glu Trp Glu Glu Arg
 245 250 255
 Arg Asp Ala Leu Lys Met Lys Leu Asn Lys Ala Arg Lys Asp His Leu
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 275 280 285
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<210> 5407
 <211> 2010
 <212> DNA
 <213> Homo sapiens

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<210> 5408

<211> 335

<212> PRT

<213> Homo sapiens

<400> 5408

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 35 40 45
 Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
 50 55 60
 Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met Phe Thr Ala
 65 70 75 80
 Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala Asp Glu Glu
 85 90 95
 Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Thr Asn
 100 105 110
 Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe
 115 120 125
 Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala
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 Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly
 145 150 155 160
 Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val
 165 170 175
 Asn Ile Arg Val Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu
 180 185 190
 Gly Leu Leu Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser
 195 200 205
 Asn Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu
 210 215 220
 Cys Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 225 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr
 245 250 255
 Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val
 260 265 270
 Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu

	275		280		285	
Ala	Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val					
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Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile						
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<210> 5409

<211> 2019

<212> DNA

<213> Homo sapiens

<400> 5409

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1200

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 1920
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<210> 5410

<211> 198

<212> PRT

<213> Homo sapiens

<400> 5410

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			20					25					30		
Gln	Ile	Glu	Gln	Gly	Met	Asp	Met	Val	Ile	Ser	Ser	Val	Ile	Gly	Glu
		35					40					45			
Ser	Tyr	Arg	Leu	Gln	Ser	Met	Gln	Cys	Ser	Ser	Leu	Phe	Gln	Phe	Asp
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Phe	Gln	Glu	Ala	Val	Lys	Asn	Phe	Phe	Pro	Pro	Gly	Asn	Glu	Val	Val
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Asn	Gly	Glu	Asn	Leu	Ser	Phe	Ala	Tyr	Glu	Phe	Lys	Ala	Asp	Ala	Leu
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Thr	Ile	Lys	Leu	Phe	Leu	Glu	Lys	Met	Ser	Glu	Pro	Leu	Ile	Arg	Arg
	130					135					140				
Ser	Ser	Phe	Ser	Asp	Arg	Lys	Phe	Ser	Val	Thr	Ser	Arg	Gly	Ser	Ile


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Asp Asp Val Phe Asn Cys Asn Leu Ser Pro Arg Ser Ser Leu Thr Glu
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<210> 5411

<211> 2802

<212> DNA

<213> Homo sapiens

<400> 5411

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<210> 5412

<211> 642

<212> PRT

<213> Homo sapiens

<400> 5412

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Gly Glu Ile Leu Tyr Asn Asn Phe Leu Phe Asp Ile Pro Lys Ile Leu
      35              40              45
Asp Leu Cys Val Leu Phe Gly Lys Gly Asn Ser Pro Leu Leu Gln Lys
 50              55              60
Met Ile Gly Asn Ile Phe Thr Gln Gln Pro Ser Tyr Tyr Ser Asp Leu
 65              70              75              80
Asp Glu Thr Leu Pro Thr Ile Leu Gln Val Phe Ser Asn Ile Leu Gln
      85              90              95
His Cys Gly Leu Gln Gly Asp Gly Ala Asn Thr Thr Pro Gln Lys Leu
      100              105              110
Glu Glu Arg Gly Arg Leu Thr Pro Ser Asp Met Pro Leu Leu Glu Leu
      115              120              125
Lys Asp Ile Val Leu Tyr Leu Cys Asp Thr Cys Thr Thr Leu Trp Ala
      130              135              140
Phe Leu Asp Ile Phe Pro Leu Ala Cys Gln Thr Phe Gln Lys His Asp
 145              150              155              160
Phe Cys Tyr Arg Leu Ala Ser Phe Tyr Glu Ala Ala Ile Pro Glu Met
      165              170              175
Glu Ser Ala Ile Lys Lys Arg Arg Leu Glu Asp Ser Lys Leu Leu Gly
      180              185              190
Asp Leu Trp Gln Arg Leu Ser His Ser Arg Lys Lys Leu Met Glu Ile
      195              200              205
Phe His Ile Ile Leu Asn Gln Ile Cys Leu Leu Pro Ile Leu Glu Ser
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Ser Cys Asp Asn Ile Gln Gly Phe Ile Glu Glu Phe Leu Gln Ile Phe
 225              230              235              240
Ser Ser Leu Leu Gln Glu Lys Arg Phe Leu Arg Asp Tyr Asp Ala Leu
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Phe Pro Val Ala Glu Asp Ile Ser Leu Leu Gln Gln Ala Ser Ser Val
      260              265              270
Leu Asp Glu Thr Arg Thr Ala Tyr Ile Leu Gln Ala Val Glu Ser Ala
      275              280              285
Trp Glu Gly Val Asp Arg Arg Lys Ala Thr Asp Ala Lys Asp Pro Ser
      290              295              300
Val Ile Glu Glu Pro Asn Gly Glu Pro Asn Gly Val Thr Val Thr Ala
 305              310              315              320
Glu Ala Val Ser Gln Ala Ser Ser His Pro Glu Asn Ser Glu Glu Glu
      325              330              335
Glu Cys Met Gly Ala Ala Ala Ala Val Gly Pro Ala Met Cys Gly Val
      340              345              350
Glu Leu Asp Ser Leu Ile Ser Gln Val Lys Asp Leu Leu Pro Asp Leu
      355              360              365
Gly Glu Gly Phe Ile Leu Ala Cys Leu Glu Tyr Tyr His Tyr Asp Pro

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Pro Leu Leu Thr Ser Arg His Asn Val Phe Gln Asn Asp Glu Phe Asp
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Val Phe Ser Arg Asp Ser Val Asp Leu Ser Arg Val His Lys Gly Lys
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Ser Thr Arg Lys Glu Glu Asn Thr Arg Ser Leu Leu Asn Asp Lys Arg
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Ala Val Ala Ala Gln Arg Gln Arg Tyr Glu Gln Tyr Ser Val Val Val
465              470              475              480
Glu Glu Val Pro Leu Gln Pro Gly Glu Ser Leu Pro Tyr His Ser Val
      485              490              495
Tyr Tyr Glu Asp Glu Tyr Asp Asp Thr Tyr Asp Gly Asn Gln Val Gly
      500              505              510
Ala Asn Asp Ala Asp Ser Met Thr Ser Ser Ser Ala Ala Gly His Ser
      515              520              525
Pro Ser Gln Val Leu Arg Thr Lys Val Pro Arg Glu Gly Gln Glu Glu
      530              535              540
Asp Asp Asp Asp Glu Glu Asp Asp Ala Asp Glu Glu Ala Pro Lys Pro
545              550              555              560
Asp His Phe Val Gln Asp Pro Ala Val Leu Arg Glu Lys Ala Glu Ala
      565              570              575
Arg Arg Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His Asp Ser Ser
      580              585              590
Thr Ala Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser Arg Glu Thr
      595              600              605
Thr Gln Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr Arg Ala Asn
      610              615              620
His Asn Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys Gly Met Ile
625              630              635              640
Pro Ser

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<210> 5413

<211> 1677

<212> DNA

<213> Homo sapiens

<400> 5413

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360

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<210> 5414

<211> 426

<212> PRT

<213> Homo sapiens

<400> 5414

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Glu Pro Lys Asn Ile Ile Asn Pro His Glu Lys Val Gln Met Lys Ser

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Lys Asn Asn Ile Lys Ala Ser Leu His Asn Val Lys Ser Ser Leu Pro
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Leu Phe Asn Thr Lys Ser Ser Thr Ser Val Gly Gln Leu Gln Ser Pro
65      70      75      80
Thr Leu Asn Ser Pro Ile Tyr Met Gln Lys Gln Gly Lys Asn Glu His
      85      90      95
Leu Ala Phe Asn Thr Lys Ser Lys Ala Ser Thr Val Gly Ser Glu Leu
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Val Leu Val Ser Thr Thr Val Pro Thr Val His His Val Ser Asp Leu
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Glu Met Ser Ser Thr Leu Asp Cys Leu Pro Val Leu Ala Asp Trp Glu
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Asp Val Val Leu Leu Pro Ala Ser Gln Pro Glu Glu Asn Val Asp Cys
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Thr Val Pro Ile Ser Asp Ser Asp Leu Glu Ile Ser Phe Asn Ser Gly
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Ile Val Tyr Lys Ser Pro His Thr Thr Ile Tyr Asn Val Lys Glu Ala
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Pro Trp Lys Ser Gly Lys Met Thr Pro Pro Leu Cys Lys Cys Gly Arg
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Arg Ser Lys Arg Leu Val Val Ser Asn Asn Gly Pro Asn His Gly Lys
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Val Phe Tyr Cys Cys Pro Ile Gly Lys Tyr Gln Glu Asn Arg Lys Cys
      355      360      365
Cys Gly Tyr Phe Lys Trp Glu Gln Thr Leu Gln Lys Glu Arg Ala Asn
      370      375      380
Ser Met Val Pro Ser His Ser Thr Gly Gly Leu Thr Phe Ser Ser Pro
385      390      395      400
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<210> 5415

<211> 1493

<212> DNA

<213> Homo sapiens

<400> 5415

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<210> 5416
 <211> 55
 <212> PRT
 <213> Homo sapiens

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 Ala Cys Leu Lys Pro Leu Ser
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<210> 5417
 <211> 2087
 <212> DNA
 <213> Homo sapiens

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<210> 5418

<211> 528

<212> PRT

<213> Homo sapiens

<400> 5418

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 Arg His Ala Glu Asn Pro His His Pro Leu Lys Thr Ser Ser Arg Ala

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Lys	Gly	Pro	Val	Ala	Val	Thr	Gly	Ala	Ser	Thr	Pro	Glu	Gly	Thr	Ala		
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Pro	Pro	Pro	Pro	Ala	Ala	Pro	Ala	Pro	Pro	Lys	Gly	Glu	Lys	Glu	Gly		
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Glu	Asp	Phe	Cys	Pro	Arg	Lys	Leu	Arg	Gln	Met	His	Leu	Met	Ile	Asp		
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Gln																	

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<210> 5419

<211> 989

<212> DNA

<213> Homo sapiens

<400> 5419

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<210> 5420

<211> 174

<212> PRT

<213> Homo sapiens

<400> 5420

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Ile Ala Arg Gly Gln Arg Tyr Tyr Gly Phe Gly Arg Thr Val Tyr Pro
    85                90                95
Glu Glu His Ser Arg Trp Arg Asp Arg Ser Arg Thr Arg Ser Arg Ser
    100                105                110
Arg Thr Pro Phe Arg Leu Ser Glu Lys Asp Arg Met Glu Leu Leu Glu
    115                120                125
Ile Ala Lys Thr Asn Ala Ala Lys Ala Leu Gly Thr Thr Asn Ile Asp
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<210> 5421

<211> 1239

<212> DNA

<213> Homo sapiens

<400> 5421

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<210> 5422

<211> 276

<212> PRT

<213> Homo sapiens

<400> 5422

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Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	Ser	Thr	Cys
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Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	Thr	Gly	Ser	Met
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Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	Phe	Ser	Val	Thr	Leu
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Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	Ala	Cys	Tyr	Ala	Ala	Leu	Phe
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Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu
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Ser	His	Gly	Arg	Ser	Arg	Asp	His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser
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Cys	Ile	Ala	Cys	Val	Ala	Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala
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Arg	Pro	Gly	Glu	Ile	Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu
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Val	Tyr	Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn
	210					215					220				
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225					230					235					240
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265

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<210> 5423
<211> 2427
<212> DNA
<213> Homo sapiens

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<210> 5424

<211> 570

<212> PRT

<213> Homo sapiens

<400> 5424

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 Leu Leu Thr Met Ser Asn Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln
 20 25 30
 Lys Tyr Gln Leu Leu Val Tyr His Ala Asp Ser Leu Phe His Asp Lys
 35 40 45
 Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys
 50 55 60
 Lys Ala Leu Ser Lys Thr Ser Lys Val Arg Pro Ser Thr Gly Asn Ser

```

65          70          75          80
Ala Ser Thr Pro Gln Ser Gln Cys Leu Pro Ser Glu Ile Glu Val Lys
      85          90          95
Tyr Lys Met Ala Glu Cys Tyr Thr Met Leu Lys Gln Asp Lys Asp Ala
      100          105          110
Ile Ala Ile Leu Asp Gly Ile Pro Ser Arg Gln Arg Thr Pro Lys Ile
      115          120          125
Asn Met Met Leu Ala Asn Leu Tyr Lys Lys Ala Gly Gln Glu Arg Pro
      130          135          140
Ser Val Thr Ser Tyr Lys Glu Val Leu Arg Gln Cys Pro Leu Ala Leu
      145          150          155          160
Asp Ala Ile Leu Gly Leu Leu Ser Leu Ser Val Lys Gly Ala Glu Val
      165          170          175
Ala Ser Met Thr Met Asn Val Ile Gln Thr Val Pro Asn Leu Asp Trp
      180          185          190
Leu Ser Val Trp Ile Lys Ala Tyr Ala Phe Val His Thr Gly Asp Asn
      195          200          205
Ser Arg Ala Ile Ser Thr Ile Cys Ser Leu Glu Lys Lys Ser Leu Leu
      210          215          220
Arg Asp Asn Val Asp Leu Glu Ser Leu Ala Asp Leu Tyr Phe Arg
      225          230          235          240
Ala Gly Asp Asn Lys Asn Ser Val Leu Lys Phe Glu Gln Ala Gln Met
      245          250          255
Leu Asp Pro Tyr Leu Ile Lys Gly Met Asp Val Tyr Gly Tyr Leu Leu
      260          265          270
Ala Arg Glu Gly Arg Leu Glu Asp Val Glu Asn Leu Gly Cys Arg Leu
      275          280          285
Phe Asn Ile Ser Asp Gln His Ala Glu Pro Trp Val Val Ser Gly Cys
      290          295          300
His Ser Phe Tyr Ser Lys Arg Tyr Ser Arg Ala Leu Tyr Leu Gly Ala
      305          310          315          320
Lys Ala Ile Gln Leu Asn Ser Asn Ser Val Gln Ala Leu Leu Leu Lys
      325          330          335
Gly Ala Ala Leu Arg Asn Met Gly Arg Val Gln Glu Ala Ile Ile His
      340          345          350
Phe Arg Glu Ala Ile Arg Leu Ala Pro Cys Arg Leu Asp Cys Tyr Glu
      355          360          365
Gly Leu Ile Glu Cys Tyr Leu Ala Ser Asn Ser Ile Arg Glu Ala Met
      370          375          380
Val Met Ala Asn Asn Val Tyr Lys Thr Leu Gly Ala Asn Ala Gln Thr
      385          390          395          400
Leu Thr Leu Leu Ala Thr Val Cys Leu Glu Asp Pro Val Thr Gln Glu
      405          410          415
Lys Ala Lys Thr Leu Leu Asp Lys Ala Leu Thr Gln Arg Pro Asp Tyr
      420          425          430
Ile Lys Ala Val Val Lys Lys Ala Glu Leu Leu Ser Arg Glu Gln Lys
      435          440          445
Tyr Glu Asp Gly Ile Ala Leu Leu Arg Asn Ala Leu Ala Asn Gln Ser
      450          455          460
Asp Cys Val Leu His Arg Ile Leu Gly Asp Phe Leu Val Ala Val Asn
      465          470          475          480
Glu Tyr Gln Glu Ala Met Asp Gln Tyr Ser Ile Ala Leu Ser Leu Asp
      485          490          495
Pro Asn Asp Gln Lys Ser Leu Glu Gly Met Gln Lys Met Glu Lys Glu

```



```

          500          505          510
Glu Ser Pro Thr Asp Ala Thr Gln Glu Asp Val Asp Asp Met Glu
          515          520          525
Gly Ser Gly Glu Glu Gly Asp Leu Glu Gly Ser Asp Ser Glu Ala Ala
          530          535          540
Gln Trp Ala Asp Gln Glu Gln Trp Phe Gly Met Ser Glu Gly Ala Ala
545          550          555          560
Ala Pro Trp Pro Gln Trp Pro Ala Leu Leu
          565          570

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<210> 5425
 <211> 639
 <212> DNA
 <213> Homo sapiens

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<400> 5425
cggcgcgcca tgtgatcaaa cggatatacag cccaggcgcc agatgagctg tcctttgagg
60
tgaggctgtg ggaagcaga ttccagctgg gctccccaca cccctgctc ctctgaccc
120
ttctcttccc accgccttc tcccagggtg gagacattgt etcggtgatc gacatgccac
180
ccacagagga tcggagctgg tggcggggca agcagagctt ccaggtcggg ttcttcccca
240
gtgagtgtgt ggaactcttc acagagcggc cagggtcggg cctgaaggcg gatgccgatg
300
gccccccatg tggcatcccg gctccccagg gtatctctgc tctgacctca gctgtgccac
360
ggcctcgtgg gaagctggcc ggcttctccc gcaccttcac gcgtcccgcc ccttctcggc
420
agcggctcgc gcagcgggga atcctcgcac agagggtgtt tggctcgcgt ctgtggcagg
480
acctcagcaa ctcaggccag gatgtgcccc gtgctgcgct gctgctccga gttcattgag
540
gccnaccggg tggtggatgg gatctaccgg ctctcaggcg tgtcttccaa catccagagg
600
cttcggcacg agtttgacag tgagaggata cggagctg
639

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<210> 5426
 <211> 98
 <212> PRT
 <213> Homo sapiens

```

<400> 5426
Pro Gln Leu Cys His Gly Leu Val Gly Ser Trp Pro Ala Cys Ser Ala
1          5          10          15
Pro Ser Cys Ala Pro Ala Leu Leu Gly Ser Gly Cys Gly Ser Gly Glu
20          25          30
Ser Cys Asp Arg Gly Cys Leu Ala Ala Ile Leu Ala Ser Thr Ser Ala
35          40          45
Thr Gln Ala Arg Met Cys Pro Val Leu Arg Cys Cys Ser Glu Phe Ile
50          55          60
Glu Ala Xaa Gly Val Val Asp Gly Ile Tyr Arg Leu Ser Gly Val Ser

```

```

65              70              75              80
Ser Asn Ile Gln Arg Leu Arg His Glu Phe Asp Ser Glu Arg Ile Pro
      85              90              95
Glu Leu

```

<210> 5427

<211> 366

<212> DNA

<213> Homo sapiens

<400> 5427

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tgatcactgt attgcactcc agtctgggca acagagcaag actctgtcat aacaaaccca
60
acaaacaaat caaaaattct tgttgagtac ctgctacatg ctaagtgtct ctctagggtgc
120
tgaggatata tcagaggggca aaatggatac agatactctg aaaaaacgtg cattctagct
180
gggattgggt cctccacact gtgtccaaaa ggtatgttgg ggttgctgaa gtatataaac
240
tggtattggc agcaggaaca gcatttatgg aacagagggg aagacacatt caaggaatga
300
aacatcgtct ggctggatca tgaaatgcaa ggcagatatg gcacaggagg cagacaaagg
360
gttgaa
366

```

<210> 5428

<211> 101

<212> PRT

<213> Homo sapiens

<400> 5428

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Met Phe His Ser Leu Asn Val Ser Ser Pro Leu Phe His Lys Cys Cys
 1              5              10              15
Ser Cys Cys Gln Tyr Gln Phe Ile Tyr Phe Ser Asn Pro Asn Ile Pro
      20              25              30
Phe Gly His Ser Val Glu Asp Pro Ile Pro Ala Arg Met His Val Phe
      35              40              45
Ser Glu Tyr Leu Tyr Pro Phe Cys Pro Leu Met Tyr Pro Gln His Leu
      50              55              60
Glu Glu His Leu Ala Cys Ser Arg Tyr Ser Thr Arg Ile Phe Asp Leu
65              70              75              80
Phe Val Gly Leu Phe Met Thr Glu Ser Cys Ser Val Ala Gln Thr Gly
      85              90              95
Val Gln Tyr Ser Asp
      100

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<210> 5429

<211> 612

<212> DNA

<213> Homo sapiens

<400> 5429

ccggcggggcg gcaaggctcc gggccagcat gggggcttcg tggtgactgt caagcaagag
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 cgcgcgagg gtccacgcgc gggcgagaag gggccccacg agggaggagt gagagtccct
 120
 gcgctgagct gggggaggcc ccgggctccc gccccagcct cgaagccccg cccagggtg
 180
 gatttgaatt gtttgtggct ccgcccacag cccattttcc tctggaagct gagaccccg
 240
 cccgtgccag ctgccacgcc cctgacaggt cctctgccac tctaagtcca ggccccgc
 300
 accgcacaat gccagctctg cccactctaa ggtcccgccc acttcacac cttggggggc
 360
 gcaccctccc cttggtcctg tgggcccgtt ctcagcaga aaaccacgcc caccaagcag
 420
 aggcacagcc cacaaccgaa gtaaacgcca accctgtact caaacctcgg cccatagttc
 480
 ctcagatccc ctcaccctg gccagggatc cctctaacc accgtgtccc gactgtgac
 540
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 600
 gcccatacgc gt
 612

<210> 5430
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 5430
 Pro Ala Gly Gly Lys Ala Pro Gly Gln His Gly Gly Phe Val Val Thr
 1 5 10 15
 Val Lys Gln Glu Arg Gly Glu Gly Pro Arg Ala Gly Glu Lys Gly Ser
 20 25 30
 His Glu Glu Glu Val Arg Val Pro Ala Leu Ser Trp Gly Arg Pro Arg
 35 40 45
 Ala Pro Ala Pro Ala Ser Lys Pro Arg Pro Arg Leu Asp Leu Asn Cys
 50 55 60
 Leu Trp Leu Arg Pro Gln Pro Ile Phe Leu Trp Lys Leu Arg Pro Arg
 65 70 75 80
 Pro Val Pro Ala Ala Thr Pro Leu Thr Gly Pro Leu Pro Leu
 85 90

<210> 5431
 <211> 3005
 <212> DNA
 <213> Homo sapiens

<400> 5431
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 aggcacctgg ccgcatggc gagacacagt gccaacacca gcattgatgc ccgcaacctg
 120
 gccattgtct gggcacccaa cctgctacgg tccatggagc tggagtgcgt gggaatgggt
 180

ggcgcggcgg cgttccggga agttcgggtg cagtcggtgg tggtagagtt tctgctcacc
240
catgtggagc tctgtttcag cgacacettc acctccgccc gcctcgaccg tgcaggccgc
300
tgccctgtcc ccaggcccaa gtcccttgcc ggagctgccc cctccaccgg cctgtgtgag
360
ctggaggaag cccaggcacg caccaggggc cggctgggga cggccacgga gcccaacaat
420
cccaaggccc cggcctcacc tgcgaaagg aggaaggagg agagagggga gaagcagcgg
480
aagccagggg gcagcagctg gaagacgttc ttgactgag gccggggccc cagtgtccct
540
cgaaagaagc cctgtccctg gctggggggc acccgtgccc caccgcagcc ttcaggcagc
600
agacccgaca ccgtcacact gagatctgcc aagagcgagg agtctctgtc atcgaggccc
660
agcggggctg gcctccagag gctgcacagg ctgcggcgac cccactccag cagcgacgct
720
ttccctgtgg gcccagcacc tgctggctcc tgcgagagcc tgctcctcgt ctcctcctcc
780
gagtcctcct cctctgagtc ctctctctcc tctctgagtc cctcagcagc tggggtgggg
840
gcactctctg ggtctccctc acaccgtacc tcagcctggc tagatgatgg tgatgatgtg
900
gacttcagcc caccgcctg cctggaggga ctccgggggc tggactttga tcccttaacc
960
ttccgctgca gcagccccc cccaggggat cccgcacctc cggccagccc agcacccccc
1020
gcccctgctc ctgccttccc acccagggtg acccccccag ccatctcgcc cggggggccc
1080
accagccccg cctcgctgc tgccctagac atctcagagc cctggctgt atcagtacca
1140
cccgctgtcc tagaactgct ggggggtggg ggagcacctg cctcagccac cccaacacca
1200
gctctcagcc cggccgggag cctgcgcccc catctcatac cctgtgtgt gcgaggagcc
1260
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1320
ggcccaactg gtcctgatat ggagtcacca ctgccacccc ctcccctgtc tctcctgcgc
1380
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1440
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1500
cctgtctccc aatccccctt ccacgcctcg ctgtctctgg aggtggggcg ggagcccctg
1560
gggacctcag ggagtgggac acctcccaac tccctagcac acccgggtgc ctgggtcccg
1620
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1680
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1740
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1800

tcacaggttc ctacccccgg cttctttctcc ccagccccca gggagtgctt gccacccttc
 1860
 ctccgggttc ccaagccagg cttgtacccc ctggggcccc catccttcca gccaggttcc
 1920
 ccagccccag tctggaggag ctctctgggc cccctgcac cactcgacag gggagagaac
 1980
 ctgtactatg agatcggggc aagtgagggg tccccctatt ctggccccac ccgctcctgg
 2040
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 2100
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 2160
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 2340
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 2460
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 2580
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 2640
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 2700
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 2760
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 2820
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 2880
 gtctgacct gtgcacgggg atggggggac aactcctacc cttctttccc cacatgcccc
 2940
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 3000
 aaaaaa
 3005

<210> 5432

<211> 863

<212> PRT

<213> Homo sapiens

<400> 5432

Xaa His Asp Val Ile Gln Gln Leu Pro Pro His Tyr Arg Thr Leu
 1 5 10 15
 Glu Tyr Leu Leu Arg His Leu Ala Arg Met Ala Arg His Ser Ala Asn
 20 25 30
 Thr Ser Met His Ala Arg Asn Leu Ala Ile Val Trp Ala Pro Asn Leu

[illegible]

```

465          470          475          480
Ala Glu Arg Ala Gln Gln Val Ala Glu Gln Ser Gln Gln Glu Cys
          485          490          495
Gly Gly Thr Pro Pro Ala Ser Gln Ser Pro Phe His Arg Ser Leu Ser
          500          505          510
Leu Glu Val Gly Gly Glu Pro Leu Gly Thr Ser Gly Ser Gly Pro Pro
          515          520          525
Pro Asn Ser Leu Ala His Pro Gly Ala Trp Val Pro Gly Pro Pro Pro
          530          535          540
Tyr Leu Pro Arg Gln Gln Ser Asp Gly Ser Leu Arg Ser Gln Arg
          545          550          555
Pro Met Gly Thr Ser Arg Arg Gly Leu Arg Gly Pro Ala Gln Val Ser
          565          570          575
Ala Gln Leu Arg Ala Gly Gly Gly Gly Arg Asp Ala Pro Glu Ala Ala
          580          585          590
Ala Gln Ser Pro Cys Ser Val Pro Ser Gln Val Pro Thr Pro Gly Phe
          595          600          605
Phe Ser Pro Ala Pro Arg Glu Cys Leu Pro Pro Phe Leu Gly Val Pro
          610          615          620
Lys Pro Gly Leu Tyr Pro Leu Gly Pro Pro Ser Phe Gln Pro Ser Ser
          625          630          635
Pro Ala Pro Val Trp Arg Ser Ser Leu Gly Pro Pro Ala Pro Leu Asp
          645          650          655
Arg Gly Glu Asn Leu Tyr Tyr Glu Ile Gly Ala Ser Glu Gly Ser Pro
          660          665          670
Tyr Ser Gly Pro Thr Arg Ser Trp Ser Pro Phe Arg Ser Met Pro Pro
          675          680          685
Asp Arg Leu Asn Ala Ser Tyr Gly Met Leu Gly Gln Ser Pro Pro Leu
          690          695          700
His Arg Ser Pro Asp Phe Leu Leu Ser Tyr Pro Pro Ala Pro Ser Cys
          705          710          715
Phe Pro Pro Asp His Leu Gly Tyr Ser Ala Pro Gln His Pro Ala Arg
          725          730          735
Arg Pro Thr Pro Pro Glu Pro Leu Tyr Val Asn Leu Ala Leu Gly Pro
          740          745          750
Arg Gly Pro Ser Pro Ala Ser Ser Ser Ser Ser Pro Pro Ala His
          755          760          765
Pro Arg Ser Arg Ser Asp Pro Gly Pro Pro Val Pro Arg Leu Pro Gln
          770          775          780
Lys Gln Arg Ala Pro Trp Gly Pro Arg Thr Pro His Arg Val Pro Gly
          785          790          795
Pro Trp Gly Pro Pro Glu Pro Leu Leu Leu Tyr Arg Ala Ala Pro Pro
          805          810          815
Ala Tyr Gly Arg Gly Gly Glu Leu His Arg Gly Ser Leu Tyr Arg Asn
          820          825          830
Gly Gly Gln Arg Gly Glu Gly Ala Gly Pro Pro Pro Pro Tyr Pro Thr
          835          840          845
Pro Ser Trp Ser Leu His Ser Glu Gly Gln Thr Arg Ser Tyr Cys
          850          855          860

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<210> 5433

<211> 385

<212> DNA

<213> Homo sapiens

<400> 5433
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 120
 ctgggtataa gaagctcttc tggctctccag agttctcgga gtaacccttc catccaagcc
 180
 acgctcaata agactgtgct ttctctcttc ttaaataacc acccacagac atctgttccc
 240
 aacgcattctg ctcttcaccc ttgctctcgt ctgttttccc ttagcaaccc atctctttcc
 300
 accacaaacc tgagcggccc gtctcggcgt cggcagcctc ccgtcagccc tctcagcgtt
 360
 tctctctggcc ctgaagcaca tcaag
 385

<210> 5434
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 5434
 Asp Leu Thr Asn Leu His Tyr Ser Thr Pro Leu Pro Ala Ser Leu Asp
 1 5 10 15
 Thr Thr Asp His His Phe Gly Ser Met Ser Val Gly Asn Ser Val Asn
 20 25 30
 Asn Ile Pro Ala Ala Met Thr His Leu Gly Ile Arg Ser Ser Ser Gly
 35 40 45
 Leu Gln Ser Ser Arg Ser Asn Pro Ser Ile Gln Ala Thr Leu Asn Lys
 50 55 60
 Thr Val Leu Ser Ser Ser Leu Asn Asn His Pro Gln Thr Ser Val Pro
 65 70 75 80
 Asn Ala Ser Ala Leu His Pro Ser Leu Arg Leu Phe Ser Leu Ser Asn
 85 90 95
 Pro Ser Leu Ser Thr Thr Asn Leu Ser Gly Pro Ser Arg Arg Arg Gln
 100 105 110
 Pro Pro Val Ser Pro Leu Thr Leu Ser Pro Gly Pro Glu Ala His Gln
 115 120 125

<210> 5435
 <211> 617
 <212> DNA
 <213> Homo sapiens

<400> 5435
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 60
 aaacagataa ttctttatat tcaacctggt gtcaaaattt ttagaaacat tttcccagtt
 120
 ccttgtataa gtatactttg tataacttct ggcaaaccat aattatgaac tcacattact
 180
 atagtactat aatactgcag aaagggatct tgcgtttcag aaatgtcact catccagttt
 240

tctctccctt tctctaaccc catctccctc ccaggctcat gggtttctgtt gcaatcctct
 300
 ttctcttac acaaggcaag aagttttctt accaatagat cagacctgtg aaggactgcc
 360
 cgacatgac tgatatgggtt gttcttcatt ttgggctgta gtattttaaa gttagaggttt
 420
 gctctgatgg tcccatcaact gcttgccatt gtctttccct ttgctctagc tatcagggga
 480
 tgttgcttta agtttggtcc ccaggcttta ctgccaagag ggaaattcat acccacttta
 540
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 600
 agttaccctt cagcgt
 617

<210> 5436

<211> 119

<212> PRT

<213> Homo sapiens

<400> 5436

Met	Asn	Phe	Pro	Leu	Gly	Ser	Lys	Ala	Trp	Gly	Thr	Asn	Leu	Lys	Gln
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His	Pro	Leu	Ile	Ala	Arg	Ala	Lys	Gly	Lys	Thr	Met	Ala	Ser	Ser	Asp
		20					25					30			
Gly	Thr	Ile	Arg	Ala	Asn	Leu	Tyr	Phe	Lys	Ile	Leu	Gln	Pro	Lys	Met
		35				40					45				
Lys	Asn	Asn	His	Ile	Arg	Ser	Cys	Arg	Ala	Val	Leu	His	Arg	Ser	Asp
	50				55					60					
Leu	Leu	Val	Arg	Lys	Leu	Leu	Ala	Leu	Cys	Lys	Glu	Lys	Glu	Asp	Cys
65			70						75					80	
Asn	Arg	Asn	His	Glu	Pro	Gly	Arg	Glu	Met	Gly	Leu	Glu	Lys	Gly	Glu
			85					90					95		
Glu	Asn	Trp	Met	Ser	Asp	Ile	Ser	Glu	Thr	Gln	Asp	Pro	Phe	Leu	Gln
		100					105					110			
Tyr	Tyr	Ser	Thr	Ile	Val	Met									
		115													

<210> 5437

<211> 1422

<212> DNA

<213> Homo sapiens

<400> 5437

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 120
 ttctcggggt ttctgacctc ctgcagcctc ctcttgccct gggtgcacca gatcttggcg
 180
 gctgaggctg gcttaccttc gagccgttcc ttcattgggat ttgctgctcc cttaccaaac
 240
 aagcgaaagg cttactcgga gcgtagaatc atgggggtact caatgcagga gatgtatgag
 300

gtgggtgtcca acgtccagga gtatcgtgag tttgtgccct ggtgtaagaa gtctctgggtg
 360
 gtatccagcc gtaaggggtca tttgaaagcc cagctggagg ttggctttcc acctgtcatg
 420
 gaacgttaca cctctgcagt ttccatgggtc aaacctcaca tgggtcaaggc tgtttgtact
 480
 gatggcaagc tcttcaacca cttagagact atttggcgat tcagccctgg tattctctgcc
 540
 tatcctcgaa cctgcactgt ggacttttcg atttcctttg aatttcgttc tctgctgcac
 600
 tcccagctgg ccaccatggt ttttgatgag gttgtcaaac agaattgtgc tgcctttgag
 660
 cgtcgggcag ccaccaagtt tggccagaa acagccatcc cccgtgaact gatgttccat
 720
 gaggtgcacc agacttgagg caagggattg ctccctgacc tccctcttac cccacttccc
 780
 tacacaattc tcttatttat ttggtttggc tcctgttcca atttgaaagg agtctgtgtt
 840
 cataatactg tttctcctct caatttccca gaaattgggt tctatgctgg ctggaaatgt
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 1020
 gttgtctctg gaccttatca agacaccta gtgtctgacc aggggacgat agtaactttt
 1080
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 1140
 tttaccctcg ctgagattcc tcaggagaaa aggcaacctg cctccagcct gaaatacata
 1200
 aagcctcatt ttaagactgt aagtccatgc tgcctggcta ctagagagca aggggctttc
 1260
 ttaccaccag tgctgaggag aaaagtactg aacggaaacg gagttgtctt tgtactcttg
 1320
 agttgtacct tattcttcca cttggcctga gtttttataa aatttcaata aattgtgaca
 1380
 gtgtgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
 1422

<210> 5438

<211> 245

<212> PRT

<213> Homo sapiens

<400> 5438

Phe Arg Gly Gly Val Leu Tyr Trp Asp Ala Gly Ala Ala Gly Thr
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 20 25 30
 Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr Ser Cys
 35 40 45
 Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu Ala Gly
 50 55 60
 Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe Thr Asn

65		70		75		80
Lys	Arg	Lys	Ala	Tyr	Ser	Glu
		85		90		95
Glu	Met	Tyr	Glu	Val	Val	Ser
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Lys	Ala	Gln	Leu	Glu	Val	Gly
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Asp	Gly	Lys	Leu	Phe	Asn	His
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Phe	Glu	Phe	Arg	Ser	Leu	Leu
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<210> 5439

<211> 4234

<212> DNA

<213> Homo sapiens

<400> 5439

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<211> 461

<212> PRT

<213> Homo sapiens

<400> 5440

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Arg	Gln	Leu	Arg	Cys	Leu	Val	Val	Asp	Glu	Ala	Asp	Arg	Met	Val	Glu
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Thr	Leu	Val	His	Gln	Ala	Pro	Ala	Arg	Ile	Leu	His	Lys	Lys	His	Thr
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Lys	Lys	Met	Asp	Lys	Thr	Ala	Lys	Leu	Asp	Leu	Leu	Met	Gln	Lys	Ile
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Pro Leu Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser Gly
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<212> DNA

<213> Homo sapiens

<400> 5441

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<211> 250

<212> PRT

<213> Homo sapiens

<400> 5442

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Val Cys Leu Ile Asp Pro Gly Cys Phe Arg Glu Ile Asp Glu Leu Ile		205
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<210> 5443

<211> 2021

<212> DNA

<213> Homo sapiens

<400> 5443

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<210> 5444

<211> 438

<212> PRT

<213> Homo sapiens

<400> 5444

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 35 40 45
 Arg Ala Trp Gln Tyr Leu Ser Gly Gly Lys Val Lys Leu Gln Gln Asn
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 Pro Gly Lys Phe Asp Glu Leu Asp Met Ser Pro Gly Asp Pro Lys Trp
 65 70 75 80
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Gln	Tyr	Glu	Thr	Ile	Glu	Arg	Leu	Arg	Ser	Leu	Ser	Pro	Lys	Ile	Met		
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Gln	Glu	Ala	Phe	Leu	Val	Gln	Glu	Val	Val	Glu	Leu	Pro	Val	Thr	Glu		
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Arg	Gln	Ile	Glu	Arg	Glu	His	Leu	Ile	Gln	Leu	Arg	Arg	Trp	Gln	Glu		
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Thr	Arg	Gly	Glu	Leu	Gln	Cys	Arg	Ser	Pro	Pro	Arg	Leu	His	Gly	Ala		
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Lys	Ala	Ile	Leu	Asp	Ala	Glu	Pro	Gly	Pro	Arg	Pro	Ala	Leu	Gln	Pro		
			325					330					335				
Ser	Pro	Ser	Ile	Arg	Leu	Pro	Leu	Asp	Ala	Pro	Leu	Pro	Gly	Ser	Lys		
			340					345					350				
Ala	Lys	Pro	Lys	Pro	Pro	Lys	Gln	Ala	Gln	Lys	Glu	Gln	Arg	Lys	Gln		
		355					360					365					
Met	Lys	Gly	Arg	Gly	Gln	Leu	Glu	Lys	Pro	Pro	Ala	Pro	Asn	Gln	Ala		
		370				375					380						
Met	Val	Val	Ala	Ala	Ala	Gly	Asp	Ala	Cys	Pro	Pro	Gln	His	Val	Pro		
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<210> 5445

<211> 1187

<212> DNA

<213> Homo sapiens

<400> 5445

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<210> 5446

<211> 107

<212> PRT

<213> Homo sapiens

<400> 5446

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 35 40 45
 Gly Thr Gln Trp Phe His Pro Gln Val Cys Ser Asn Arg His His Ser
 50 55 60
 Pro Arg Pro His Ala Asp Ser Asp Thr Arg Ala His Ser Pro Arg Ser

65		70		75		80									
His	Ala	Asp	Ser	Asp	Met	Arg	Ala	His	Ser	Leu	Ser	His	Asp	Ser	Gln
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<210> 5447

<211> 1444

<212> DNA

<213> Homo sapiens

<400> 5447

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1260

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<210> 5448
 <211> 189
 <212> PRT
 <213> Homo sapiens

<400> 5448
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 35 40 45
 Val Thr Asp Val Phe Gln Gly Ser Met Arg Ile Phe Thr Lys Lys Leu
 50 55 60
 Pro His Pro Asp Leu Pro Ala Glu Glu Lys Glu Gln Leu Leu His Asn
 65 70 75 80
 Asp Glu Tyr Gln Glu Thr Met Val Glu Ser Thr Phe Met Tyr Leu Thr
 85 90 95
 Leu Asp Leu Pro Thr Ala Pro Leu Tyr Lys Asp Glu Lys Glu Gln Leu
 100 105 110
 Ile Ile Pro Gln Val Pro Leu Phe Asn Ile Leu Ala Lys Phe Asn Gly
 115 120 125
 Ile Thr Glu Lys Glu Tyr Lys Thr Tyr Lys Glu Asn Phe Leu Lys Arg
 130 135 140
 Phe Gln Leu Thr Lys Leu Pro Pro Tyr Leu Ile Phe Cys Ile Lys Arg
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<210> 5449
 <211> 1359
 <212> DNA
 <213> Homo sapiens

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<210> 5450

<211> 293

<212> PRT

<213> Homo sapiens

<400> 5450

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 35 40 45
 Pro Ser Ile Leu Asp His Leu Ile Asn Asn Asp Arg Lys Leu Pro Pro
 50 55 60
 Glu Tyr Asn Leu Pro His Thr Tyr Val Glu Met Gln Ser Leu Gln Ile

65		70		75		80
Ala	Ala	Phe	Leu	Phe	Thr	Val
		85		90		95
Trp	Phe	Thr	Asp	Leu	Ser	Leu
		100		105		110
Val	Lys	Pro	Ser	Thr	Pro	Ser
		115		120		125
Gly	Ser	Asp	Glu	Gly	Thr	Glu
		130		135		140
Asn	Lys	Ala	Arg	Arg	Glu	Asp
		145		150		155
His	Leu	Met	Ile	Asp	Gln	Leu
		165		170		175
Gly	Thr	Leu	Ser	Met	Leu	Gln
		180		185		190
Asp	Phe	Leu	Asp	Ser	Glu	Val
		195		200		205
Ser	Glu	Ala	Glu	Ser	Glu	Asn
		210		215		220
Pro	Leu	Phe	Ser	Leu	Leu	Pro
		225		230		235
Ser	Leu	Val	Ser	Lys	Leu	Arg
		245		250		255
Gln	Leu	Ser	His	Thr	Ile	Leu
		260		265		270
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<210> 5451

<211> 1184

<212> DNA

<213> Homo sapiens

<400> 5451

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540

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<210> 5452

<211> 206

<212> PRT

<213> Homo sapiens

<400> 5452

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		20					25						30			
Ser	Ser	Pro	Glu	Leu	Ser	Val	Ala	Phe	His	His	Ser	Gly	Pro	Ser	Cys	
		35				40					45					
Leu	Ser	Pro	Ala	Leu	Ser	Gln	Thr	Thr	Gln	Lys	Ser	Gly	His	Leu	Trp	
	50				55					60						
Ala	Pro	Gly	Met	Val	Thr	Glu	Glu	Lys	His	Ala	Val	Pro	Val	Ser	Pro	
65				70					75					80		
Gly	Phe	Cys	Gln	Lys	Ile	Glu	Gln	Val	Gln	Leu	Thr	His	Cys	Tyr	Cys	
			85					90					95			
Arg	Ser	Leu	Lys	Leu	Pro	Gly	Leu	Val	Leu	Asp	Pro	Ser	Arg	Asn	His	
		100				105						110				
Gln	Val	Arg	His	Leu	Glu	Pro	Pro	Gly	Glu	Gly	Pro	Pro	Ser	Arg	Ala	
		115				120						125				
Leu	Lys	Glu	Leu	His	Glu	Ile	Arg	Asn	Cys	Leu	Met	Lys	Cys	Ile	Ser	
	130				135					140						
Leu	Tyr	Leu	Glu	Asp	Glu	Ala	Gln	Thr	Pro	Thr	Pro	Leu	Ser	Pro	Pro	
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Gly	Leu	Gly	Met	Ser	Pro	Ala	Ala	Arg	Pro	Arg	Ser	Phe	Pro	Gly	Gly	
			165					170					175			
Leu	Gly	Glu	Val	Gly	Ala	Gly	Thr	Ile	Ser	Val	Pro	Ser	Thr	Leu	Thr	
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<210> 5453
 <211> 1974
 <212> DNA
 <213> Homo sapiens

<400> 5453
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 1974

<210> 5454

<211> 320

<212> PRT

<213> Homo sapiens

<400> 5454

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			20				25						30		
Arg	Ile	Asp	Ser	Lys	Ala	Trp	Arg	Glu	Thr	Leu	Thr	Leu	Gln	Lys	Gln
	35					40					45				
Leu	Arg	Tyr	Arg	Phe	Pro	Glu	Leu	Ala	Asp	Pro	Asp	Thr	Cys	Tyr	Gly
	50				55					60					
Phe	Arg	Phe	Cys	His	Gln	Leu	Asp	Phe	Ser	Thr	Ser	Gly	Ala	Leu	Cys
65				70					75					80	
Val	Ala	Leu	Asn	Lys	Ala	Ala	Ala	Gly	Ser	Ala	Tyr	Arg	Cys	Phe	Lys
			85					90					95		
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	100						105					110			
Gln	Glu	Ser	Arg	Val	Thr	Ile	Ser	His	Ala	Ile	Gly	Arg	Asn	Ser	Thr
	115					120					125				
Glu	Gly	Arg	Ala	His	Thr	Met	Cys	Ile	Glu	Gly	Ser	Gln	Gly	Val	Ala
	130				135						140				
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			165					170					175		
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	180					185					190				
His	Pro	Val	Val	Gly	Asp	Leu	Thr	Tyr	Gly	Glu	Val	Ser	Gly	Arg	Glu
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	245	250
Gln Leu Val Gln Ala Leu Arg Ala Thr Pro Asp Pro Asp Pro Glu Asp		255
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Arg Pro Pro Pro Pro Thr Lys Pro Pro Glu Thr Glu Ala Gln Arg		285
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<210> 5455

<211> 975

<212> DNA

<213> Homo sapiens

<400> 5455

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 120
 tgagcctaag gtaccacagt tagtctcatt tgccctctgt cctgtgaact ccacttagaa
 180
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 240
 agctagaatt accattagag gcacaaaccc ctgagaatac acaagggggc acgcttcag
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 480
 aatagccacc ttccaggcgt gagtctctga gataaaaatg gattttaacc taggactgcc
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 660
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 720
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 780
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 840
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<210> 5456

<211> 149

<212> PRT

<213> Homo sapiens

<400> 5456

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Pro Arg Thr Ala Gly Ser Trp Pro Ser Ala Ala Ala Gln Thr Arg Ala
 1             5             10             15
Val Cys Ala Gly Ser Arg Leu Phe Pro Val Ser Asn Trp Leu Val Ser
      20             25             30
Leu Tyr Gly Leu Ala Ser Phe Arg Pro Gly Val Gly Pro His Pro Thr
      35             40             45
His Cys Pro Leu Ala Val Arg Leu Ala Cys Pro Ala Val Pro Thr Thr
      50             55             60
Val Val Lys Gln Arg Leu Gln Met Tyr Asn Ser Gln His Arg Ser Ala
      65             70             75             80
Ile Ser Cys Ile Arg Thr Val Trp Arg Thr Glu Gly Leu Gly Ala Phe
      85             90             95
Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met Asn Ile Pro Phe Gln Ser
      100            105            110
Ile His Phe Ile Thr Tyr Glu Phe Leu Gln Glu Gln Val Asn Pro His
      115            120            125
Arg Thr Tyr Asn Pro Gln Ser His Ile Ile Ser Gly Gly Leu Ala Gly
      130            135            140
Ala Leu Ala Ala Ala
145

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<210> 5457

<211> 448

<212> DNA

<213> Homo sapiens

<400> 5457

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cgcagcggga gcgtgggcag ccaggcgggtg gcgcggagga tggatgggga cagccgagat
 60
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 120
tccgtgtcca cccacatgac agcaggagcg atggccggga tcttgaggca ctcggtcatg
 180
taccgggtgg actcgggtgaa ggtaatgtgg actgtggagc tctgtgctgg tcactttcaa
 240
ccctgaacct gatgctactt attttgagcgt tctaagtga aagtcggcct ggtggatgct
 300
tccattata atattaaatt tgcttcttcg tgaggtcaca cctcacatcc ccagtgtcac
 360
tttaataact agtggttttt acatgggtggg ccatgaccca ttagtggact ctgcatttaa
 420
aaataataaa ataaataaaa gaaaaaaaa
448

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<210> 5458

<211> 81

<212> PRT

<211> Homo sapiens

<400> 5458

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Arg Ser Gly Ser Val Gly Ser Gln Ala Val Ala Arg Arg Met Asp Gly
 1           5           10           15
Asp Ser Arg Asp Gly Gly Gly Gly Lys Asp Ala Thr Gly Ser Glu Asp
      20           25           30
Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr His Met Thr Ala
      35           40           45
Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met Tyr Pro Val Asp
      50           55           60
Ser Val Lys Val Met Trp Thr Val Glu Leu Cys Ala Gly His Phe Gln
65           70           75           80
Pro

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<210> 5459

<211> 1468

<212> DNA

<213> Homo sapiens

<400> 5459

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120
cggtatggagc tgcgcagcgg gagcgtgggc agccaggcgg tggcgcgagg gatggatggg
180
gacagccgag atggcggcgg cggaaggac gccaccgggt cggaggacta cgagaacctg
240
ccgactagcg cctccgtgtc caccacatg acagcaggag cgatggccgg gatcctggag
300
cactcggta tgtaccgggt ggactcgggt aagacacgaa tgcagagttt gagtccagat
360
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420
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480
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600
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660
cccgcttgct cacgaataaa gaactcagag ttgtgtgtgc aatgcacacc cagacacacg
720
cagcacaca cgcgcgcgcg cacacacatg cttttttctg tccccctcgg ctttctgaag
780
cctgggggaga aatcagtgac agaggtgttt tggttttatt gttatgtggg ttttcttttg
840
tatttttttt gtttgttttg tttttaaaca ttcaaaagca attaatgatc agacatagga
900
gaaaccttga atagaataaa aacttttgaa tgctgggattc aaaaaaaaaa aaaagttatc
960

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tggacagctt ctttgagact atttaaaac tggatacaaca ggtctctaca acgccaagat
 1020
 ctaactaagc tttaaaaggt caagaagttt tatggctgac aaaggactcg cgcaacgcag
 1080
 aaggcccttc ccaccttaag cttccgggga tctgggaatt ttaccccat tctcttctgt
 1140
 ttgtctgagt ctcactcttc tgcaagcaag ggctgaaatc attttgtttg ggatagctgg
 1200
 gagtatggcc accctgctcc acgatgcggt aatgaatcca gcagaaggta atgtttcatg
 1260
 gtcccaggga ggggcagtag gggtatgtgca aaggggcaca aaaaaatggt tgtgggagag
 1320
 tggagaggac tgaaggtggg cagacggctc ctagtctcca gtcagagcag acaggagaa
 1380
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 1440
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 1468

<210> 5460

<211> 155

<212> PRT

<213> Homo sapiens

<400> 5460

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 Met Asp Gly Asp Ser Arg Asp Gly Gly Gly Lys Asp Ala Thr Gly
 20 25 30
 Ser Glu Asp Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr His
 35 40 45
 Met Thr Ala Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met Tyr
 50 55 60
 Pro Val Asp Ser Val Lys Thr Arg Met Gln Ser Leu Ser Pro Asp Pro
 65 70 75 80
 Lys Ala Gln Tyr Thr Ser Ile Tyr Gly Ala Leu Lys Lys Ile Met Gln
 85 90 95
 Thr Glu Gly Phe Trp Arg Pro Leu Arg Gly Val Asn Val Met Ile Met
 100 105 110
 Gly Ala Gly Pro Ala His Ala Met Tyr Phe Ala Cys Tyr Glu Asn Met
 115 120 125
 Lys Arg Thr Leu Asn Asp Val Phe His His Gln Gly Asn Ser His Leu
 130 135 140
 Ala Asn Gly Ile Leu Lys Ala Phe Val Trp Ser
 145 150 155

<210> 5461

<211> 1725

<212> DNA

<213> Homo sapiens

<400> 5461

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120
ccggaggagca gcaacgcaag gagccaaaat agtttctttg ccggaatgct ttaattctcc
180
atatggagcg aaatatcttc ctgaatatgc agagaaaatt cctggtgaat ccacacagaa
240
gctttctgaa gtacgaaagg aatgcagcat atatctcatt ggaggtaact tcctacccac
300
aaggctctat cctgaagag gatgctggga aattatataa cacctgtgct gtgtttgggc
360
ctgatggaac tttagtagca aagtatagaa agatccatct gtttgacatt gatgttctcg
420
gaaaaattac atttcaagaa tctaaaacat tgagtccggg tgatagtctt tccacatttg
480
atattcgtat gtaccagata agtttgcttc tttagcaatc tcagtagaag acaatcaggt
540
atttattctt tttttgtctc tctccgattt cttcacataa cctaactgaa agaccataag
600
tgagaaaggc agagaatcat cacagatctg gaaagttcgg gcttatttga gaactaagga
660
tttgacacga ttttgccctt tgatttgatt gtagcttcct gttacgggctt ccagagtata
720
cctattaggc tacagttgag tacctcccat ctgataata agcattcaat tagaatgaat
780
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840
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900
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960
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1020
gacatgcggt ttgcagagct tgcacaaatc tacgcacaga gaggctgcc a gctgttggtta
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1140
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1200
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1260
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1320
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1560
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1620
tcttcacata ttaagttgcc tccaagcagt ttgtgaaagt atcagatcct ggtatcctgg
1680

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1725

<210> 5462

<211> 159

<212> PRT

<213> Homo sapiens

<400> 5462

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Phe His Leu Cys Ile Phe Cys Leu Glu Thr Ala Tyr Cys Arg Val Gly
          20           25           30
Leu Gly Ile Cys Tyr Asp Met Arg Phe Ala Glu Leu Ala Gln Ile Tyr
          35           40           45
Ala Gln Arg Gly Cys Gln Leu Leu Val Tyr Pro Gly Ala Phe Asn Leu
          50           55           60
Thr Thr Gly Pro Ala His Trp Glu Leu Leu Gln Arg Ser Arg Ala Val
  65           70           75           80
Asp Asn Gln Val Tyr Val Ala Thr Ala Ser Pro Ala Arg Asp Asp Lys
          85           90           95
Ala Ser Tyr Val Ala Trp Gly His Ser Thr Val Val Asn Pro Trp Gly
          100          105          110
Glu Val Leu Ala Lys Ala Gly Thr Glu Ala Ile Val Tyr Ser Asp
          115          120          125
Ile Asp Leu Lys Lys Leu Ala Glu Ile Arg Gln Gln Ile Pro Val Phe
          130          135          140
Arg Gln Lys Arg Ser Asp Leu Tyr Ala Val Glu Met Lys Lys Pro
  145          150          155
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<210> 5463

<211> 792

<212> DNA

<213> Homo sapiens

<400> 5463

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  120
gacaaaaggcg agggacaaga gagagttaac atctagacag tggaaaaagc catggtgtgt
  180
ggtttctggg aaccaccaac acttgcaggt ttactgtttt cccaggggtg actacaagaa
  240
agaaaaaccat gtttttgcga gattaaaatg tgggttgagt tgcctaaatt aaccatcccc
  300
atttttatca tatttccacc atcacttcag ggttttaaga gtcagtgtcc acctgggcgg
  360
agctggtagt acattttgct tcttagaaag ctaagtcctg ggttcctgtc gatttttaggt
  420
tccaggaact tctgagaac acccgatcgc agagggtaat tttctggagt ttgttttgca
  480
gggatagctg ggagtatggc caccctgtcc cactgatcgg taatgaatcc agcagaagtg
  540
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gtgaagcagc gcttgcagat gtacaactcg cagcaccggt cagcaatcag ctgcatccgg
 600
 acgggtgtgga ggaccgaggg gttggggggcc ttctaccgga gctacaccac gcagctgacc
 660
 atgaacatcc cettccagtc catccacttc atcacctatg agttcctgca ggagcaggtc
 720
 aacccccacc ggacctacaa cccgcagtc cccatcatct caggcgggct ggccggggcc
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<210> 5464

<211> 111

<212> PRT

<213> Homo sapiens

<400> 5464

Phe	Ser	Gly	Val	Cys	Phe	Ala	Gly	Ile	Ala	Gly	Ser	Met	Ala	Thr	Leu
1				5					10					15	
Leu	His	Asp	Ala	Val	Met	Asn	Pro	Ala	Glu	Val	Val	Lys	Gln	Arg	Leu
			20					25					30		
Gln	Met	Tyr	Asn	Ser	Gln	His	Arg	Ser	Ala	Ile	Ser	Cys	Ile	Arg	Thr
		35					40					45			
Val	Trp	Arg	Thr	Glu	Gly	Leu	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr
		50				55				60					
Gln	Leu	Thr	Met	Asn	Ile	Pro	Phe	Gln	Ser	Ile	His	Phe	Ile	Thr	Tyr
65					70				75					80	
Glu	Phe	Leu	Gln	Glu	Gln	Val	Asn	Pro	His	Arg	Thr	Tyr	Asn	Pro	Gln
			85					90					95		
Ser	His	Ile	Ile	Ser	Gly	Gly	Leu	Ala	Gly	Ala	Leu	Ala	Ala		
			100				105						110		

<210> 5465

<211> 497

<212> DNA

<213> Homo sapiens

<400> 5465

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 120
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 300
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 360
 aacccccggc aggagacctc cctgacccc tctgctgcct ctctgtggg accctccagt
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gcagccacgc agtgcac
497

<210> 5466

<211> 134

<212> PRT

<213> Homo sapiens

<400> 5466

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Met Ala Pro Pro Leu Gln Gly Pro Gly Gly Ala Ala Gly Gly Arg Thr
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Asp Gly Gln Ala Ala Trp Val Ala Gly Pro Arg Lys Ala Gly Val Asp
           20           25           30
Val Arg Asp Glu Pro Pro Ala Lys Pro Val Gly Met Ser Gly Pro Ser
           35           40           45
Trp Trp Asp Cys Leu Gly His Arg His Gln His Gly Val Arg Ala Ile
           50           55           60
Ser Gly Asp Ile Gly Gly Ala Thr Thr Arg Trp Gly Ile Phe Asn Arg
65           70           75           80
Leu Glu Pro Leu Arg Leu Glu Arg Pro Thr Pro Gly Arg Arg Pro Pro
           85           90           95
Leu Thr Pro Leu Leu Pro Leu Leu Trp Asp Pro Pro Val Asp Thr Pro
           100          105          110
Asp Glu Asp Thr Gln Glu Ala Ser Ser Gln Asp Arg Arg Gln Leu Pro
           115          120          125
Gly Gln Pro Arg Ser Ala
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<210> 5467

<211> 1329

<212> DNA

<213> Homo sapiens

<400> 5467

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cccggatcca gttcctgga cttgggggat ctgaacgagt cggacttctc caacaatgcg
180
cactttcctg agcacctgga ccactttacg gagaacatgg aggacttctc caatgacctg
240
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360
gcgcccaga gcccccttgt gcccatcaag atggaggaca ccaccaaga tgcagagcat
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480
gagctgcccc tggacctctt ggctgccccc toggccatgg ctgcgcgcgc cgccatggcc
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600
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ggagagatga ctcagctgcc agtgcataaa gcagagcctc tggaggtgaa ccagttcctc
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 720
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 1329

<210> 5468

<211> 363

<212> PRT

<213> Homo sapiens

<400> 5468

Met Asp Ala Val Leu Glu Pro Phe Pro Ala Asp Arg Leu Phe Pro Gly
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 Ser Ser Phe Leu Asp Leu Gly Asp Leu Asn Glu Ser Asp Phe Leu Asn
 20 25 30
 Asn Ala His Phe Pro Glu His Leu Asp His Phe Thr Glu Asn Met Glu
 35 40 45
 Asp Phe Ser Asn Asp Leu Phe Ser Ser Phe Phe Asp Asp Pro Val Leu
 50 55 60
 Asp Glu Lys Ser Pro Leu Leu Asp Met Glu Leu Asp Ser Pro Thr Pro
 65 70 75 80
 Gly Ile Gln Ala Glu His Ser Tyr Ser Leu Ser Gly Asp Ser Ala Pro
 85 90 95
 Gln Ser Pro Leu Val Pro Ile Lys Met Glu Asp Thr Thr Gln Asp Ala
 100 105 110
 Glu His Gly Ala Trp Ala Leu Gly His Lys Leu Cys Ser Ile Met Val
 115 120 125
 Lys Gln Glu Gln Ser Pro Glu Leu Pro Val Asp Pro Leu Ala Ala Pro
 130 135 140
 Ser Ala Met Ala Ala Ala Ala Met Ala Thr Thr Pro Leu Leu Gly
 145 150 155 160
 Leu Ser Pro Leu Ser Arg Leu Pro Ile Pro His Gln Ala Pro Gly Glu

165 170 175
 Met Thr Gln Leu Pro Val Ile Lys Ala Glu Pro Leu Glu Val Asn Gln
 180 185 190
 Phe Leu Lys Val Thr Pro Glu Asp Leu Val Gln Met Pro Thr Pro
 195 200 205
 Pro Ser Ser His Gly Ser Asp Ser Asp Gly Ser Gln Ser Pro Arg Ser
 210 215 220
 Leu Pro Pro Ser Ser Pro Val Arg Pro Met Ala Arg Ser Ser Thr Ala
 225 230 235 240
 Ile Ser Ser Ser Pro Leu Leu Thr Ala Pro His Lys Leu Gln Gly Thr
 245 250 255
 Ser Gly Pro Leu Val Leu Thr Glu Glu Lys Arg Thr Leu Ile Ala
 260 265 270
 Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr Lys Ser Glu Glu
 275 280 285
 Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn Lys Ile Ser Ala
 290 295 300
 Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp Ser Leu Glu Lys
 305 310 315 320
 Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu Arg Lys Lys Val
 325 330 335
 Glu Thr Leu Glu Asn Ala Asn Ser Phe Ser Ser Gly Ile Gln Pro Leu
 340 345 350
 Leu Cys Ser Leu Ile Gly Leu Glu Asn Pro Thr
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<210> 5469

<211> 1292

<212> DNA

<213> Homo sapiens

<400> 5469

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 180
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 300
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 360
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 420
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 540
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 660

gaagagcccc gctgggagga ggaggaagag gagctcatgg gcatttcacc catatctcca
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 aaagagggcaa aggttcctgt ggccaaaatt tctacattcc ctgaaggaga acctggcccc
 780
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 1260
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 1292

<210> 5470

<211> 427

<212> PRT

<213> Homo sapiens

<400> 5470

Xaa Ala Ala Ala Ser Thr Glu Gly Glu Asp Val Gly Trp Trp Arg Ser
 1 5 10 15
 Trp Leu Gln Gln Ser Tyr Gln Ala Val Lys Glu Lys Ser Ser Glu Ala
 20 25 30
 Leu Glu Phe Met Lys Arg Asp Leu Thr Glu Phe Thr Gln Val Val Gln
 35 40 45
 His Asp Thr Ala Cys Thr Ile Ala Ala Thr Ala Ser Val Val Lys Glu
 50 55 60
 Lys Leu Ala Thr Glu Gly Ser Ser Gly Ala Thr Glu Lys Met Lys Lys
 65 70 75 80
 Gly Leu Ser Asp Phe Leu Gly Val Ile Ser Asp Thr Phe Ala Pro Ser
 85 90 95
 Pro Asp Lys Thr Ile Asp Cys Asp Val Ile Thr Leu Met Gly Thr Pro
 100 105 110
 Ser Gly Thr Ala Glu Pro Tyr Asp Gly Thr Lys Ala Arg Leu Tyr Ser
 115 120 125
 Leu Gln Ser Asp Pro Ala Thr Tyr Cys Asn Glu Pro Asp Gly Pro Pro
 130 135 140
 Glu Leu Phe Asp Ala Trp Leu Ser Gln Phe Cys Leu Glu Glu Lys Lys
 145 150 155 160
 Gly Glu Ile Ser Glu Leu Leu Val Gly Ser Pro Ser Ile Arg Ala Leu
 165 170 175
 Tyr Thr Lys Met Val Pro Ala Ala Val Ser His Ser Glu Phe Trp His
 180 185 190
 Arg Tyr Phe Tyr Lys Val His Gln Leu Glu Gln Glu Ala Arg Arg

195 200 205
 Asp Ala Leu Lys Gln Arg Ala Glu Gln Ser Ile Ser Glu Glu Pro Gly
 210 215 220
 Trp Glu Glu Glu Glu Glu Glu Leu Met Gly Ile Ser Pro Ile Ser Pro
 225 230 235 240
 Lys Glu Ala Lys Val Pro Val Ala Lys Ile Ser Thr Phe Pro Glu Gly
 245 250 255
 Glu Pro Gly Pro Gln Ser Pro Cys Glu Glu Asn Leu Val Thr Ser Val
 260 265 270
 Glu Pro Pro Ala Glu Val Thr Pro Ser Glu Ser Ser Glu Ser Ile Ser
 275 280 285
 Leu Val Thr Gln Ile Ala Asn Pro Ala Thr Ala Pro Glu Ala Arg Val
 290 295 300
 Leu Pro Lys Asp Leu Ser Gln Lys Leu Leu Glu Ala Ser Leu Glu Glu
 305 310 315 320
 Gln Gly Leu Ala Val Asp Val Gly Glu Thr Gly Pro Ser Pro Pro Ile
 325 330 335
 His Ser Lys Pro Leu Thr Pro Ala Gly His Thr Gly Gly Pro Glu Pro
 340 345 350
 Arg Pro Pro Ala Arg Val Glu Thr Leu Arg Glu Glu Ala Pro Thr Asp
 355 360 365
 Leu Arg Val Phe Glu Leu Asn Ser Asp Ser Gly Lys Ser Thr Pro Ser
 370 375 380
 Asn Asn Gly Lys Lys Gly Ser Ser Thr Asp Ile Ser Glu Asp Trp Glu
 385 390 395 400
 Lys Asp Phe Asp Leu Asp Met Thr Glu Glu Glu Val Gln Met Ala Leu
 405 410 415
 Ser Lys Val Asp Ala Ser Gly Glu Leu Lys Met
 420 425

<210> 5471
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 5471
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 120
 ttgccagggtg tggcgacatg gtgtgccctg gggcagagta cagagacaca agcttgtgtg
 180
 gacacgaatg tgtagctatg tgcgagtga caccgagtgg tgagtgcagg gacccacaggc
 240
 cggcctgcgt cggtgcgcag ggcataatagg ggcgtgcacg cagtcttgga ggtgtgtgca
 300
 cagagccccc ggcacccgcg tgtgtgcaaa gacacaggaa cccgtctgcg tggcgctgtg
 360
 tgtgcaaccc aaggagggtg gcgcttgga tccaaagtgt gcgcttatcc ggaatgtggat
 420
 gtggggggcag ccgggggacag ggctgggtgt gcgtgactcg ggtgtgccgg gacccacaga
 480
 gcatatgtgt ccatgccttg tgctgtgact catgtccctg ggggtgggac gcgt
 534

<210> 5472

<211> 161

<212> PRT

<213> Homo sapiens

<400> 5472

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Met Leu Cys Gly Ser Arg His Thr Arg Val Thr His Thr Gln Pro Cys
 1             5             10             15
Pro Arg Leu Pro Pro His Pro His Pro Asp Lys Arg Thr Leu Trp Ser
      20             25             30
Pro Ser Ala His Leu Leu Gly Leu His Thr Gln Arg His Ala Asp Gly
      35             40             45
Phe Leu Cys Leu Cys Thr His Ala Gly Ala Gly Gly Ser Val His Thr
      50             55             60
Pro Pro Arg Leu Arg Ala Arg Pro Tyr Met Pro Cys Ala Pro Thr Gln
      65             70             75             80
Ala Gly Leu Gly Ser Leu His Ser Pro Leu Arg Val His Ser His Ile
      85             90             95
Ala Thr His Ser Cys Pro His Lys Leu Val Ser Leu Tyr Ser Ala His
      100            105            110
Gly His Thr Cys Ala Pro His Leu Ala Thr Arg Thr Pro Gly Leu Cys
      115            120            125
Ile Pro His Pro Gly Ser Gly Pro Arg Val Val Gly Pro Ala Gly Ser
      130            135            140
Ala Ala Ala Ser Ala Arg Thr Val Leu Phe Leu Arg Pro Arg Gly Ala
      145            150            155            160
Ala

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<210> 5473

<211> 691

<212> DNA

<213> Homo sapiens

<400> 5473

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gcgaccagca gcgctggtgg ccattgctctt ggacactacg gcctggcggg cagccctcgc
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cgctgccgcg ccccgcgccc ccaggaggcc gcaccctgcg ccagggcccg gagacagcaa
120
catcttcttg ggccctgcagg agacctgaca gatgccaaa caaaggaaca gttgggatcc
180
aggcagcatg aggtagaatg gcaaacctac cagggtattc tgaagaagac aagagtcgatg
240
gaaaaaacca agtggctgga tatcaaagga aatcatgaaa aagatggagg agctcttatt
300
actggccaag gaaagcagtc ggagcaacca tacaatttgg tttggacact ttacaacatc
360
cactattctt tctccatcac caggaatccg gtcaataatg agttcggcta tagcttattt
420
gtgtgggcat ctccatacac ttggtggact gatgcctgtt ttgcacactc gtcacttcca
480
gggcactttg gaacttgagg tgggagactg gaaggataat aggaggtacc ggatttttgc
540

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ttttgatcac gacctcttta gctttgcaga tttgatcttt gggaagtggc ctgtgggtct
 600
 tatcaccaat cctaaatcac tcctttatag ttgtggtgaa catgaaccac tagaaagact
 660
 ttttcaactca acccacatta gattggtaac a
 691

<210> 5474
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 5474
 Met Lys Lys Met Glu Glu Leu Leu Leu Ala Lys Glu Ser Ser Arg
 1 5 10 15
 Ser Asn His Thr Ile Trp Phe Gly His Phe Thr Thr Ser Thr Ile Leu
 20 25 30
 Ser Pro Ser Pro Gly Ile Arg Ser Ile Met Ser Ser Ala Ile Ala Tyr
 35 40 45
 Leu Cys Gly His Leu His Thr Leu Gly Gly Leu Met Pro Val Leu His
 50 55 60
 Thr Arg His Phe Gln Gly Thr Leu Glu Leu Glu Val Gly Asp Trp Lys
 65 70 75 80
 Asp Asn Arg Arg Tyr Arg Ile Phe Ala Phe Asp His Asp Leu Phe Ser
 85 90 95
 Phe Ala Asp Leu Ile Phe Gly Lys Trp Pro Val Val Leu Ile Thr Asn
 100 105 110
 Pro Lys Ser Leu Leu Tyr Ser Cys Gly Glu His Glu Pro Leu Glu Arg
 115 120 125
 Leu Leu His Ser Thr His Ile Arg Leu Val Thr
 130 135

<210> 5475
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 5475
 ggccacacacg aaacagcctt cctgggaccc aaggacctgt tccctacga caaatgtaaa
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 gacaagtacg ggaagcccaa caagaggaaa ggcttcaatg aaggcgctgtg ggagatccag
 120
 aacaaccccc acgccagcta cagcgccctt ccgccagtga gctcctccga cagcgaggcc
 180
 cccgaggcca accccgcga cggcagtgac gctgacgagg acgatgagga cccggggggtc
 240
 atggccgtca cagcggtaac cgccacagct gccagcgaca ggatggagag cgactcagac
 300
 tcagacaaga gtagcgacaa cagtggcctg aagaggaaga cgcctgcgct aaagatgtcg
 360
 gtctcgaaac gagccgaaa ggcctccagc gacctggatc agggccagct gtccccatcc
 420
 gaagaggaga actcgaaaag ctcatctgag tcggagaaga ccagcgacca ggacttcaca
 480

cctgagaaga aagcagcggc cggggcgcca cggagggggc ctctgggggg acggaaaaaa
 540
 aagaaggcgc cgtcagcctc cgactccgac tccaaggcgc attcggacgc ggccaagcct
 600
 gagccggtgg ccatggcgcg gtcggcgt
 628

<210> 5476
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 5476
 Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro Tyr
 1 5 10 15
 Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys Gly Phe
 20 25 30
 Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala Ser Tyr Ser
 35 40 45
 Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala Pro Glu Ala Asn
 50 55 60
 Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp Glu Asp Arg Gly Val
 65 70 75 80
 Met Ala Val Thr Ala Val Thr Ala Thr Ala Ser Asp Arg Met Glu
 85 90 95
 Ser Asp Ser Asp Ser Asp Lys Ser Ser Asp Asn Ser Gly Leu Lys Arg
 100 105 110
 Lys Thr Pro Ala Leu Lys Met Ser Val Ser Lys Arg Ala Arg Lys Ala
 115 120 125
 Ser Ser Asp Leu Asp Gln Ala Ser Val Ser Pro Ser Glu Glu Asn
 130 135 140
 Ser Glu Ser Ser Ser Glu Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr
 145 150 155 160
 Pro Glu Lys Lys Ala Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly
 165 170 175
 Gly Arg Lys Lys Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys
 180 185 190
 Ala Asp Ser Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser
 195 200 205
 Ala

<210> 5477
 <211> 727
 <212> DNA
 <213> Homo sapiens

<400> 5477
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 120
 gggcccttct cactgagctc gtgaagtgcc tcagtcaagg caaggtcccc tggccatat
 180

gggtcccccc gcccatgggg ttgggtggt ccttatagtg cctacgttag tctgtgtgga
 240
 gccccctggcc agcgggggag aaaaagggtg cttctgggtcc gtctgtataa aacatggccc
 300
 ctccactgtc gggccccccac acagctggca ggctgggtg gcctctcacc cctggcctcc
 360
 cctggacccc tggtgtggtc ctcaacttca ctctccgcac ttagtgcccc gccgccccca
 420
 gactcatcgt cgctcagccc atagggaagc ccaggcctgg cccccagaga gtctccttec
 480
 gagtctctct cgaagcccat gagctggtca ctgttgccgt cgccttcctc ctcttctctt
 540
 tcctctctca actccagatc ctggcctagt agcaaatcac tctccaatac caggggccccg
 600
 ggtcctctct cgaggagtc ttcagtatcc actttgaccc cctcgcatth caggggctgc
 660
 ggggtggcttt gcttctctcg gggcatcgtg accgggtcca gcccgacgcg cctccggcct
 720
 gcggccg
 727

<210> 5478

<211> 99

<212> PRT

<213> Homo sapiens

<400> 5478

Ser	Ala	Ser	Val	Lys	Ala	Arg	Ser	Pro	Gly	Pro	Tyr	Gly	Pro	Pro	Arg
1				5					10					15	
Pro	Trp	Gly	Trp	Ala	Gly	Pro	Tyr	Ser	Ala	Tyr	Val	Ser	Leu	Cys	Gly
		20						25					30		
Ala	Pro	Gly	Gln	Arg	Gly	Arg	Lys	Arg	Trp	Leu	Leu	Val	Arg	Leu	Tyr
		35					40					45			
Lys	Thr	Trp	Pro	Leu	Thr	Cys	Arg	Pro	Pro	Thr	Gln	Leu	Ala	Gly	Trp
		50				55				60					
Ala	Gly	Leu	Ser	Pro	Leu	Ala	Ser	Pro	Gly	Pro	Leu	Ala	Gly	Ser	Ser
65					70					75				80	
Thr	Ser	Leu	Ser	Ala	Leu	Ser	Ala	Arg	Pro	Pro	Pro	Asp	Ser	Ser	Ser
				85					90					95	

Leu Ser Pro

<210> 5479

<211> 1386

<212> DNA

<213> Homo sapiens

<400> 5479

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 cgaggagcagc gggagcgca ggagcaggag cggaggctgc aggcagaaag ggacaagcga
 120
 atgcgagagg agcagctggc acgggaggcc gagggccggg cggagcggga ggcggaggcc
 180

cgagagcggg aggagcagga ggcacgagag aaggcgcagg ccgagcagga ggagcaggag
 240
 cggctgcaga agcagaaaga ggagccgaa gctcggctgc gggaagaggc ggagcggcag
 300
 cgtctggagc gggaagagca cttccagcag caggagcaag agcggcaaga gcgcagaaag
 360
 cgtctggagg agatcatgaa gaggactcgg aagtcagaag tttctgaaac caagcagaag
 420
 caggacagca aggaggccaa cgccaacggt tccagcccag agcctgtgaa agctgtggag
 480
 gctcggctcc cagggtctga gaaggaggct gtgcagaaag aggagcccat cccacaggag
 540
 cctcagtgga gtctcccaag caaggagttg ccagcgtccc tggatgaatgg cctgcagcct
 600
 ctcccagcac accaggagaa tggcttctcc accaacggac cctctgggga caagagtctg
 660
 agccgaacac cagagacact cctgcccttt gcagaggcag aagccttctt caagaaagct
 720
 gtggtgcagt cccgcaggt cacaagaagtc ctttaagagg gtttgccctg gatccgggca
 780
 cagttgtgag ggctcctctg catcacctac caggatgtct ggaggagaaa aagacagaaac
 840
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 900
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 960
 cgcacgcgca gacatccctt ctccccata cacacatata cactcacagc ctctctggcc
 1020
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 1080
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 1200
 aggggggatcc caggctctgg gatgggggac accttgggac acaggatact ggttgcctta
 1260
 ggggtaccca tgccccctgc cctcgccttg aatcagtggt actgcatctg attaaatgtc
 1320
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 1380
 aaaaaa
 1386

<210> 5480
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 5480
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 20 25 30
 Leu Gln Ala Glu Arg Asp Lys Arg Met Arg Glu Glu Gln Leu Ala Arg

35 40 45
 Glu Ala Glu Ala Arg Ala Glu Arg Glu Ala Glu Ala Arg Arg Arg Glu
 50 55 60
 Glu Gln Glu Ala Arg Glu Lys Ala Gln Ala Glu Gln Glu Glu Gln Glu
 65 70 75 80
 Arg Leu Gln Lys Gln Lys Glu Glu Ala Glu Ala Arg Ser Arg Glu Glu
 85 90 95
 Ala Glu Arg Gln Arg Leu Glu Arg Glu Lys His Phe Gln Gln Gln Glu
 100 105 110
 Gln Glu Arg Gln Glu Arg Arg Lys Arg Leu Glu Glu Ile Met Lys Arg
 115 120 125
 Thr Arg Lys Ser Glu Val Ser Glu Thr Lys Gln Lys Gln Asp Ser Lys
 130 135 140
 Glu Ala Asn Ala Asn Gly Ser Ser Pro Glu Pro Val Lys Ala Val Glu
 145 150 155 160
 Ala Arg Ser Pro Gly Leu Gln Lys Glu Ala Val Gln Lys Glu Glu Pro
 165 170 175
 Ile Pro Gln Glu Pro Gln Trp Ser Leu Pro Ser Lys Glu Leu Pro Ala
 180 185 190
 Ser Leu Val Asn Gly Leu Gln Pro Leu Pro Ala His Gln Glu Asn Gly
 195 200 205
 Phe Ser Thr Asn Gly Pro Ser Gly Asp Lys Ser Leu Ser Arg Thr Pro
 210 215 220
 Glu Thr Leu Leu Pro Phe Ala Glu Ala Glu Ala Phe Leu Lys Lys Ala
 225 230 235 240
 Val Val Gln Ser Pro Gln Val Thr Glu Val Leu
 245 250

<210> 5481

<211> 1513

<212> DNA

<213> Homo sapiens

<400> 5481

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 120
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 180
 cccctaaccg tgaggctgcc gcgcggcggt cactgcgcgg gggtagtggg cccagtggt
 240
 gcgctctctg gccgttcctt acactttgct tcaggctcca gtgcaggggc gtatggggat
 300
 atggccaact cgggctgcaa ggacgtcacg ggtccagatg aggagagttt tctgtacttt
 360
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 420
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 480
 agtcaaaact ggcatggagg gatagccacc atttttcaga gtcctggcga tgaattgtgg
 540
 ggagtagtat ggaaatgaa caaaagcaat ttaaattctc tggatgagca agaaggggtt
 600

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aaaagtggaa tgtatgttgt aatagaagtt aaagttgcaa ctcaagaagg aaaagaaata
660
acctgtcgaa gttatctgat gacaaattac gaaagtgctc ccccatcccc acagtataaa
720
aagattattt gcatgggtgc aaaagaaaaa ggtttgccgc tggagtatca agagaagtta
780
aaagcaatag aaccaaatga ctatacagga aaggctctcag aagaaattga agacatcatc
840
aaaaaggggg aaacacaaac tctttagaac ataacagaat atatctaagg gtattctatg
900
tgctaataata aaatatTTTT aacacttgag aacagggatc tgggggatct ccacgtttga
960
tccattttca gcagtgtctc gaaggagtat cttacttggg tgattccttg tttttagact
1020
ataaaaagaa actgggatag gagtttagaca atttaaaagg ggtgatagag ggcctgaaat
1080
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1140
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1260
agacaattga taataacatt ttgaaaattg gaaagatggg atactgtttt tagaggaata
1320
aacgtatttg tggttttaaa aaaaaagagc aacttccttt gcactgtata cccttttgta
1380
ttattaggat ttatactat gtttatatgt tgcctattta ataaatcgct taaagtata
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1500
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<210> 5482

<211> 188

<212> PRT

<213> Homo sapiens

<400> 5482

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Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly Pro Asp Glu Glu Ser
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Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Thr Glu Arg Ile His
          20             25             30
Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Asp
          35             40             45
Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys Thr Ser Gln Thr Trp
          50             55             60
His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro Gly Asp Glu Leu Trp
          65             70             75             80
Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu Asn Ser Leu Asp Glu
          85             90             95
Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val Ile Glu Val Lys Val
          100            105            110
Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg Ser Tyr Leu Met Thr

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	115		120		125	
Asn	Tyr	Glu	Ser	Ala	Pro	Pro
130					135	
Met	Gly	Ala	Lys	Glu	Asn	Gly
145				150		155
Lys	Ala	Ile	Glu	Pro	Asn	Asp
				165		170
Glu	Asp	Ile	Ile	Lys	Lys	Gly
				180		185

<210> 5483

<211> 1552

<212> DNA

<213> Homo sapiens

<400> 5483

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 120
 ttcacctaca tcgagtctgc ctccggagctc agaggggggt ttgactggag cctccacttc
 180
 cagtgggagc agctctcccc agagcagaag gctcggcgcc tggaccaccac ggagcccatc
 240
 aggactccta tcatagctgg agggctcttc gtgatcgaca aagcttgggt tgattacctg
 300
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 360
 gtgtggatgt gcgggggagc cctagagatc gtcccctgca gccagtgagg gcacgtcttc
 420
 cggaagaagc accctctacgt ttccctgat ggaatgccac acacgtatat aaagaacacc
 480
 aagcggagac ctgaagtgtg gatggatgaa tacaagcaat actattacgc tgcccggcca
 540
 ttccgacctg agaggccctt cgggaatggt gagagcagat tggacctgag gaagaatctg
 600
 cgctgccaga gcttcaagtg gtacctggag aatatctacc ctgaactcag catccccaag
 660
 gaggcttcca tccagaaggc caatatccga cagagacaga agtgccctgga atctcaaagg
 720
 cagaacaacc aagaaccccc aaacctaag ttgagccctc gtgccaaagt caaaggcgaa
 780
 gatgcaagt cccaggtatg ggccttcaca tacaccaga agatcctcca ggaggagctg
 840
 tgcctgtcag tcatcacctt gttccctggc gcccagtggt ttcttgtcct ttgcaagaat
 900
 ggagatgacc gacagcaatg gacccaaact ggttccaca tcgagcacat agcatccac
 960
 ctctgcctcg atacagatat gttcgtgtat ggcaccgaga acggcaaggaa aatcgctgct
 1020
 aacctcatgt agtctcact catgagccag cactgggaca tggtagctc ttgaggacc
 1080
 ctgccagaag cagcaagggc catgggggtg tgcttccctg gaccagaaca gactggaaac
 1140

tgggcagcaa gcagcctgca accacctcag acatcctgga ctgggaggtg gaggcagagc
 1200
 cccccaggagc aggagcaact gtctcaggga ggacagagga aaacatcaca agccaatggg
 1260
 gctcaagac aaatcccaca tgttctcaag gccgttaagt tccagtcctg gccagtcatt
 1320
 ccctgattgg tatctggaga cagaaacctta atgggaagtg tttattgttc cttttcctac
 1380
 aaaggaagca gtctctggag gccagaaaga aaagccttct ttttactag gccaggacta
 1440
 cattgagaga tgaagaatgg aggttggttc caaaagaaat aaagagaaac ttagaagttg
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 1552

<210> 5484
 <211> 357
 <212> PRT
 <213> Homo sapiens

<400> 5484
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 Leu Xaa Asp Arg Val Lys Glu Asp Tyr Thr Arg Val Val Cys Pro Val
 20 25 30
 Ile Asp Ile Ile Asn Leu Asp Thr Phe Thr Tyr Ile Glu Ser Ala Ser
 35 40 45
 Glu Leu Arg Gly Gly Phe Asp Trp Ser Leu His Phe Gln Trp Glu Gln
 50 55 60
 Leu Ser Pro Glu Gln Lys Ala Arg Arg Leu Asp Pro Thr Glu Pro Ile
 65 70 75 80
 Arg Thr Pro Ile Ile Ala Gly Gly Leu Phe Val Ile Asp Lys Ala Trp
 85 90 95
 Phe Asp Tyr Leu Gly Lys Tyr Asp Met Asp Met Asp Ile Trp Gly Gly
 100 105 110
 Glu Asn Phe Glu Ile Ser Phe Arg Val Trp Met Cys Gly Gly Ser Leu
 115 120 125
 Glu Ile Val Pro Cys Ser Arg Val Gly His Val Phe Arg Lys Lys His
 130 135 140
 Pro Tyr Val Phe Pro Asp Gly Asn Ala Asn Thr Tyr Ile Lys Asn Thr
 145 150 155 160
 Lys Arg Thr Ala Glu Val Trp Met Asp Glu Tyr Lys Gln Tyr Tyr Tyr
 165 170 175
 Ala Ala Arg Pro Phe Ala Leu Glu Arg Pro Phe Gly Asn Val Glu Ser
 180 185 190
 Arg Leu Asp Leu Arg Lys Asn Leu Arg Cys Gln Ser Phe Lys Trp Tyr
 195 200 205
 Leu Glu Asn Ile Tyr Pro Glu Leu Ser Ile Pro Lys Glu Phe Ser Ile
 210 215 220
 Gln Lys Gly Asn Ile Arg Gln Arg Gln Lys Cys Leu Glu Ser Gln Arg
 225 230 235 240
 Gln Asn Asn Gln Glu Thr Pro Asn Leu Lys Leu Ser Pro Cys Ala Lys
 245 250 255
 Val Lys Gly Glu Asp Ala Lys Ser Gln Val Trp Ala Phe Thr Tyr Thr

	260		265		270
Gln Lys Ile	Leu Gln Glu	Glu Leu Cys Leu	Ser Val Ile Thr	Leu Phe	
	275		280	285	
Pro Gly Ala	Pro Val Val	Leu Val Leu Cys	Lys Asn Gly Asp	Asp Arg	
	290	295	300		
Gln Gln Trp	Thr Lys Thr	Gly Ser His Ile	Glu His Ile Ala	Ser His	
305		310	315	320	
Leu Cys Leu	Asp Thr Asp	Met Phe Gly Asp	Gly Thr Glu Asn	Gly Lys	
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<210> 5485

<211> 1549

<212> DNA

<213> Homo sapiens

<400> 5485

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<210> 5486

<211> 290

<212> PRT

<213> Homo sapiens

<400> 5486

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			20					25					30		
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		35				40					45				
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		50				55					60				
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65					70					75				80	
Tyr	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Arg	Tyr	Arg	Glu	Arg
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		115				120						125			
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130						135					140				
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Pro	Thr	Gln	Gln	Arg	Ser	Ile	Ala	Phe	Ser	Ser	Asn	Asn	Ser	Val	Ala
				245					250					255	
Lys	Pro	Ile	Gln	Lys	Ser	Ala	Lys	Ala	Ala	Thr	Glu	Glu	Ala	Ser	Ser
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<210> 5487

<211> 1716

<212> DNA

<213> Homo sapiens

<400> 5487

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<210> 5488

<211> 272

<212> PRT

<213> Homo sapiens

<400> 5488

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			35				40				45				
Gly	Pro	Ala	His	Ala	Met	Tyr	Phe	Ala	Cys	Tyr	Glu	Asn	Met	Lys	Arg
			50			55					60				
Thr	Leu	Asn	Asp	Val	Phe	His	His	Gln	Gly	Asn	Ser	His	Leu	Ala	Asn
65				70					75						80
Gly	Ile	Ala	Gly	Ser	Met	Ala	Thr	Leu	Leu	His	Asp	Ala	Val	Met	Asn
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Pro	Ala	Glu	Val	Val	Lys	Gln	Arg	Leu	Gln	Met	Tyr	Asn	Ser	Gln	His
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Arg	Ser	Ala	Ile	Ser	Cys	Ile	Arg	Thr	Val	Trp	Arg	Thr	Glu	Gly	Leu
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Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Ile	Pro
			130			135					140				
Phe	Gln	Ser	Ile	His	Phe	Ile	Thr	Tyr	Glu	Phe	Leu	Gln	Glu	Gln	Val
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Leu	Ala	Gly	Ala	Leu	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val	Cys
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Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Asn	Val	Ala	Leu	Ser	Leu	Ala	Asn
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<210> 5489

<211> 1600

<212> DNA

<213> Homo sapiens

<400> 5489

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<211> 357

<212> PRT

<213> Homo sapiens

<400> 5490

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Leu	Glu	Lys	Ile	Leu	Gln	Arg	Gln	Phe	Ser	Ser	Ser	Asn	Ser	Pro	Arg
		35					40					45			
Gly	Ile	Ile	Phe	Thr	Arg	Thr	Arg	Gln	Ser	Ala	His	Ser	Leu	Leu	Leu
	50					55					60				
Trp	Leu	Gln	Gln	Gln	Gln	Gly	Leu	Gln	Thr	Val	Asp	Ile	Arg	Ala	Gln
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Arg	Asp	Gln	Gln	Glu	Val	Ile	Gln	Lys	Phe	Gln	Asp	Gly	Thr	Leu	Asn
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Leu	Leu	Val	Ala	Thr	Ser	Val	Ala	Glu	Gly	Leu	Asp	Ile	Pro	His	
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Cys	Asn	Val	Val	Val	Arg	Tyr	Gly	Leu	Leu	Thr	Asn	Glu	Ile	Ser	Met
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Val	Gln	Ala	Arg	Gly	Arg	Ala	Arg	Ala	Asp	Gln	Ser	Val	Tyr	Ala	Phe
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Ala	Leu	Glu	Thr	Leu	Met	Glu	Gln	Ala	Val	Ala	Ala	Val	Gln	Lys	Met
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Asp	Gln	Ala	Glu	Tyr	Gln	Ala	Lys	Ile	Arg	Asp	Leu	Gln	Gln	Ala	Ala
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	210				215					220					
Gln	Phe	Pro	Val	Glu	His	Val	Gln	Leu	Leu	Cys	Ile	Asn	Cys	Met	Val
225				230					235					240	
Ala	Val	Gly	His	Gly	Ser	Asp	Leu	Arg	Lys	Val	Glu	Gly	Thr	His	His
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Val	Asn	Val	Asn	Pro	Asn	Phe	Ser	Asn	Tyr	Tyr	Asn	Val	Ser	Arg	Asp

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	290		295		300
Lys Ser Val Lys Leu Pro Val Leu Lys Val Arg Ser Met Leu Leu Glu					
305		310		315	320
Thr Pro Gln Gly Arg Ile Gln Ala Lys Lys Trp Ser Arg Val Pro Phe					
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Ser Val Pro Asp Phe Asp Phe Leu Gln His Cys Ala Glu Asn Leu Ser					
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<210> 5491

<211> 5555

<212> DNA

<213> Homo sapiens

<400> 5491

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<211> 602

<212> PRT

<213> Homo sapiens

<400> 5492

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<211> 6538

<212> DNA

<213> Homo sapiens

<400> 5493

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<213> Homo sapiens

<400> 5494

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Val Phe Val Arg Val	Thr Asn Pro Val Asp Leu Trp Ser Ala Pro					
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Ser Ser Gln Ala Arg	Leu Glu Lys Glu Tyr Phe Asp Gln His Phe Gly					
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Pro Phe Phe Arg Thr	Glu Gln Leu Ile Ile Arg Ala Pro Leu Thr Asp					
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Lys His Ile Tyr Gln	Pro Tyr Pro Ser Gly Ala Asp Val Pro Phe Gly					
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Pro Pro Leu Asp Ile	Gln Ile Leu His Gln Val Leu Asp Leu Gln Ile					
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Ala Ile Glu Asn Ile	Thr Ala Ser Tyr Asp Asn Glu Thr Val Thr Leu					
450		455		460		
Gln Asp Ile Cys Leu	Ala Pro Leu Ser Pro Tyr Asn Thr Asn Cys Thr					
465		470		475		480
Ile Leu Ser Val Leu	Asn Tyr Phe Gln Asn Ser His Ser Val Leu Asp					
	485		490			495
His Lys Lys Gly Asp	Asp Phe Phe Val Tyr Ala Asp Tyr His Thr His					
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Phe Leu Tyr Cys Val	Arg Ala Pro Ala Ser Leu Asn Asp Thr Ser Leu					
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Leu His Asp Pro Cys	Leu Gly Thr Phe Gly Gly Pro Val Phe Pro Trp					
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Leu Val Leu Gly Gly	Tyr Asp Asp Gln Asn Tyr Asn Asn Ala Thr Ala					
545		550		555		560
Leu Val Ile Thr Phe	Pro Val Asn Asn Tyr Tyr Asn Asp Thr Glu Lys					
	565		570			575
Leu Gln Arg Ala Gln	Ala Trp Glu Lys Glu Phe Ile Asn Phe Val Lys					

580										585										590										
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Val	Ile	Ser	Tyr	Ala	Ile	Met	Phe	Leu	Tyr	Ile	Ser	Leu	Ala	Leu	Gly															
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Gly	Val	Phe	Ser	Tyr	Ile	Gly	Leu	Pro	Leu	Thr	Leu	Ile	Val	Ile	Glu															
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Val	Ile	Pro	Phe	Leu	Val	Leu	Ala	Val	Gly	Val	Asp	Asn	Ile	Phe	Ile															
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Leu	Val	Gln	Ala	Tyr	Gln	Arg	Asp	Glu	Arg	Leu	Gln	Gly	Glu	Thr	Leu															
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Gly	Asp	Phe	Met	Arg	Phe	Leu	Pro	Met	Phe	Leu	Ser	Asp	Asn	Pro	Asn															
			995				1000					1005																		
Pro	Lys	Cys	Gly	Lys	Gly	Gly	His	Ala	Ala	Tyr	Ser	Ser	Ala	Val	Asn															

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 Tyr His Thr Val Leu Gln Thr Ser Ala Asp Phe Ile Asp Ala Leu Lys
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 Gly Ser Ala Tyr Arg Val Phe Pro Tyr Ser Val Phe Tyr Val Phe Tyr
 1075 1080 1085
 Glu Gln Tyr Leu Thr Ile Ile Asp Asp Thr Ile Phe Asn Leu Gly Val
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 Ser Leu Val Asn Leu Val Met Ser Cys Gly Ile Ser Val Glu Phe Cys
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 Ser His Ile Thr Arg Ala Phe Thr Val Ser Met Lys Gly Ser Arg Val
 1170 1175 1180
 Glu Arg Ala Glu Glu Ala Leu Ala His Met Gly Ser Ser Val Phe Ser
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 Gly Ile Thr Leu Thr Lys Phe Gly Gly Ile Val Val Leu Ala Phe Ala
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 Lys Ser Gln Ile Phe Gln Ile Phe Tyr Phe Arg Met Tyr Leu Ala Met
 1220 1225 1230
 Val Leu Leu Gly Ala Thr His Gly Leu Ile Phe Leu Pro Val Leu Leu
 1235 1240 1245
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<210> 5495

<211> 2414

<212> DNA

<213> Homo sapiens

<400> 5495

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<210> 5496

<211> 345

<212> PRT

<213> Homo sapiens

<400> 5496

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			20					25				30			
Leu	Leu	Gly	Ser	Met	Ala	Leu	Ser	Asn	His	Tyr	Arg	Ser	Glu	Asp	Leu
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Leu	Asp	Val	Asp	Thr	Ala	Ala	Gly	Gly	Phe	Gln	Gln	Arg	Gln	Gly	Leu
	50					55					60				
Lys	Tyr	Cys	Leu	Pro	Leu	Thr	Phe	Cys	Ile	His	Thr	Gly	Leu	Ser	Gln
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Tyr	Ile	Ala	Val	Glu	Ala	Ala	Glu	Gly	Arg	Asn	Lys	Asn	Glu	Val	Phe
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Tyr	Gln	Cys	Pro	Asp	Gln	Met	Ala	Arg	Asn	Pro	Ala	Ala	Ile	Asp	Met
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Phe	Ile	Ile	Gly	Ala	Thr	Phe	Thr	Asp	Trp	Phe	Thr	Ser	Tyr	Val	Lys
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Asn	Val	Val	Ser	Gly	Gly	Phe	Pro	Ile	Ile	Arg	Asp	Gln	Ile	Phe	Arg
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Tyr	Val	His	Asp	Pro	Glu	Cys	Val	Ala	Thr	Thr	Gly	Asp	Ile	Thr	Val
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Ser	Val	Ser	Thr	Ser	Phe	Leu	Pro	Glu	Leu	Ser	Ser	Val	His	Pro	Pro
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His	Tyr	Phe	Phe	Thr	Tyr	Arg	Ile	Arg	Ile	Glu	Met	Ser	Lys	Asp	Ala
	180							185					190		
Leu	Pro	Glu	Lys	Ala	Cys	Gln	Leu	Asp	Ser	Arg	Tyr	Trp	Arg	Ile	Thr
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Asn	Ala	Lys	Gly	Asp	Val	Glu	Glu	Val	Gln	Gly	Pro	Gly	Val	Val	Gly
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Glu	Phe	Pro	Ile	Ile	Ser	Pro	Gly	Arg	Val	Tyr	Glu	Tyr	Thr	Ser	Cys
225					230					235					240
Thr	Thr	Phe	Ser	Thr	Thr	Ser	Gly	Tyr	Met	Glu	Gly	Tyr	Tyr	Thr	Phe
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<210> 5498

<211> 150

<212> PRT

<213> Homo sapiens

<400> 5498

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Ala Gln Leu Trp Trp Ser Ser Pro Phe Ile His Ser Pro Gly Glu Thr
      35             40             45
Asn Ile Pro His Thr Leu Thr Glu Pro His Ser Val Pro Gly Trp Cys
      50             55             60
Trp Asp Thr Leu Arg Arg His Gly Ala Gly Gln Gly His Pro Gly Met
65             70             75             80
Ala Arg Ser Gly Thr Gly Glu Gly Gln Arg Glu Gly Asp Ile Glu Arg
      85             90             95
Glu Glu Asp Glu Glu Glu Gly Asn Arg Ser Arg Lys Ser Arg Asp Ser
      100            105            110
Arg Ser Gln Val Lys Gly Leu Pro Leu His Ser Arg Glu Gln Arg Asp
      115            120            125
Pro Ser Ala Gly Ala Ser Glu Lys Ser Arg Asn Pro Ser Arg Met Gly
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Thr Trp Gly Val Asn Phe
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<210> 5499

<211> 1918

<212> DNA

<213> Homo sapiens

<400> 5499

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<210> 5500

<211> 426

<212> PRT

<213> Homo sapiens

<400> 5500

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 His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro
 50 55 60
 Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Asp Glu Asp Arg
 65 70 75 80
 Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
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 Asp Ile Ala His Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
 100 105 110
 Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
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 Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
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 Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
 145 150 155 160
 Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
 165 170 175
 Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
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 Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
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 Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
 210 215 220
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
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 245 250 255
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
 260 265 270
 Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala
 275 280 285
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 290 295 300
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 305 310 315 320
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
 325 330 335
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 340 345 350
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 355 360 365
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 370 375 380
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
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 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
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 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
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<210> 5501

<211> 568

<212> DNA

<213> Homo sapiens

<400> 5501

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<210> 5502

<211> 110

<212> PRT

<213> Homo sapiens

<400> 5502

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Gly	Ala	Ala	Leu	Gln	Val	Leu	Ala	His	Ala	Gln	Gln	Ala	Pro	His	Ser
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Phe	Val	Thr	Thr	Lys	Gly	Thr	Val	Leu	Phe	Thr	Ala	Pro	Pro	Ala	Ser
				50			55				60				
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65					70				75					80	
Leu	Ala	Arg	Gln	Gly	Pro	Ala	Leu	Lys	Glu	Ile	Ser	Leu	Pro	Asp	Pro
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Trp	Thr	Trp	Lys	Trp	Arg	Leu	His	Val	Pro	Ala	Leu	Ala	Ala		
			100				105						110		

<210> 5503

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 5503

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120
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1260
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1440
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1560
agagggttaa ctgagaggag cacagagtgg tacaggagat ggggatgaaa gggataaggg
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1679

<210> 5504
 <211> 392
 <212> PRT
 <213> Homo sapiens

<400> 5504
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 35 40 45
 Ser Gly Glu Ala Thr Gly Ala Asp Ala Gly Arg Leu Cys Pro Pro Pro
 50 55 60
 Arg Ser Arg Ala Pro His Lys Asp Arg Thr Leu Ala Arg Ser Arg Pro
 65 70 75 80
 Gln Thr Gln Gly Glu Asp Cys Ser Leu Pro Val Gly Glu Val Lys Ile
 85 90 95
 Gly Lys Arg Ser Tyr Ser Pro Ala Pro Gly Lys Gln Lys Lys Pro Asn
 100 105 110
 Ala Met Gly Leu Ala Pro Thr Ser Ser Pro Gly Ala Pro Asn Ser Ala
 115 120 125
 Arg Ala Thr His Asn Pro Val Pro Cys Gly Ser Gly Arg Gly Pro Cys
 130 135 140
 His Leu Ala Asn Leu Leu Ser Thr Leu Ala Gln Ser Asn Gln Asn Arg
 145 150 155 160
 Asp His Lys Gln Gly Pro Pro Glu Val Thr Cys Gln Ile Arg Lys Lys
 165 170 175
 Thr Arg Thr Leu Tyr Arg Ser Asp Gln Leu Glu Glu Leu Glu Lys Ile
 180 185 190
 Phe Gln Glu Asp His Tyr Pro Asp Ser Asp Lys Arg Arg Glu Ile Ala
 195 200 205
 Gln Thr Val Gly Val Thr Pro Gln Arg Ile Met Val Lys Gly Ala Gly
 210 215 220
 Ser Leu Val Ala Gly Trp Ser Gly Gly Gly Pro Thr Ile Glu Thr Leu
 225 230 235 240
 Glu Leu Gln Ser Glu Arg Ser Ala Val Ala Trp Val Trp Phe Gln Asn
 245 250 255
 Arg Arg Ala Lys Trp Arg Lys Met Glu Lys Leu Asn Gly Lys Glu Ser
 260 265 270
 Lys Asp Asn Pro Ala Ala Pro Gly Pro Ala Ser Ser Gln Cys Ser Ser
 275 280 285
 Ala Ala Glu Ile Leu Pro Ala Val Pro Met Glu Pro Lys Pro Asp Pro
 290 295 300
 Phe Pro Gln Glu Ser Pro Leu Asp Thr Phe Pro Glu Pro Pro Met Leu
 305 310 315 320
 Leu Thr Ser Asp Gln Thr Leu Ala Pro Thr Gln Pro Ser Glu Gly Ala
 325 330 335
 Gln Arg Val Val Thr Pro Pro Leu Phe Ser Pro Pro Pro Val Arg Arg
 340 345 350
 Ala Asp Leu Pro Phe Pro Leu Gly Pro Val His Thr Pro Gln Leu Met
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 Pro Leu Leu Met Asp Val Ala Gly Ser Asp Ser Ser His Lys Asp Gly

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<210> 5505
<211> 1099
<212> DNA
<213> Homo sapiens

<400> 5505
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120
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180
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240
ttcatcactg aggactggga ccagcccggt gccgactgga agatcttcta cttcttacgg
300
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420
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480
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660
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780
gccggctggt acggcccgag ggtcaccaac agcagcatca ccacgtggcc cccgtgtccc
840
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960
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1099

<210> 5506
<211> 280
<212> PRT
<213> Homo sapiens

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<400> 5506

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 35 40 45
 Arg Gln Leu Leu Leu Asn Cys Arg Leu Val Cys Ser Leu Trp Arg Asp
 50 55 60
 Leu Ile Asp Leu Val Thr Leu Trp Lys Arg Lys Cys Leu Arg Glu Gly
 65 70 75 80
 Phe Ile Thr Glu Asp Trp Asp Gln Pro Val Ala Asp Trp Lys Ile Phe
 85 90 95
 Tyr Phe Leu Arg Ser Leu His Arg Asn Leu Leu His Asn Pro Cys Ala
 100 105 110
 Glu Glu Gly Phe Glu Phe Trp Ser Leu Asp Val Asn Gly Gly Asp Glu
 115 120 125
 Trp Lys Val Glu Asp Leu Ser Arg Asp Gln Arg Lys Glu Phe Pro Asn
 130 135 140
 Asp Gln Val Lys Lys Tyr Phe Val Thr Ser Tyr Trp Thr Cys Leu Lys
 145 150 155 160
 Ser Gln Val Val Asp Leu Lys Ala Glu Gly Tyr Trp Glu Glu Leu Leu
 165 170 175
 Asp Thr Phe Arg Pro Asp Ile Val Val Lys Asp Trp Phe Ala Ala Arg
 180 185 190
 Ala Asp Cys Gly Cys Thr Tyr Gln Leu Lys Val Gln Leu Leu Ser Ala
 195 200 205
 Asp Tyr Phe Val Leu Ala Ser Phe Glu Pro Asp Pro Ala Thr Ile Gln
 210 215 220
 Gln Lys Ser Asp Ala Lys Trp Arg Glu Val Ser His Thr Phe Ser Asn
 225 230 235 240
 Tyr Pro Pro Gly Val Arg Tyr Ile Trp Phe Gln His Gly Gly Val Asp
 245 250 255
 Thr His Tyr Trp Ala Gly Trp Tyr Gly Pro Arg Val Thr Asn Ser Ser
 260 265 270
 Ile Thr Ile Gly Pro Pro Leu Pro
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<210> 5507

<211> 1658

<212> DNA

<213> Homo sapiens

<400> 5507

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 aagcaatttc tcaccttga caaacaggtc cttcgattct atgcaatctg ggatgataca
 180
 gacagcatgt atggtgaatg tcggacctac atcattcatt actatcttat ggatgatacg
 240
 gtggaaattc gagaggtcca cgaacggaat gatgggagag atcctttccc atcctctaag
 300

aaccgccagc gtgtgcccaa agttttgggtg gaaaatgcaa agaacttccc tcagtgtgtg
360
ctagaaatct ctgaccaaga agtgttgga tggtatactg ctaagactt cattgttggg
420
aagtcactca ctatccttgg gagaactttc ttcatttatg attgtgatcc atttactcga
480
cggtattaca aagagaagtt tggaaatcact gatttaccac gtattgatgt gagcaagcgg
540
gaaccacctc cagtaaaaca ggagttgcct ccttataacg gttttggact agtggaagat
600
tctgtctcaga attgttttgc tctcattcca aaagctccaa aaaaagacgt tattaaaatg
660
ctgggtaatg ataacaaggt gcttcgttat ttggctgtac tggaatcccc catcccagaa
720
gacaaagacc gcagatttgt cttctcttac tttctagcta ccgacatgat cagtatcttt
780
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840
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1020
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1080
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1140
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1560
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1658

<210> 5508

<211> 448

<212> PRT

<213> Homo sapiens

<400> 5508

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	20	25	30	
Thr Pro Ser Asp Phe Asp Gln Leu Lys Gln Phe Leu Thr Phe Asp Lys				
	35	40	45	
Gln Val Leu Arg Phe Tyr Ala Ile Trp Asp Asp Thr Asp Ser Met Tyr				
	50	55	60	
Gly Glu Cys Arg Thr Tyr Ile Ile His Tyr Tyr Leu Met Asp Asp Thr				
	65	70	75	
Val Glu Ile Arg Glu Val His Glu Arg Asn Asp Gly Arg Asp Pro Phe				
	85	90	95	
Pro Leu Leu Met Asn Arg Gln Arg Val Pro Lys Val Leu Val Glu Asn				
	100	105	110	
Ala Lys Asn Phe Pro Gln Cys Val Leu Glu Ile Ser Asp Gln Glu Val				
	115	120	125	
Leu Glu Trp Tyr Thr Ala Lys Asp Phe Ile Val Gly Lys Ser Leu Thr				
	130	135	140	
Ile Leu Gly Arg Thr Phe Phe Ile Tyr Asp Cys Asp Pro Phe Thr Arg				
	145	150	155	
Arg Tyr Tyr Lys Glu Lys Phe Gly Ile Thr Asp Leu Pro Arg Ile Asp				
	165	170	175	
Val Ser Lys Arg Glu Pro Pro Pro Val Lys Gln Glu Leu Pro Pro Tyr				
	180	185	190	
Asn Gly Phe Gly Leu Val Glu Asp Ser Ala Gln Asn Cys Phe Ala Leu				
	195	200	205	
Ile Pro Lys Ala Pro Lys Lys Asp Val Ile Lys Met Leu Val Asn Asp				
	210	215	220	
Asn Lys Val Leu Arg Tyr Leu Ala Val Leu Glu Ser Pro Ile Pro Glu				
	225	230	235	
Asp Lys Asp Arg Arg Phe Val Phe Ser Tyr Phe Leu Ala Thr Asp Met				
	245	250	255	
Ile Ser Ile Phe Glu Pro Pro Val Arg Asn Ser Gly Ile Ile Gly Gly				
	260	265	270	
Lys Tyr Leu Gly Arg Thr Lys Val Val Lys Pro Tyr Ser Thr Val Asp				
	275	280	285	
Asn Pro Val Tyr Tyr Gly Pro Ser Asp Phe Phe Ile Gly Ala Val Ile				
	290	295	300	
Glu Val Phe Gly His Arg Phe Ile Ile Leu Asp Thr Asp Glu Tyr Val				
	305	310	315	
Leu Lys Tyr Met Glu Ser Asn Ala Ala Gln Tyr Ser Pro Glu Ala Leu				
	325	330	335	
Ala Ser Ile Gln Asn His Val Arg Lys Arg Glu Ala Pro Ala Pro Glu				
	340	345	350	
Ala Glu Ser Lys Gln Thr Glu Lys Asp Pro Gly Val Gln Glu Leu Glu				
	355	360	365	
Ala Leu Ile Asp Thr Ile Gln Lys Gln Leu Lys Asp His Ser Cys Lys				
	370	375	380	
Asp Asn Ile Arg Glu Ala Phe Gln Ile Tyr Asp Lys Glu Ala Ser Gly				
	385	390	395	
Tyr Val Asp Arg Asp Met Phe Phe Lys Ile Cys Glu Ser Leu Asn Val				
	405	410	415	
Pro Val Asp Asp Ser Leu Val Lys Glu Leu Ile Arg Met Cys Ser His				
	420	425	430	
Gly Glu Gly Lys Ile Asn Tyr Tyr Asn Phe Val Arg Ala Phe Ser Asn				

435 440 445

<210> 5509
 <211> 818
 <212> DNA
 <213> Homo sapiens

<400> 5509
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 240
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 480
 ggacgcaaac cctgtgaata tcaggaatgt agacagaagg catatacatg taagccatgt
 540
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 720
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 818

<210> 5510
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 5510
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 Ala Phe Ser Gln Ile Pro Gly His Asn Leu Asn Lys Lys Thr Pro Pro
 20 25 30
 Gly Val Lys Pro Pro Glu Ser His Val Cys Gly Glu Val Gly Val Gly
 35 40 45
 Tyr Pro Ser Thr Glu Arg His Ile Arg Asp Arg Leu Gly Arg Lys Pro
 50 55 60
 Cys Glu Tyr Gln Glu Cys Arg Gln Lys Ala Tyr Thr Cys Lys Pro Cys
 65 70 75 80
 Gly Asn Ala Phe Arg Phe His His Ser Phe His Ile His Glu Arg Pro

85 90 95
 His Ser Gly Glu Asn Leu Tyr Glu Cys
 100 105

<210> 5511

<211> 379

<212> DNA

<213> Homo sapiens

<400> 5511

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 120
 ctctgctgag ttgctgagag tctgtgttcc tctctccact tataggatgg gtccatcatc
 180
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 240
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 379

<210> 5512

<211> 101

<212> PRT

<213> Homo sapiens

<400> 5512

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 Ile Glu Glu Phe Ser Ile Ile Pro Glu Ala Pro Met Arg Ser Ser Gln
 20 25 30
 Val Ser Ala Leu Gly Leu Glu Ala Gln Glu Asp Glu Asp Pro Ser Tyr
 35 40 45
 Lys Trp Arg Glu Glu His Arg Leu Ser Ala Thr Gln Gln Ser Glu Leu
 50 55 60
 Arg Asp Val Cys Asp Tyr Ala Ile Glu Thr Met Pro Ser Phe Pro Lys
 65 70 75 80
 Glu Gly Ser Ala Asp Val Glu Pro Asn Gln Glu Ser Leu Val Ala Glu
 85 90 95
 Ala Cys Asp Thr Pro
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<210> 5513

<211> 837

<212> DNA

<213> Homo sapiens

<400> 5513

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120
agactcgggg agccattgac catcgtctct gaggatggag actggtggag ggtgctgtct
180
gaagtctcag gcagagagta taacatcccc agcgtccacg tggccaaagt ctccatggg
240
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360
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480
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720
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837

<210> 5514

<211> 248

<212> PRT

<213> Homo sapiens

<400> 5514

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			20					25				30			
Gly	Gly	Pro	Ala	Glu	Leu	Ser	Leu	Arg	Leu	Gly	Glu	Pro	Leu	Thr	Ile
			35				40				45				
Val	Ser	Glu	Asp	Gly	Asp	Trp	Trp	Thr	Val	Leu	Ser	Glu	Val	Ser	Gly
			50			55					60				
Arg	Glu	Tyr	Asn	Ile	Pro	Ser	Val	His	Val	Ala	Lys	Val	Ser	His	Gly
			65			70				75				80	
Trp	Leu	Tyr	Glu	Gly	Leu	Ser	Arg	Glu	Lys	Ala	Glu	Asp	Leu	Leu	Leu
			85						90					95	
Leu	Pro	Gly	Asn	Pro	Gly	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Gln	Thr
			100					105						110	
Arg	Arg	Gly	Ser	Tyr	Ser	Leu	Ser	Val	Arg	Leu	Ser	Arg	Pro	Ala	Ser
			115				120					125			
Trp	Asp	Arg	Ile	Arg	His	Tyr	Arg	Ile	His	Cys	Leu	Asp	Asn	Gly	Trp
			130			135						140			
Leu	Tyr	Ile	Ser	Pro	Arg	Leu	Thr	Phe	Pro	Ser	Leu	Gln	Ala	Leu	Val
			145			150				155				160	
Asp	His	Tyr	Ser	Glu	Leu	Ala	Asp	Asp	Ile	Cys	Cys	Leu	Leu	Lys	Glu

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                165                170                175
Pro Cys Val Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro
      180      185      190
Leu Pro Val Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp
      195      200      205
Ser Ser Leu Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu
      210      215      220
Ser Glu Gly Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp
      225      230      235      240
Glu Ala Val Ser Leu Asp Asp Ala
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<210> 5515

<211> 420

<212> DNA

<213> Homo sapiens

<400> 5515

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120
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180
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240
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300
ctttgtcacc agcacctgct tcatagtctc tctggagtcg caggaacggg tcatatagat
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<210> 5516

<211> 120

<212> PRT

<213> Homo sapiens

<400> 5516

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      20      25      30
Arg Gln Lys Lys Leu Glu Met Glu Lys Leu Gln Leu Gln Ala Leu Glu
      35      40      45
Gln Glu His Lys Lys Leu Ala Ala Arg Leu Glu Glu Glu Arg Gly Lys
      50      55      60
Asn Lys Gln Val Val Leu Met Leu Val Lys Glu Cys Lys Gln Leu Ser
      65      70      75      80
Ser Lys Val Ile Glu Glu Ala Gln Lys Leu Glu Asp Val Met Ala Lys
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Val Pro Gly Thr Gly His Ile Asp

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 Gly Asp Met Val Ile Val Pro Thr Cys Cys Ser Val Ile Cys Arg Ala
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 Ser Asp Trp Phe Lys

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 Gly Asn Ala Arg Arg Asn Met Val Ser Ser Glu Ala His Gly Cys Phe
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 Trp Val Met Leu Glu Ala Gly Ala Glu Thr Asp Val Val Asn Ser Val
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<211> 6190

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 5524

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 Ser Glu Glu Phe Lys His Val Gly Leu Thr Ala Ala Val Leu Ser Ala
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 His Thr Gln Lys Glu Glu Gln Asn Tyr Val Asp Lys Phe Arg Glu Lys
 675 680 685
 Ile Leu Ser Ser Pro Tyr Ser Ser Tyr Leu Gln Glu Ser Arg Ser
 690 695 700
 Lys Ala Lys Tyr Ser Tyr Phe Gln Gly Asp Ser Thr Ser Lys Gln Thr
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 Arg Ser Ala Gly Cys Arg Lys Gly Lys His Lys Arg Lys Lys Leu Pro
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 Glu Pro Pro Asp Ser Ser Ser Ser Asn Thr Gly Ser Gly Pro Arg Arg
 740 745 750
 Gly Ala His Gln Asn Ala Gln Pro Cys Cys Pro Ser Ala Ala Ser Ser
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 Pro His Thr Ser Ser Pro Thr Phe Pro Pro Ala Ala Met Val Pro Ser
 770 775 780
 Gln Ala Pro Tyr Leu Val Pro Ala Phe Pro Leu Pro Ala Ala Thr Ser
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 Pro Gly Arg Glu Tyr Ala Ala Pro Gly Thr Ala Pro Glu Gly Leu His
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 Gly Pro Pro Leu Ser Glu Gly Leu Gln Pro Tyr Pro Ala Phe Pro Phe
 820 825 830
 Pro Tyr Leu Asp Thr Phe Met Thr Val Phe Leu Pro Asp Pro Pro Val
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 Cys Pro Leu Leu Ser Pro Ser Phe Leu Pro Cys Pro Phe Leu Gly Ala
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 Lys Trp Glu Ala Gln Ser Glu Gly His Pro Phe Ile Thr Ser Arg Ser
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Tyr Gln Cys Val Thr Gly Asn Asn Gly Ser Glu Ser Ser Pro Ala Thr
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 980 985 990
 Ser His Pro Thr Ala Ser Ala Leu Ser Thr Gly Ser Pro Pro Met Lys
 995 1000 1005
 Asn Pro Ser His Pro Thr Ala Ser Thr Leu Ser Met Gly Leu Pro Pro
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 Val Leu Lys Glu Asp Leu Glu Lys Leu Glu Ser Met Arg Gln Gln Gln
 1125 1130 1135
 Pro Gln Phe Ser His Gly Gln Lys Glu Glu Leu Ala Lys Val Tyr Asn
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 Trp Ile Gln Ser Gln Thr Val Thr Gln Glu Ile Asp Ile Gln Ala Cys
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<211> 761

<212> DNA

<213> Homo sapiens

<400> 5525

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<211> 102

<212> PRT

<213> Homo sapiens

<400> 5526

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 35 40 45
 Glu Ile Thr Gln Leu Glu Ser Trp Glu Glu Pro Phe Met Pro Ala Trp
 50 55 60
 Glu Val Val Thr Ser Ala Ile Pro Arg Glu Thr Leu Arg Met Ala Phe
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<210> 5527

<211> 728

<212> DNA

<213> Homo sapiens

<400> 5527

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<211> 176

<212> PRT

<213> Homo sapiens

<400> 5528

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 Val Thr Gly Leu Lys Leu Ser Gln Asp Leu Asp Asp Leu Ala Ile Leu
 35 40 45
 Tyr Leu Ala Thr Val Gln Ala Ile Ala Leu Gly Thr Arg Phe Ile Ile
 50 55 60
 Glu Ala Met Glu Ala Ala Gly His Ser Ile Ser Thr Leu Phe Leu Cys
 65 70 75 80
 Gly Gly Leu Ser Lys Asn Pro Leu Phe Val Gln Met His Ala Asp Ile
 85 90 95
 Thr Gly Met Pro Val Val Leu Ser Gln Glu Val Glu Ser Val Leu Val
 100 105 110
 Gly Ala Ala Val Leu Gly Ala Cys Ala Ser Gly Asp Phe Ala Ser Val
 115 120 125
 Gln Glu Ala Met Ala Lys Met Ser Lys Val Gly Lys Val Val Phe Pro
 130 135 140
 Arg Leu Gln Asp Lys Lys Tyr Tyr Asp Lys Lys Tyr Gln Val Phe Leu
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 Lys Leu Val Glu His Gln Lys Glu Tyr Leu Ala Ile Met Asn Asp Asp
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<210> 5529

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 5529

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<211> 603

<212> PRT

<213> Homo sapiens

<400> 5530

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 35 40 45
 Arg Leu Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp
 50 55 60
 Glu Gln Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro
 65 70 75 80
 Lys Arg Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln
 85 90 95
 Arg Thr Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe
 100 105 110
 Leu Lys Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr
 115 120 125
 Glu Ser Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser
 130 135 140
 Ile Gly Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu

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Ser	Asn	Lys	Gln	Leu	Phe	Glu	Leu	Leu	Cys	Tyr	Ala	Glu	Ser	Ile	Asp					
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Asp	Gln	Leu	Asn	Thr	Leu	Leu	Lys	Glu	Phe	Gln	Leu	Thr	Glu	Glu	Asn					
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Thr	Lys	Leu	Arg	Tyr	Leu	Thr	Cys	Ser	Leu	Ile	Glu	Asp	Met	Ala	Ala					
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Ala	Tyr	Phe	Pro	Asp	Cys	Ile	Val	Arg	Pro	Phe	Gly	Ser	Ser	Val	Asn					
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Thr	Phe	Gly	Lys	Leu	Gly	Cys	Asp	Leu	Asp	Met	Phe	Leu	Asp	Leu	Asp					
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Glu	Thr	Arg	Asn	Leu	Ser	Ala	His	Lys	Ile	Ser	Gly	Asn	Phe	Leu	Met					
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Glu	Phe	Gln	Val	Lys	Asn	Val	Pro	Ser	Glu	Arg	Ile	Ala	Thr	Gln	Lys					
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Ile	Leu	Ser	Val	Leu	Gly	Glu	Cys	Leu	Asp	His	Phe	Gly	Pro	Gly	Cys					
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Val	Gly	Val	Gln	Lys	Ile	Leu	Asn	Ala	Arg	Cys	Pro	Leu	Val	Arg	Phe					
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Ser	His	Gln	Ala	Ser	Gly	Phe	Gln	Cys	Asp	Leu	Thr	Thr	Asn	Asn	Arg					
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Ser	Arg	Val	Arg	Ala	Leu	Val	Phe	Ser	Val	Arg	Cys	Trp	Ala	Arg	Ala					
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His	Ser	Leu	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Trp	Ile	Thr	Asn	Phe	Ser					
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Cys	Val	Ile	Glu	Gly	Asn	Asn	Cys	Thr	Phe	Val	Arg	Asp	Leu	Ser	Arg					
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Ile	Lys	Pro	Ser	Gln	Asn	Thr	Glu	Thr	Leu	Glu	Leu	Leu	Lys	Glu						
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Phe	Phe	Glu	Tyr	Phe	Gly	Asn	Phe	Ala	Phe	Asp	Lys	Asn	Ser	Ile	Asn					
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Ile	Arg	Gln	Gly	Arg	Glu	Gln	Asn	Lys	Pro	Asp	Ser	Ser	Pro	Leu	Tyr					
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Gln	Ser	Gln	Leu	Gln	Lys	Phe	Val	Asp	Leu	Ala	Arg	Glu	Ser	Ala	Trp					
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Ile	Leu	Gln	Gln	Glu	Asp	Thr	Asp	Arg	Pro	Ser	Ile	Ser	Ser	Asn	Arg					
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Pro	Trp	Gly	Leu	Val	Ser	Leu	Leu	Leu	Pro	Ser	Ala	Pro	Asn	Arg						

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<210> 5531
 <211> 3056
 <212> DNA
 <213> Homo sapiens

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<210> 5532

<211> 593

<212> PRT

<213> Homo sapiens

<400> 5532

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 35 40 45
 Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Glu Gly
 50 55 60
 Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg
 65 70 75 80
 Asp Val Tyr Glu Asp Glu Leu Val Pro Val Phe Glu Ala Val Gly Arg
 85 90 95
 Ile Tyr Glu Leu Arg Leu Met Met Asp Phe Asp Gly Lys Asn Arg Gly
 100 105 110
 Tyr Ala Phe Val Met Tyr Cys His Lys His Glu Ala Lys Arg Ala Val
 115 120 125
 Arg Glu Leu Asn Asn Tyr Glu Ile Arg Pro Gly Arg Leu Leu Gly Val
 130 135 140
 Cys Cys Ser Val Asp Asn Cys Arg Leu Phe Ile Gly Gly Ile Pro Lys
 145 150 155 160
 Met Lys Lys Arg Glu Glu Ile Leu Glu Glu Ile Ala Lys Val Thr Glu
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 Gly Val Leu Asp Val Ile Val Tyr Ala Ser Ala Ala Asp Lys Met Lys
 180 185 190
 Asn Arg Gly Phe Ala Phe Val Glu Tyr Glu Ser His Arg Ala Ala Ala
 195 200 205
 Met Ala Arg Arg Lys Leu Met Pro Gly Arg Ile Gln Leu Trp Gly His
 210 215 220
 Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp
 225 230 235 240
 Val Met Glu Thr Val Lys Ile Leu Tyr Val Arg Asn Leu Met Ile Glu
 245 250 255
 Thr Thr Glu Asp Thr Ile Lys Lys Ser Phe Gly Gln Phe Asn Pro Gly
 260 265 270
 Cys Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe
 275 280 285
 Thr Ser Arg Glu Asp Ala Val His Ala Met Asn Asn Leu Asn Gly Thr
 290 295 300
 Glu Leu Glu Gly Ser Cys Leu Glu Val Thr Leu Ala Lys Pro Val Asp
 305 310 315 320
 Lys Glu Gln Tyr Ser Arg Tyr Gln Lys Ala Ala Arg Gly Gly Gly Ala
 325 330 335
 Ala Glu Ala Ala Gln Gln Pro Ser Tyr Val Tyr Ser Cys Asp Pro Tyr


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          340          345          350
Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn
          355          360          365
Arg Asp Tyr Phe Val Lys Ala Gly Ser Ile Arg Gly Arg Gly Gly
          370          375          380
Ala Ala Gly Asn Arg Ala Pro Gly Pro Arg Gly Ser Tyr Leu Gly Gly
          385          390          395          400
Tyr Ser Ala Gly Arg Gly Ile Tyr Ser Arg Tyr His Glu Gly Lys Gly
          405          410          415
Lys Gln Gln Glu Lys Gly Tyr Glu Leu Val Pro Asn Leu Glu Ile Pro
          420          425          430
Thr Val Asn Pro Val Ala Ile Lys Pro Gly Thr Val Ala Ile Pro Ala
          435          440          445
Ile Gly Ala Gln Tyr Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met
          450          455          460
Ile Glu Asp Gly Lys Ile His Thr Val Glu His Met Ile Ser Pro Ile
          465          470          475          480
Ala Val Gln Pro Asp Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala
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Ala Ala Ala Ala Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro
          500          505          510
Phe Gln Gly Arg Pro Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val
          515          520          525
Gln Arg Ile Pro Thr Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe
          530          535          540
Ala Ala Pro Ala Thr Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala
          545          550          555          560
Ala Ala Ala Ala Val Tyr Gly Gly Tyr Ala Gly Tyr Ile Pro Gln Ala
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<210> 5533

<211> 505

<212> DNA

<213> Homo sapiens

<400> 5533

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300
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420

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<210> 5534
 <211> 168
 <212> PRT
 <213> Homo sapiens

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 Tyr Arg Arg Gly Leu Ser Lys Tyr Glu Ser Ile Asp Glu Asp Glu Leu
 35 40 45
 Leu Ala Ser Leu Ser Ala Glu Leu Lys Glu Leu Glu Arg Glu Leu
 50 55 60
 Glu Asp Ile Glu Pro Asp Arg Asn Leu Pro Val Gly Leu Arg Gln Lys
 65 70 75 80
 Ser Leu Thr Glu Lys Thr Pro Thr Gly Thr Phe Ser Arg Glu Ala Leu
 85 90 95
 Met Ala Tyr Trp Glu Lys Glu Ser Gln Lys Leu Leu Glu Lys Glu Arg
 100 105 110
 Leu Gly Glu Cys Gly Lys Val Ala Glu Asp Lys Glu Glu Ser Glu Glu
 115 120 125
 Glu Leu Ile Phe Thr Glu Ser Asn Ser Glu Val Ser Glu Glu Val Tyr
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 145 150 155 160
 Ser Asp Glu Glu Glu Arg Thr Ile
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<210> 5535
 <211> 1887
 <212> DNA
 <213> Homo sapiens

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720
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1887

<210> 5536

<211> 306

<212> PRT

<213> Homo sapiens

<400> 5536

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Pro Gly Glu Thr Pro Lys His Gln Pro Gly Ser Pro Arg Gly Ser Gly
35      40      45
Arg Glu Glu Asp Asp Glu Leu Leu Gly Asn Asp Asp Ser Asp Lys Thr
50      55      60
Glu Leu Leu Ala Gly Gln Lys Lys Ser Ser Pro Phe Trp Thr Phe Glu
65      70      75      80
Tyr Tyr Gln Thr Phe Phe Asp Val Asp Thr Tyr Gln Val Phe Asp Arg
85      90      95
Ile Lys Gly Ser Leu Leu Pro Ile Pro Gly Lys Asn Phe Val Arg Leu
100     105     110
Tyr Ile Arg Ser Asn Pro Asp Leu Tyr Gly Pro Phe Trp Ile Cys Ala
115     120     125
Thr Leu Val Phe Ala Ile Ala Ile Ser Gly Asn Leu Ser Asn Phe Leu
130     135     140
Ile His Leu Gly Glu Lys Thr Tyr His Tyr Val Pro Glu Phe Arg Lys
145     150     155     160
Val Ser Ile Ala Ala Thr Ile Ile Tyr Ala Tyr Ala Trp Leu Val Pro
165     170     175
Leu Ala Leu Trp Gly Phe Leu Met Trp Arg Asn Ser Lys Val Met Asn
180     185     190
Ile Val Ser Tyr Ser Phe Leu Glu Ile Val Cys Val Tyr Gly Tyr Ser
195     200     205
Leu Phe Ile Tyr Ile Pro Thr Ala Ile Leu Trp Ile Ile Pro Gln Lys
210     215     220
Ala Val Arg Trp Ile Leu Val Met Ile Ala Leu Gly Ile Ser Gly Ser
225     230     235     240
Leu Leu Ala Met Thr Phe Trp Pro Ala Val Arg Glu Asp Asn Arg Arg
245     250     255
Val Ala Leu Ala Thr Ile Val Thr Ile Val Leu Leu His Met Leu Leu
260     265     270
Ser Val Gly Cys Leu Ala Tyr Phe Phe Asp Ala Pro Glu Met Asp His
275     280     285
Leu Pro Thr Thr Thr Ala Thr Pro Asn Gln Thr Val Ala Ala Ala Lys
290     295     300
Ser Ser
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<210> 5537

<211> 2881

<212> DNA

<213> Homo sapiens

<400> 5537

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120

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 2881

<210> 5538

<211> 352

<212> PRT

<213> Homo sapiens

<400> 5538

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 20 25 30
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 35 40 45
 Leu Gln Gln Leu Gln Ala Val Val Pro Gln Ile Asp Met Glu Gly Asp

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      50              55              60
Arg Asn Ile Trp Ile Val Lys Pro Gly Ala Lys Ser Arg Gly Arg Gly
65              70              75              80
Ile Met Cys Met Asp His Leu Glu Glu Met Leu Lys Leu Val Asn Gly
      85              90              95
Asn Pro Val Val Met Lys Asp Gly Lys Trp Val Val Gln Lys Tyr Ile
      100             105             110
Glu Arg Pro Leu Leu Ile Phe Gly Thr Lys Phe Asp Leu Arg Gln Trp
      115             120             125
Phe Leu Val Thr Asp Trp Asn Pro Leu Thr Val Trp Phe Tyr Arg Asp
      130             135             140
Ser Tyr Ile Arg Phe Ser Thr Gln Pro Phe Ser Leu Lys Asn Leu Asp
      145             150             155
Asn Ser Val His Leu Cys Asn Asn Ser Ile Gln Lys His Leu Glu Asn
      165             170             175
Ser Cys His Arg His Pro Leu Leu Pro Pro Asp Asn Met Trp Ser Ser
      180             185             190
Gln Arg Phe Gln Ala His Leu Gln Glu Met Gly Ala Pro Asn Ala Trp
      195             200             205
Ser Thr Ile Ile Val Pro Gly Met Lys Asp Ala Val Ile His Ala Leu
      210             215             220
Gln Thr Ser Gln Asp Thr Val Gln Cys Arg Lys Ala Ser Phe Glu Leu
      225             230             235
Tyr Gly Ala Asp Phe Val Phe Gly Glu Asp Phe Gln Pro Trp Leu Ile
      240             245             250
Glu Ile Asn Ala Ser Pro Thr Met Ala Pro Ser Thr Ala Val Thr Ala
      255             260             265
Arg Leu Cys Ala Gly Val Gln Ala Asp Thr Leu Arg Val Val Ile Asp
      270             275             280
Arg Arg Leu Asp Arg Asn Cys Asp Thr Gly Ala Phe Glu Leu Ile Tyr
      285             290             295
Lys Gln Pro Val Thr Thr Ser Pro Ala Ser Thr Pro Arg Pro Ser Cys
      300             305             310
Leu Leu Pro Met Tyr Ser Asp Thr Arg Ala Arg Ser Ser Asp Asp Ser
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<210> 5539

<211> 1887

<212> DNA

<213> Homo sapiens

<400> 5539

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300

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1887

<210> 5540
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 5540
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 35 40 45
 Ala Pro Trp Cys Ser Val Ser Ser Gly Pro Ser Arg Tyr Val Leu Gly
 50 55 60
 Met Gln Glu Leu Phe Arg Gly His Ser Lys Thr Arg Glu Phe Leu Ala
 65 70 75 80
 His Ser Ala Lys Val His Ser Val Ala Trp Ser Cys Asp Gly Arg Arg
 85 90 95
 Leu Ala Ser Gly Ser Phe Asp Lys Thr Ala Ser Val Phe Leu Leu Glu
 100 105 110
 Arg Thr Gly Trp Ser Lys Lys Thr Ile Ile Gly Asp Met Gly Ile Xaa
 115 120 125
 Val Asp Gln Leu Cys Trp His Pro Ser Asn Pro Asp Leu Phe Val Thr
 130 135 140
 Ala Ser Gly Asp Lys Thr Ile Arg Ile Trp Asp Val Arg Thr Thr Lys
 145 150 155 160
 Cys Ile Ala Thr Val Asn Thr Lys Gly Glu Asn Ile Asn Ile Cys Trp
 165 170 175
 Ser Pro Asp Gly Gln Thr Ile Ala Val Gly Asn Lys Asp Asp Val Val
 180 185 190
 Thr Phe Ile Asp Ala Lys Thr His Arg Ser Lys Ala Glu Gln Phe
 195 200 205
 Lys Phe Glu Val Asn Glu Ile Ser Trp Asn Asn Asp Asn Asn Met Phe
 210 215 220
 Phe Leu Thr Asn Gly Asn Gly Cys Ile Asn Ile Leu Ser Tyr Pro Glu
 225 230 235 240
 Leu Lys Pro Val Gln Ser Ile Asn Ala His Pro Ser Asn Cys Ile Cys
 245 250 255
 Ile Lys Phe Asp Pro Met Gly Lys Tyr Phe Ala Thr Gly Ser Ala Asp
 260 265 270
 Ala Leu Val Ser Leu Trp Asp Val Asp Glu Leu Val Cys Val Arg Cys
 275 280 285
 Phe Ser Arg Leu Asp Trp Pro Val Arg Thr Leu Ser Phe Ser His Asp
 290 295 300
 Gly Lys Met Leu Ala Ser Ala Ser Glu Asp His Phe Ile Asp Ile Ala
 305 310 315 320
 Glu Val Glu Thr Gly Asp Lys Leu Trp Glu Val Gln Cys Glu Ser Pro
 325 330 335
 Thr Phe Thr Val Ala Trp His Pro Lys Arg Pro Leu Leu Ala Phe Ala
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 Val Lys Leu Phe Gly Leu Pro Asn Asp Ser

370

<210> 5541
 <211> 1854
 <212> DNA
 <213> Homo sapiens

375

<400> 5541
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<210> 5548

<211> 167

<212> PRT

<213> Homo sapiens

<400> 5548

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 20 25 30
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 35 40 45
 Phe Val Ile Pro Lys Lys Asn Val Pro Thr Ser Lys Arg Glu Thr Tyr
 50 55 60
 Thr Glu Asp Phe Ile Lys Lys Gln Ile Glu Glu Phe Asn Ile Gly Lys
 65 70 75 80
 Arg His Leu Ala Asn Met Met Gly Glu Asp Pro Glu Thr Phe Thr Gln
 85 90 95
 Glu Asp Ile Asp Arg Ala Ile Ala Tyr Leu Phe Pro Ser Gly Leu Phe
 100 105 110
 Glu Lys Arg Ala Arg Pro Val Met Lys His Pro Glu Gln Ile Phe Pro
 115 120 125
 Arg Gln Arg Ala Ile Gln Trp Gly Glu Asp Gly Arg Pro Phe His Tyr

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<210> 5549
 <211> 1865
 <212> DNA
 <213> Homo sapiens

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 1260

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 1380
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<210> 5550

<211> 242

<212> PRT

<213> Homo sapiens

<400> 5550

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			20					25					30		
Arg	Trp	Ser	Arg	Tyr	Ser	Pro	Glu	Phe	Lys	Asp	Pro	Leu	Ile	Asp	Lys
		35					40				45				
Glu	Tyr	Tyr	Arg	Lys	Pro	Val	Glu	Glu	Leu	Thr	Glu	Glu	Glu	Lys	Tyr
	50					55					60				
Val	Arg	Glu	Leu	Lys	Lys	Thr	Gln	Leu	Ile	Lys	Ala	Ala	Pro	Ala	Gly
65					70					75					
Lys	Thr	Ser	Ser	Val	Phe	Glu	Asp	Pro	Val	Ile	Ser	Lys	Phe	Thr	Asn
			85						90				95		
Met	Met	Met	Ile	Gly	Gly	Asn	Lys	Val	Leu	Ala	Arg	Ser	Leu	Met	Ile
			100					105					110		
Gln	Thr	Leu	Glu	Ala	Val	Lys	Arg	Lys	Gln	Phe	Glu	Lys	Tyr	His	Ala
		115					120					125			
Ala	Ser	Ala	Glu	Glu	Gln	Ala	Thr	Ile	Glu	Arg	Asn	Pro	Tyr	Thr	Ile
		130				135					140				
Phe	His	Gln	Ala	Leu	Lys	Asn	Cys	Glu	Pro	Met	Ile	Gly	Leu	Val	Pro
145					150					155					
Ile	Leu	Lys	Gly	Gly	Arg	Phe	Tyr	Gln	Val	Pro	Val	Pro	Leu	Pro	Asp
			165					170					175		
Arg	Arg	Arg	Arg	Phe	Leu	Ala	Met	Lys	Trp	Met	Ile	Thr	Glu	Cys	Arg
			180					185					190		
Asp	Lys	Lys	His	Gln	Arg	Thr	Leu	Met	Pro	Glu	Lys	Leu	Ser	His	Lys

	195		200		205										
Leu	Leu	Glu	Ala	Phe	His	Asn	Gln	Gly	Pro	Val	Ile	Lys	Arg	Lys	His
	210					215						220			
Asp	Leu	His	Lys	Met	Ala	Glu	Ala	Asn	Arg	Ala	Leu	Ala	His	Tyr	Arg
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<210> 5551

<211> 1689

<212> DNA

<213> Homo sapiens

<400> 5551

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360
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<210> 5552

<211> 104

<212> PRT

<213> Homo sapiens

<400> 5552

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		20						25					30		
Tyr	Leu	Leu	Asp	Pro	Tyr	Val	Asn	Leu	Ala	Pro	Gly	Cys	Arg	Ser	Leu
		35					40					45			
Phe	Ser	Val	Ile	Val	Arg	Val	Val	Gly	Asp	Leu	Met	Leu	Arg	Ile	Gln
	50				55					60					
Arg	Ile	Gln	Asp	Phe	Thr	Pro	Lys	Leu	Leu	Leu	Val	Arg	Lys	Arg	Leu
65					70				75					80	
Leu	Gly	Leu	Glu	Pro	Glu	Gly	Pro	Ile	Ser	Asp	Leu	Glu	Pro	Val	Glu
			85					90						95	
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<210> 5553

<211> 274

<212> DNA

<213> Homo sapiens

<400> 5553

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274

<210> 5554
<211> 90
<212> PRT
<213> Homo sapiens

<400> 5554
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35 40 45
Gly Pro Ala Thr Ala Pro Ala Val Val Leu Ser His Tyr Arg Gly Cys
50 55 60
Tyr Phe Pro Ser Gln Cys Pro Trp Gln Pro Trp Lys Pro Met Lys Gln
65 70 75 80
Ala Leu Thr Gln Glu Ser Leu Cys Ile Phe
85 90

<210> 5555
<211> 414
<212> DNA
<213> Homo sapiens

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414

<210> 5556
<211> 115
<212> PRT
<213> Homo sapiens

<400> 5556
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Gly Gln Arg Ser Asp Val Gly Phe Arg Lys Gln Gly Pro Gly Gly Asp
20 25 30
Glu Ser Gln Gly Cys Asp Ser Arg Arg Asp Ser Cys Glu Gly Pro Gly

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      35              40              45
Gln Ala Lys Leu Glu Asp Ser Pro Asp Leu Arg Gly Ser Thr Arg Ser
  50              55              60
Arg Cys Leu Leu Asp Leu Ser His Ser Ala His Pro Asn Leu Asn Pro
  65              70              75              80
Ala Pro Gly Pro Thr Pro Val Pro Trp Leu Glu Thr Gly Ala Ser Ala
      85              90              95
Gln Leu Phe Pro Phe Ser His Ser Leu Ser Ala Ala Cys Arg Val His
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Ser Ala Ser
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<210> 5557

<211> 1970

<212> DNA

<213> Homo sapiens

<400> 5557

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  1080

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<210> 5558

<211> 360

<212> PRT

<213> Homo sapiens

<400> 5558

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			20					25					30		
Ser	Val	Pro	Arg	Glu	Pro	Ile	Asp	Arg	Lys	Arg	Leu	Lys	Lys	Asp	Val
		35					40				45				
Glu	Pro	Ser	Cys	Ser	Gly	Ser	Ser	Leu	Gly	Pro	Asp	Lys	Gly	Leu	Ala
		50				55					60				
Gln	Ser	Pro	Pro	Ser	Ser	Ser	Leu	Thr	Ala	Thr	Arg	Gln	Lys	Pro	Ser
65					70					75				80	
Gln	Ser	Pro	Ser	Ala	Pro	Pro	Ala	Asp	Val	Thr	Pro	Lys	Pro	Ala	Thr
			85						90					95	
Glu	Ala	Val	Gln	Ser	Glu	His	Ser	Asp	Ala	Ser	Pro	Met	Ser	Ile	Asn
			100					105					110		
Glu	Val	Ile	Leu	Ser	Ala	Ser	Gly	Ala	Cys	Lys	Leu	Ile	Asp	Ser	Leu
		115					120					125			
His	Ser	Tyr	Cys	Phe	Ser	Ser	Arg	Gln	Asn	Lys	Ser	Gln	Val	Cys	Cys

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Gln Arg Val Ser Arg Ser Asp Ser Gln Val Arg	Lys Leu Gln Glu Lys				
	165	170	175		
Leu Asp Glu Leu Arg Arg Val Ser Val Pro Tyr	Pro Ser Ser Leu Leu				
	180	185	190		
Ser Pro Ser Arg Glu Pro Pro Lys Met Asn Pro Val Val Glu Pro Leu					
	195	200	205		
Ser Trp Met Leu Gly Thr Trp Leu Ser Asp Pro Pro Gly Ala Gly Thr					
	210	215	220		
Tyr Pro Thr Leu Gln Pro Phe Gln Tyr Leu Glu Val His Ile Ser					
225	230	235	240		
His Val Gly Gln Pro Met Leu Asn Phe Ser Phe Asn Ser Phe His Pro					
	245	250	255		
Asp Thr Arg Lys Pro Met His Arg Glu Cys Gly Phe Ile Arg Leu Lys					
	260	265	270		
Pro Asp Thr Asn Lys Val Ala Phe Val Ser Ala Gln Asn Thr Gly Val					
	275	280	285		
Val Glu Val Glu Glu Gly Glu Val Asn Gly Gln Glu Leu Cys Ile Ala					
	290	295	300		
Ser His Ser Ile Ala Arg Ile Ser Phe Ala Lys Glu Pro His Val Glu					
305	310	315	320		
Gln Ile Thr Arg Lys Phe Arg Leu Asn Ser Glu Gly Lys Leu Glu Gln					
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Val Thr Tyr Lys Lys Val Thr Pro					
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<210> 5559

<211> 3866

<212> DNA

<213> Homo sapiens

<400> 5559

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<211> 1165

<212> PRT

<213> Homo sapiens

<400> 5560

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<211> 2089

<212> DNA

<213> Homo sapiens

<400> 5561

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<211> 372

<212> PRT

<213> Homo sapiens

<400> 5562

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<210> 5563

<211> 2878

<212> DNA

<213> Homo sapiens

<400> 5563

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<210> 5564

<211> 683

<212> PRT

<213> Homo sapiens

<400> 5564

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 35 40 45
 Leu Ser Asn Arg Arg Leu Lys His Phe Pro Arg Gly Ala Ala Arg Ser
 50 55 60
 Tyr Asp Leu Ser Asp Ile Thr Gln Ala Asp Leu Ser Arg Asn Arg Phe
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 Pro Glu Val Pro Glu Ala Ala Cys Gln Leu Val Ser Leu Glu Gly Leu
 85 90 95
 Ser Leu Tyr His Asn Cys Leu Arg Cys Leu Asn Pro Ala Leu Gly Asn
 100 105 110
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 Leu Pro Pro Tyr Ile Cys Gln Leu Pro Leu Arg Val Leu Ile Val Ser
 130 135 140
 Asn Asn Lys Leu Gly Ala Leu Pro Pro Asp Ile Gly Thr Leu Gly Ser
 145 150 155 160
 Leu Arg Gln Leu Asp Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Ser
 165 170 175
 Glu Leu Cys Gly Leu Ser Ser Leu Arg Asp Leu Asn Val Arg Arg Asn
 180 185 190
 Gln Leu Ser Thr Leu Pro Glu Glu Leu Gly Asp Leu Pro Leu Val Arg
 195 200 205
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 210 215 220
 Arg Leu Arg His Leu Gln Val Ile Leu Leu Asp Ser Asn Pro Leu Gln
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 Tyr Leu Ser Thr Glu Ala Gly Gln Arg Gly Ser Ala Leu Gly Asp Leu

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 385 390 395 400
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 Ser Thr Gln Ala Met His Asn Gly Ser Pro Lys Ser Ser Ala Ser Gln
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 485 490 495
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 Ser Gln Ser Gly Ser Gly Pro Ser Ser Pro Asp Ser Val Leu Arg Pro
 515 520 525
 Arg Arg Tyr Pro Gln Val Pro Asp Glu Lys Asp Leu Met Thr Gln Leu
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 565 570 575
 Leu Arg Pro Arg Ser Val Pro Phe Ile His Val Pro Ser Pro Ala Val
 580 585 590
 Pro Lys Leu Ser Ala Leu Lys Ala Arg Lys Asn Val Glu Ser Phe Leu
 595 600 605
 Glu Ala Cys Arg Lys Met Gly Val Pro Glu Ala Asp Leu Cys Ser Pro
 610 615 620
 Ser Asp Leu Leu Gln Gly Thr Ala Arg Gly Leu Arg Thr Ala Leu Glu
 625 630 635 640
 Ala Val Lys Arg Val Gly Gly Lys Ala Leu Pro Pro Leu Trp Pro Pro
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 Ser Gly Leu Gly Gly Phe Val Val Phe Tyr Val Val Leu Met Leu Leu
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 <211> 472
 <212> DNA
 <213> Homo sapiens

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<210> 5566
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 5566
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 Leu Asp Leu Gln Gly Ser Ser Asp Pro Pro Ala Ser Ala Ser Arg Ala
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 Ala Gly Ser Thr Gly Ala Tyr His Ala Trp Leu Phe
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<210> 5567
 <211> 968
 <212> DNA
 <213> Homo sapiens

<400> 5567
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<210> 5568

<211> 130

<212> PRT

<213> Homo sapiens

<400> 5568

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 His Arg Ser Ile His Leu Ala Pro Leu Gln Ile Trp Val Leu Cys Lys
 35 40 45
 Ile Leu Pro Trp Asp Thr Glu Gly Lys Ser Asp Thr Ala Leu Leu Ser
 50 55 60
 Ser Ser Gln Thr Leu Arg Tyr Pro Asp Thr Thr Ala Leu Ile Val Ser
 65 70 75 80
 Glu Asn Thr Ala Thr Ser Ala Gly Lys Tyr Gln Arg Cys Phe Thr Arg
 85 90 95
 Tyr Met Tyr Gln Ile Leu Lys Ala Val Pro Lys Tyr His Lys Leu
 100 105 110
 His Gly Leu Lys Gln Gln Lys Phe Ile Pro Ser Gln Ser Trp Arg Pro
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 Asp Val
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<210> 5569

<211> 876

<212> DNA

<213> Homo sapiens

<400> 5569

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<210> 5570

<211> 169

<212> PRT

<213> Homo sapiens

<400> 5570

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20      25      30
Gly Ser Pro Leu Val Val Ile Ser Gln Gly Lys Ile Val Phe Glu Asp
35      40      45
Gly Asn Ile Asn Val Asn Lys Gly Met Gly Arg Phe Ile Pro Arg Lys
50      55      60
Ala Phe Pro Glu His Ser Ser Thr Trp Leu Glu Leu His Asn His Gly
65      70      75      80
Arg Arg His Val Cys Glu Ala Ser Trp Gly Cys Thr Ala Asp Pro Leu
85      90      95
Leu Ser Pro Leu Ala Leu Ser Ala Ala Phe Met Trp Leu Ser Pro Ser

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          100              105              110
Val Leu Gln Ala Phe Ile Ser Phe Arg Ala Ala Pro Ser Leu Cys Pro
          115              120              125
Gly Thr Leu Ala Lys Met Gln Cys Leu Pro Asn Ser His Ile Ser Phe
          130              135              140
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Gln Val Gln Val Pro Val Cys Asp Gly
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<210> 5571

<211> 405

<212> DNA

<213> Homo sapiens

<400> 5571

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<210> 5572

<211> 135

<212> PRT

<213> Homo sapiens

<400> 5572

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Gln Leu Arg Asp Pro Thr Ser Pro Lys Phe Pro Glu Asp Phe Asp Asp
35     40     45
Gly Glu His Ala Lys Gln Lys Ser Val Ile Ser Trp Leu Leu Asn His
50     55     60
Asp Pro Ala Lys Arg Pro Thr Ala Thr Glu Leu Lys Ser Glu Leu
65     70     75     80
Leu Pro Pro Pro Gln Met Glu Glu Ser Glu Leu His Glu Val Leu His
85     90     95
His Thr Leu Thr Asn Val Asp Gly Lys Ala Tyr Arg Thr Met Met Ala
100    105    110
Gln Ile Phe Ser Gln Arg Leu Ala Gly Ala Gly Gly Gly Tyr Arg
115    120    125
Ser Arg Leu Gly Val Pro Arg

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130

135

<210> 5573

<211> 1279

<212> DNA

<213> Homo sapiens

<400> 5573

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<211> 312
 <212> PRT
 <213> Homo sapiens

<400> 5574
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 Tyr Arg Leu Leu Gly Arg Met Phe Arg Arg Asp Glu Asn Arg Lys Val
 50 55 60
 Ala Leu Val Gly Leu Thr Ala Glu Thr Ser His Ala Leu Val Pro Lys
 65 70 75 80
 Glu Ile Pro Gly Lys Gly Gly Ile Trp Arg Val Ile Phe Lys Pro Pro
 85 90 95
 Asp Pro Asp Asn Thr Phe Leu Ser Arg Leu Asn Glu Phe Leu Ala Gly
 100 105 110
 Glu Gly Met Thr Val Gly Glu Leu Ser Arg Ala Leu Gly His Glu Asn
 115 120 125
 Gly Ser Leu Asp Pro Glu Gln Gly Met Ile Pro Glu Met Trp Ala Pro
 130 135 140
 Met Leu Ala Gln Ala Leu Glu Ala Leu Gln Pro Ala Leu Gln Cys Leu
 145 150 155 160
 Lys Tyr Lys Lys Leu Arg Val Phe Ser Gly Arg Glu Ser Pro Glu Pro
 165 170 175
 Gly Glu Glu Glu Phe Gly Arg Trp Met Phe His Thr Thr Gln Met Ile
 180 185 190
 Lys Ala Trp Gln Val Pro Asp Val Glu Lys Arg Arg Leu Leu Glu
 195 200 205
 Ser Leu Arg Gly Pro Ala Leu Asp Val Ile Arg Val Leu Lys Ile Asn
 210 215 220
 Asn Pro Leu Ile Thr Val Asp Glu Cys Leu Gln Ala Leu Glu Glu Val
 225 230 235 240
 Phe Gly Val Thr Asp Asn Pro Arg Glu Leu Gln Val Lys Tyr Leu Thr
 245 250 255
 Thr Tyr Gln Lys Asp Glu Glu Lys Leu Ser Ala Tyr Val Leu Arg Leu
 260 265 270
 Glu Pro Leu Leu Gln Lys Leu Val Gln Arg Gly Ala Ile Glu Arg Asp
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<210> 5575
 <211> 2405
 <212> DNA
 <213> Homo sapiens

<400> 5575
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 2100
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 2160
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 2220
 ggcagaactc tgaacgacaa tacgtctctc tgagcagaga ccccttctgt cttgttatcc
 2280
 acccatatgg acttggaatc aatcttgcca aatatttgga gagattgtgt ggatttaaga
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 cttga
 2405

<210> 5576

<211> 367

<212> PRT

<213> Homo sapiens

<400> 5576

Met	Ala	Asp	Phe	Gly	Ile	Ser	Ala	Gly	Gln	Phe	Val	Ala	Val	Val	Trp
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Asp	Lys	Ser	Ser	Pro	Val	Glu	Ala	Leu	Lys	Gly	Leu	Val	Asp	Lys	Leu
			20					25					30		
Gln	Ala	Leu	Thr	Gly	Asn	Glu	Gly	Arg	Val	Ser	Val	Glu	Asn	Ile	Lys
		35					40					45			
Gln	Leu	Leu	Gln	Cys	Leu	Val	Pro	Gly	Ser	Thr	Thr	Leu	His	Ser	Ala
		50				55					60				
Glu	Ile	Leu	Ala	Glu	Ile	Ala	Arg	Ile	Leu	Arg	Pro	Gly	Gly	Cys	Leu
65					70				75					80	
Phe	Leu	Lys	Glu	Pro	Val	Glu	Thr	Ala	Val	Asp	Asn	Asn	Ser	Lys	Val
				85					90				95		
Lys	Thr	Ala	Ser	Lys	Leu	Cys	Ser	Ala	Leu	Thr	Leu	Ser	Gly	Leu	Val
		100						105					110		
Glu	Val	Lys	Glu	Leu	Gln	Arg	Glu	Pro	Leu	Thr	Pro	Glu	Glu	Val	Gln
		115					120					125			
Ser	Val	Arg	Glu	His	Leu	Gly	His	Glu	Ser	Asp	Asn	Leu	Leu	Phe	Val
		130				135					140				
Gln	Ile	Thr	Gly	Lys	Lys	Pro	Asn	Phe	Glu	Val	Gly	Ser	Ser	Arg	Gln
				150					155					160	
Leu	Lys	Leu	Ser	Ile	Thr	Lys	Lys	Ser	Ser	Pro	Ser	Val	Lys	Pro	Ala

	165		170		175
Val Asp Pro Ala Ala Ala Lys Leu Trp Thr Leu Ser Ala Asn Asp Met					
	180		185		190
Glu Asp Asp Ser Met Cys Ile Phe Cys Gly Cys Ser Leu Thr His Arg					
	195		200		205
Trp Pro Leu Glu His Val Val Arg Leu Asn Met Met Ile Asn Gln Lys					
	210		215		220
Glu Asp Arg Val Asp Thr Phe Phe Thr Leu Asp Ser Lys Phe Pro Leu					
	225		230		235
Glu Ala Cys Ser His Phe Ser Phe Ser Leu Ala Glu Thr Thr Thr Val					
	245		250		255
Ser Leu Ile Ala Leu Asn Thr Leu Gln Asp Leu Ile Asp Ser Asp Glu					
	260		265		270
Leu Leu Asp Pro Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg					
	275		280		285
Ala Ala Ser Cys Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys					
	290		295		300
Thr Cys Gly Leu Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln					
	305		310		315
Met Ser Ser Gln Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp					
	325		330		335
Ala Phe Arg Cys Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys					
	340		345		350
Pro Gly Glu Lys Val Leu Leu Ser Asp Ser Asn Leu His Asp Ala					
	355		360		365

<210> 5577

<211> 659

<212> DNA

<213> Homo sapiens

<400> 5577

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 120
 cctgtggccg acatgagggc actcctgaca ggcaaggact gccccatgt ccgggagaag
 180
 ggctccggga agcagaacaa ggacctctat gagttggcct tctcaatcag ctatgaccgt
 240
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 300
 acagatgggc tcagtgcctt gctgggcagt cccatgggca gcgagcagac acggctggac
 360
 ctggagcagc tgctgacctt ggagaccaag ctgcgtctgc tggagctgga gaactgtccc
 420
 atccccgagc ggccaccccc tgtgccccca cccccacca acttcaactt ctgctatgac
 480
 tgagcatcg ctgaaccttg acagtgtggc tggccatggg ccacagctgc ggccactgca
 540
 gcagccatga agggcagtg gtagaggagt gcaggcaccc tgaccagcag agattgctgc
 600
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 659

<210> 5578
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 5578
 Leu His Ala Asp Lys Leu Trp Phe Cys Cys Leu Ser Pro Asn His Lys
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 Leu Leu Gln Tyr Gly Asp Met Glu Gly Xaa Gln Pro Ala Tyr Pro
 20 25 30
 Xaa Glu Ser Leu Pro Glu Gln Leu Pro Val Ala Asp Met Arg Ala Leu
 35 40 45
 Leu Thr Gly Lys Asp Cys Pro His Val Arg Glu Lys Gly Ser Gly Lys
 50 55 60
 Gln Asn Lys Asp Leu Tyr Glu Leu Ala Phe Ser Ile Ser Tyr Asp Arg
 65 70 75 80
 Gly Glu Glu Glu Ala Tyr Leu Asn Phe Ile Ala Pro Ser Lys Arg Glu
 85 90 95
 Phe Tyr Leu Trp Thr Asp Gly Leu Ser Ala Leu Leu Gly Ser Pro Met
 100 105 110
 Gly Ser Glu Gln Thr Arg Leu Asp Leu Glu Gln Leu Leu Thr Met Glu
 115 120 125
 Thr Lys Leu Arg Leu Leu Glu Leu Glu Asn Val Pro Ile Pro Glu Arg
 130 135 140
 Pro Pro Pro Val Pro Pro Pro Pro Thr Asn Phe Asn Phe Cys Tyr Asp
 145 150 155 160
 Cys Ser Ile Ala Glu Pro
 165

<210> 5579
 <211> 1312
 <212> DNA
 <213> Homo sapiens

<400> 5579
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 120
 cacttactac ctacagctcc aactaccgtg aatgtaacac atcgtccagt aactcaggtg
 180
 acccaagac tccctgtacc aagagctcct gcaaaccacc aggtgggtta tacaactctt
 240
 cctgcaccac cagctcaggc tccttgcga ggaactgtta tgcaggctcc tgctgttcgg
 300
 cagggtcaatc cccaaaatag tggtacagtt cgagtgcctc aaacaaccac atatgttgta
 360
 aacaatggac taacctggg atcaacagga cctcagctca cagtgcata cggaccacca
 420
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 480
 ccacagcgtc tgccccaga agctgccagc acatctctgc ctcagaagcc acattggaag
 540

tttagcacgcg ttcagagtca aaatggcata gtactgtcat ggagtgtcct ggaggtggat
 600
 cgaagctgtg ccactgttga tagctacat ctctatgctt accatgagga acccagtgcc
 660
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 720
 tgtactctca ccagtttgt atctggttagc aaatactact ttgcagtacg agccaaggat
 780
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 840
 cagagcagtt aaaccttggc gcctttatat tttcctcttt taaaatttcc accttttggt
 900
 cttgttttta atcttgtgca tgatacccca tgtaaaatcc accttgtgca agatttcttg
 960
 gacagatgtg tgtatacact acatttgttt ataaccagaa gcaaaaataaa ctcagccac
 1020
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 1080
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<210> 5580

<211> 283

<212> PRT

<213> Homo sapiens

<400> 5580

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 20 25 30
 Ser Gly Pro Ser Gln Thr Thr Ile His Leu Leu Pro Thr Ala Pro Thr
 35 40 45
 Thr Val Asn Val Thr His Arg Pro Val Thr Gln Val Thr Thr Arg Leu
 50 55 60
 Pro Val Pro Arg Ala Pro Ala Asn His Gln Val Val Tyr Thr Thr Leu
 65 70 75 80
 Pro Ala Pro Pro Ala Gln Ala Pro Leu Arg Gly Thr Val Met Gln Ala
 85 90 95
 Pro Ala Val Arg Gln Val Asn Pro Gln Asn Ser Val Thr Val Arg Val
 100 105 110
 Pro Gln Thr Thr Thr Tyr Val Val Asn Asn Gly Leu Thr Leu Gly Ser
 115 120 125
 Thr Gly Pro Gln Leu Thr Val His His Arg Pro Pro Gln Val His Thr
 130 135 140
 Glu Pro Pro Arg Pro Val His Pro Ala Pro Leu Pro Glu Ala Pro Gln
 145 150 155 160
 Pro Gln Arg Leu Pro Pro Glu Ala Ala Ser Thr Ser Leu Pro Gln Lys

```

                165                170                175
Pro His Leu Lys Lys Leu Ala Arg Val Gln Ser Gln Asn Gly Ile Val Leu
                180                185                190
Ser Trp Ser Val Leu Glu Val Asp Arg Ser Cys Ala Thr Val Asp Ser
                195                200                205
Tyr His Leu Tyr Ala Tyr His Glu Glu Pro Ser Ala Thr Val Pro Ser
                210                215                220
Gln Trp Lys Lys Ile Gly Glu Val Lys Ala Leu Pro Leu Pro Met Ala
                225                230                235                240
Cys Thr Leu Thr Gln Phe Val Ser Gly Ser Lys Tyr Tyr Phe Ala Val
                245                250                255
Arg Ala Lys Asp Ile Tyr Gly Arg Phe Gly Pro Phe Cys Asp Pro Gln
                260                265                270
Ser Thr Asp Val Ile Ser Ser Thr Gln Ser Ser
                275                280

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<210> 5581

<211> 720

<212> DNA

<213> Homo sapiens

<400> 5581

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120
gcgtcccgcg agctgcctgt ctgcgtctgg caggtcacccg agccgtcaag caagaatctg
180
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240
gtcaaacagg agcctgtgat tacgggttgcg ccagtagagg aaatgctttt tcatggcttc
300
agtgcagagc actattttcc ggtttcccat ttcacatga tctcacgtac accctgtcct
360
caagataaat cggaaacaat caacccaaaa acatgttttc ccaaagaata ttggaaact
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480
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540
ttattatcag atgatagctc attatcttgg taccatcagg ttgttctcca gatgacccct
600
tcgggagggg aagcctgtgt ttggggtcac ttaccaggtt ccagccacac catctagtgt
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<210> 5582

<211> 212

<212> PRT

<213> Homo sapiens

<400> 5582

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Met Ala Ala Pro Arg Gln Ile Pro Ser His Ile Val Arg Leu Lys Pro

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Ser Cys Ser Thr Asp Ser Ser Phe Thr Arg Thr Pro Val Pro Thr Val
      20             25             30
Ser Leu Ala Ser Arg Glu Leu Pro Val Ser Ser Trp Gln Val Thr Glu
      35             40             45
Pro Ser Ser Lys Asn Leu Trp Glu Gln Ile Cys Lys Glu Tyr Glu Ala
      50             55             60
Glu Gln Pro Pro Phe Pro Glu Gly Tyr Lys Val Lys Gln Glu Pro Val
      65             70             75             80
Ile Thr Val Ala Pro Val Glu Glu Met Leu Phe His Gly Phe Ser Ala
      85             90             95
Glu His Tyr Phe Pro Val Ser His Phe Thr Met Ile Ser Arg Thr Pro
      100            105            110
Cys Pro Gln Asp Lys Ser Glu Thr Ile Asn Pro Lys Thr Cys Ser Pro
      115            120            125
Lys Glu Tyr Leu Glu Thr Phe Ile Phe Pro Val Leu Leu Pro Gly Met
      130            135            140
Ala Ser Leu Leu His Gln Ala Lys Lys Glu Lys Cys Phe Glu Val Ser
      145            150            155            160
Cys Leu Ala Gly Phe Leu Tyr Phe Glu Ile Leu Asn His Ser Leu Leu
      165            170            175
Ser Asp Asp Ser Ser Leu Ser Trp Tyr His Gln Val Val Leu Gln Met
      180            185            190
Thr Pro Ser Gly Gly Lys Ala Cys Val Trp Gly His Leu Pro Ser Ser
      195            200            205
Ser His Thr Ile
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<210> 5583

<211> 2101

<212> DNA

<213> Homo sapiens

<400> 5583

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120
gtgggggccc ctgccggccc agcccccatt gccttcacca gtaccttgga gaaggctcga
180
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240
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300
ctggatgaga cggtgctgtg ggtggtgcac gtctctggcc ccattaaccc ccagggtgctc
360
aaaagcaaa cagccaagga gctcaaggcg ctgcaggact tggcagggaa ggaatgtcg
420
gagctcttgg acatgccagc ggcggagctg cttcaagacc accagctcct ctgggctcag
480
ctcttcagcc caggagtga aatgaagaag atcactgaca cccacacgcc gtctggcctc
540
accgtgaacc tgacgtctta ttacatgtc tcctgtctgc cagccccact gctcagcccc
600

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tccctgagcc acagggagcg agaccagatg gaggcgacgc tcaactatga agatcactgc
660
ttcagcgggc acgccaccat gcacgccgag aacctgtggc cggggcggct gtccctccgtc
720
cagcagatcc tgcagctctc tgacctgtgg aggctgaccc tccagaagcg tggtgtcaag
780
gggctgtga aggtgggtgc ccagggcatc ctgcagggga ttgtgtctcag ctttgggggg
840
ctgcagtta cagagaacca cctccagttc caggccgacc ccgagctgct gcacaacagc
900
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960
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1020
tatgcctgca aggcaggctg cctggacgag ccagtggagc tgacctcgcc gccacgggc
1080
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1200
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1260
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1320
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1380
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1560
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1620
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1680
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1920
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1980
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2100
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2101

<210> 5584

<211> 454

<212> PRT

<213> Homo sapiens

<400> 5584

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Xaa Gly Arg Asp Cys Val Leu Leu Gln Glu Asp Phe Leu Ala His Arg
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Gly Arg Pro His Val Tyr Leu Gln Arg Ile Gln Leu Asn Asn Pro Thr
          20           25           30
Glu Arg Val Ala Ala Leu Gln Thr Val Gly Pro Thr Ala Gly Pro Ala
          35           40           45
Pro Asn Ala Phe Thr Ser Thr Leu Glu Lys Val Gly Asp His Gln Phe
          50           55           60
Leu Leu Tyr Ser Gly Arg Ser Pro Pro Thr Pro Thr Gly Leu Val His
65          70          75          80
Leu Val Val Val Ala Ala Lys Lys Leu Val Asn Arg Leu Gln Val Ala
          85          90          95
Pro Lys Thr Gln Leu Asp Glu Thr Val Leu Trp Val Val His Val Ser
          100          105          110
Gly Pro Ile Asn Pro Gln Val Leu Lys Ser Lys Ala Ala Lys Glu Leu
          115          120          125
Lys Ala Leu Gln Asp Leu Ala Arg Lys Glu Met Leu Glu Leu Leu Asp
          130          135          140
Met Pro Ala Ala Glu Leu Leu Gln Asp His Gln Leu Leu Trp Ala Gln
145          150          155          160
Leu Phe Ser Pro Gly Val Glu Met Lys Lys Ile Thr Asp Thr His Thr
          165          170          175
Pro Ser Gly Leu Thr Val Asn Leu Thr Leu Tyr Tyr Met Leu Ser Cys
          180          185          190
Ser Pro Ala Pro Leu Leu Ser Pro Ser Leu Ser His Arg Glu Arg Asp
          195          200          205
Gln Met Glu Ser Thr Leu Asn Tyr Glu Asp His Cys Phe Ser Gly His
210          215          220
Ala Thr Met His Ala Glu Asn Leu Trp Pro Gly Arg Leu Ser Ser Val
225          230          235          240
Gln Gln Ile Leu Gln Leu Ser Asp Leu Trp Arg Leu Thr Leu Gln Lys
          245          250          255
Arg Gly Cys Lys Gly Leu Val Lys Val Gly Ala Pro Gly Ile Leu Gln
          260          265          270
Gly Met Val Leu Ser Phe Gly Gly Leu Gln Phe Thr Glu Asn His Leu
275          280          285
Gln Phe Gln Ala Asp Pro Asp Val Leu His Asn Ser Tyr Ala Leu His
290          295          300
Gly Ile Arg Tyr Lys Asn Asp His Ile Asn Leu Ala Val Leu Arg Met
305          310          315          320
Pro Arg Ala Ser Pro Thr Tyr Thr Cys Pro Trp Ser Pro Val Ala Ser
          325          330          335
Leu Ser Xaa Ile Tyr Ala Cys Lys Ala Gly Cys Leu Asp Glu Pro Val
          340          345          350
Glu Leu Thr Ser Ala Pro Thr Gly His Thr Phe Ser Val Met Val Thr
          355          360          365
Gln Pro Ile Thr Pro Leu Leu Tyr Ile Ser Thr Asp Leu Thr His Leu
          370          375          380
Gln Asp Leu Arg His Thr Leu His Leu Lys Ala Ile Leu Ala His Asp

```

```

385          390          395          400
Glu His Met Ala Gln Gln Asp Pro Gly Leu Pro Phe Leu Phe Trp Phe
          405          410          415
Ser Val Ala Ser Leu Ile Thr Leu Phe His Leu Phe Leu Lys Leu
          420          425          430
Ile Tyr Asn Glu Tyr Cys Gly Pro Gly Ala Lys Pro Leu Phe Arg Ser
          435          440          445
Lys Glu Asp Pro Ser Val
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<210> 5585

<211> 740

<212> DNA

<213> Homo sapiens

<400> 5585

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120
ctcacagaag taaaatatac aatgctacat tgagtgggta aaaatacaca aaaaagttagt
180
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240
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300
gagggatctg acaggatgct ggaaaaaatg actcagggaa gccgggcagc atgggctcct
360
ttggagattc aggagcggag ctacagttcca cctcactgca gttccctggg gccaacgagc
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480
cccaacccaa agactcctct aaacttcttt gcagcatgac agctgcctgc cctacactga
540
gtctacttga ctttcaattg cgtctcgcga gagaggtagg agagggacac tgccccattc
600
tggaacttgac ataagtaccc cagccacatg gccttcatcc ttatgacctg gcaggcagaa
660
caggggaccaa gcagcttcta ttttgtcaaa ctcccttggg caaatattca acattcaaca
720
acaagctttg taaacctaac
740

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<210> 5586

<211> 87

<212> PRT

<213> Homo sapiens

<400> 5586

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Met Gly Ser Phe Gly Asp Ser Gly Ala Glu Leu Ser Ser Thr Ser Leu
1          5          10          15
Gln Phe Pro Gly Ala Lys Gln Pro Ser Ser Pro Gln Tyr Leu Ser His
          20          25          30
Leu Lys Arg Ser Cys Pro Thr Tyr Leu Ser Pro Pro Gln Pro Lys Asp

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35	40	45
Ser Ser Lys Leu Leu Cys Ser Met Thr Ala Ala Cys Pro Thr Leu Ser		
50	55	60
Leu Leu Asp Leu Gln Leu Arg Leu Arg Arg Glu Val Gly Glu Gly His		
65	70	75
Cys Pro Ile Leu Asp Leu Thr		80
85		

<210> 5587

<211> 853

<212> DNA

<213> Homo sapiens

<400> 5587

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 aatattcagt gcactctggtt ggggccaaca tggatgatga cgtgtttctc ataagccctt
 120
 ttcattgttt tctcaatttg cttcagaaaa acttgcggga ttcgtccaca taaagtgtgc
 180
 acagctctcca aaaacttcag ctgaaggggg taatacatgg attgaaagag attgtcttga
 240
 aagggaataat cccgtattgc ttcataagagt gctctgaacg ttggttgctt atcgtcatgg
 300
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 360
 cttccgtaca tgcagtgatc gggacggtag ttccactggc aggggaatac atagagacac
 420
 tctgggttga aataaaaaat aatatattaat aaatcctggt ctccccacgt gatggcattc
 480
 ttgtacttct ggtacagagg gtacaacatg toctcccaag ccaggcctgt tggaatcatg
 540
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 660
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 720
 cagatgtcat caacaggtct cagaaagagg acatcggtgt ccacgtagag aagtgaagtc
 780
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 853

<210> 5588

<211> 204

<212> PRT

<213> Homo sapiens

<400> 5588

Met Ala Pro Glu His Glu Ile Pro Lys Ile Gly Trp Tyr Ser Arg Phe
1 5 10 15
Ala Arg His Pro Phe Tyr Gly Ser Ala Gly Val Asn Ser Gly Val Met

	20						25				30				
Leu	Met	Asn	Leu	Thr	Arg	Ile	Arg	Ser	Thr	Gln	Phe	Lys	Asn	Ser	Met
		35					40					45			
Ile	Pro	Thr	Gly	Leu	Ala	Trp	Glu	Asp	Met	Leu	Tyr	Pro	Leu	Tyr	Gln
	50					55				60					
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<211> 1327

<212> DNA

<213> Homo sapiens

<400> 5589

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<211> 207

<212> PRT

<213> Homo sapiens

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<211> 2194

<212> DNA

<213> Homo sapiens

<400> 5591

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<211> 580

<212> PRT

<213> Homo sapiens

<400> 5592

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 85 90 95Pro Phe Leu
 Gln Ala Pro Ser Gly Ala Glu Leu Trp Val Trp Phe
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 Gln Asp Thr Val Thr Asp Val Asp Lys Ser Trp Arg Glu Leu Ser Asn
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<211> 3078

<212> DNA

<213> Homo sapiens

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<211> 296

<212> PRT

<213> Homo sapiens

<400> 5594

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His Val Arg Arg Met Phe His Pro Gly Arg Gly Leu Gly Gly Pro Arg
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<210> 5596
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<400> 5596
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<211> 312

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<213> Homo sapiens

<400> 5598

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<212> DNA

<213> Homo sapiens

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<212> PRT

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Tyr	Phe	Pro	Phe	Met	Asp	Leu	Lys	Leu	Arg	Ala	Ala	Ser	Pro	Ile	Ile
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          355          360          365
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Ser Thr Ile Glu Val Ile Ala Gln Glu Pro Phe Gly Ala Asn Gln Thr
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Ile Ile Val Ala Val Lys Val Ser Pro Val Ser Tyr Leu Arg Val Ser
          405          410          415
Met Ser Pro Val Leu His Thr Gln Asn Lys Glu Ala Leu Val Ala Val
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<210> 5601

<211> 670

<212> DNA

<213> Homo sapiens

<400> 5601

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 gaacagagaa ggacgacagc ttctttgttg cgcaaaactga ctacagcctc caatggaggg
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 420
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 480
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 670

<210> 5602
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 5602
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 Leu Thr Trp Ala Cys Met Ala Arg Gln Thr Arg His Leu Gly Glu Gln
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 Arg Arg Thr Thr Ala Ser Leu Leu Arg Lys Leu Thr Thr Ala Ser Asn
 35 40 45
 Gly Gly Val Ile Glu Glu Leu Ser Cys Val Arg Ser Asn Asn Tyr Val
 50 55 60
 Gln Glu Pro Glu Cys Arg Arg Asn Leu Val Gln Cys Leu Leu Glu Lys
 65 70 75 80
 Gln Gly Thr Pro Val Val Gln Gly Ser Leu Glu Leu Glu Arg Val Met
 85 90 95
 Ser Ser Leu Leu Asp Met Gly Phe Ser Asn Ala His Ile Asn Glu Leu
 100 105 110
 Leu Ser Val Arg Arg Gly Ala Ser Leu Gln Gln Leu Leu Asp Ile Ile
 115 120 125
 Ser Glu Phe Ile Leu Leu Gly Leu Asn Pro Glu Pro Val Cys Val Val
 130 135 140
 Leu Lys Lys Ser Pro Gln Leu Leu Lys Leu Pro Ile Met Gln Met Arg
 145 150 155 160
 Lys Arg Ser Ser Tyr Leu Gln Lys Leu Gly Leu Gly Glu Gly Lys Leu
 165 170 175
 Lys Arg Val Leu Tyr Cys Cys Pro Glu Ile Phe Thr Met Arg Gln Gln
 180 185 190
 Asp Ile Asn Asp Thr Val Arg Leu Leu Lys Glu Lys Cys Leu Phe Thr
 195 200 205
 Val Pro Leu His Ala
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<210> 5603
 <211> 2070
 <212> DNA
 <213> Homo sapiens

<400> 5603
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 120
 catgatggag acccttcaaa ttgtcttatg ttcttttttc gcctatagac cagatataat
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 aattagcttt tcttctcttg cagattccag agagtctctt atttcatatg tgccttccag
 240
 aacatctctt gtggtattca ctacttggct tctgtgttca tgggagtcac ccctcatcat
 300
 gtctgcaggc ccccgagcaa tgtgagtcag gttgttttcc ataactactc taattggagat
 360

ttggaggaca cgggggccct gttgtcttca ggccagaaag attatgttac ggtgcagttg
420
cagaatggtg agatctggga gctctcaagg tgtagcagga ataagagga gaacacatcg
480
agtttgggct atgaatacac tggcagtaag aaagagtctt cttgtgtgga tggtacata
540
tatgaccaga acacatggaa aagcactgcy gtgaccaggt ggaacctggt ctgtgaccga
600
aaatggcttg caatgctgat ccagccccta tttatgtttg gagtcctact gggatcggtg
660
acttttggct acttttctga caggctagga cgccgggtgg tcttgtgggc cacaagcagt
720
agcatgtttt tgtttggaa agcagcggcg tttgcagttg attattacac cttcatggct
780
gctcgctttt ttcttgccat ggttgcaagt ggctatcttg tgggtgggtt tgcctatgtg
840
atggaattca ttggcatgaa gtctcggaca tgggcgtctg tccatttgca ttctttttt
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960
cagatgatec tctccacagt gactgtcccc tttatcctgt gctgttgggt gctcccagag
1020
acaccttttt ggctctctc agagggacga tatgaagaag cacaaaaaat agttgacatc
1080
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1140
caaggtcctg ttagtaatag cccactgaa gttcagaagc acaacctatc atatctgttt
1200
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1320
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1380
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1620
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1680
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1800
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1860
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1920
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1980

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 2040
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 2070

<210> 5604

<211> 560

<212> PRT

<213> Homo sapiens

<400> 5604

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 20 25 30
 His Val Cys Arg Pro Pro Gly Asn Val Ser Gln Val Val Phe His Asn
 35 40 45
 His Ser Asn Trp Ser Leu Glu Asp Thr Gly Ala Leu Leu Ser Ser Gly
 50 55 60
 Gln Lys Asp Tyr Val Thr Val Gln Leu Gln Asn Gly Glu Ile Trp Glu
 65 70 75 80
 Leu Ser Arg Cys Ser Arg Asn Lys Arg Glu Asn Thr Ser Ser Leu Gly
 85 90 95
 Tyr Glu Tyr Thr Gly Ser Lys Lys Glu Phe Pro Cys Val Asp Gly Tyr
 100 105 110
 Ile Tyr Asp Gln Asn Thr Trp Lys Ser Thr Ala Val Thr Gln Trp Asn
 115 120 125
 Leu Val Cys Asp Arg Lys Trp Leu Ala Met Leu Ile Gln Pro Leu Phe
 130 135 140
 Met Phe Gly Val Leu Leu Gly Ser Val Thr Phe Gly Tyr Phe Ser Asp
 145 150 155 160
 Arg Leu Gly Arg Arg Val Val Leu Trp Ala Thr Ser Ser Ser Met Phe
 165 170 175
 Leu Phe Gly Ile Ala Ala Ala Phe Ala Val Asp Tyr Tyr Thr Phe Met
 180 185 190
 Ala Ala Arg Phe Phe Leu Ala Met Val Ala Ser Gly Tyr Leu Val Val
 195 200 205
 Gly Phe Val Tyr Val Met Glu Phe Ile Gly Met Lys Ser Arg Thr Trp
 210 215 220
 Ala Ser Val His Leu His Ser Phe Phe Ala Val Gly Thr Leu Leu Val
 225 230 235 240
 Ala Leu Thr Gly Tyr Leu Val Arg Thr Trp Trp Leu Tyr Gln Met Ile
 245 250 255
 Leu Ser Thr Val Thr Val Pro Phe Ile Leu Cys Cys Trp Val Leu Pro
 260 265 270
 Glu Thr Pro Phe Trp Leu Leu Ser Glu Gly Arg Tyr Glu Glu Ala Gln
 275 280 285
 Lys Ile Val Asp Ile Met Ala Lys Trp Asn Arg Ala Ser Ser Cys Lys
 290 295 300
 Leu Ser Glu Leu Leu Ser Leu Asp Leu Gln Gly Pro Val Ser Asn Ser
 305 310 315 320
 Pro Thr Glu Val Gln Lys His Asn Leu Ser Tyr Leu Phe Tyr Asn Trp
 325 330 335
 Ser Ile Thr Lys Arg Thr Leu Thr Val Trp Leu Ile Trp Phe Thr Gly

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          340          345          350
Ser Leu Gly Phe Tyr Ser Phe Ser Leu Asn Ser Val Asn Leu Gly Gly
          355          360          365
Asn Glu Tyr Leu Asn Leu Phe Leu Leu Gly Val Val Glu Ile Pro Ala
          370          375          380
Tyr Thr Phe Val Cys Ile Ala Met Asp Lys Val Gly Arg Arg Thr Val
          385          390          400
Leu Ala Tyr Ser Leu Phe Cys Ser Ala Leu Ala Cys Gly Val Val Met
          405          410          415
Val Ile Pro Gln Lys His Tyr Ile Leu Gly Val Val Thr Ala Met Val
          420          425          430
Gly Lys Phe Ala Ile Gly Ala Ala Phe Gly Leu Ile Tyr Leu Tyr Thr
          435          440          445
Ala Glu Leu Tyr Pro Thr Ile Val Arg Ser Leu Ala Val Gly Ser Gly
          450          455          460
Ser Met Val Cys Arg Leu Ala Ser Ile Leu Ala Pro Phe Ser Val Asp
          465          470          475          480
Leu Ser Ser Ile Trp Ile Phe Ile Pro Gln Leu Phe Val Gly Thr Met
          485          490          495
Ala Leu Leu Ser Gly Val Leu Thr Leu Lys Leu Pro Glu Thr Leu Gly
          500          505          510
Lys Arg Leu Ala Thr Thr Trp Glu Glu Ala Ala Lys Leu Glu Ser Glu
          515          520          525
Asn Glu Ser Lys Ser Ser Lys Leu Leu Leu Thr Thr Asn Asn Ser Gly
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Leu Glu Lys Thr Glu Ala Ile Thr Pro Arg Asp Ser Gly Leu Gly Glu
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<210> 5605

<211> 376

<212> DNA

<213> Homo sapiens

<400> 5605

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120
catccaggga ggcctctcca gggaggatga cggaacatca gaggaagaa gcaaggagaa
180
ccagccacac tcagagctgg gaaagagcag caggaagatg ggggcagtga gtgccagggc
240
tctgcaggga tgggcttgcc tggcaggag caataccaag gaagttagta gggcccgggt
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<210> 5606

<211> 101

<212> PRT

<213> Homo sapiens

<400> 5606

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Met Thr Arg Ala Leu Leu Thr Ser Leu Val Leu Leu Pro Ala Arg Gln
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Ala His Pro Cys Arg Ala Leu Ala Leu Thr Ala Pro Ile Phe Leu Leu
      20           25           30
Leu Phe Pro Ser Ser Glu Cys Gly Trp Phe Ser Leu Leu Ser Ser
      35           40           45
Asp Val Pro Ser Ser Ser Leu Glu Arg Pro Pro Trp Met Thr Glu Glu
      50           55           60
Val Thr Thr Thr Ser Ser Arg Ser Thr Pro Arg Pro Ser Val Ser Pro
 65           70           75           80
Ser Gln Cys Leu Ala Pro Ser Asn Ile Ala Phe Cys Val Tyr His Gln
      85           90           95
Phe Pro Phe Thr Arg
      100

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<210> 5607

<211> 320

<212> DNA

<213> Homo sapiens

<400> 5607

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120
gggaagctgc tggaccagtg tgtggagacc ctgcagaagc agaccagggt tggcaaggct
180
ggcaccaaca agccccccag gtgccgggga agagggggcca ggctgtgggg ccgcccagct
240
cctcggaatg tgtttgactt cctcaatgaa aagctgcaag gtcaggctcc tggggcccta
300
caagccgggc ggccctcagca
320

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<210> 5608

<211> 106

<212> PRT

<213> Homo sapiens

<400> 5608

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Val His Thr Arg Gly Ile Gly Ser Arg Leu Leu Thr Lys Met Gly Tyr
 1           5           10           15
Glu Phe Gly Lys Gly Leu Gly Arg His Ala Glu Gly Arg Val Glu Pro
      20           25           30
Ile His Ala Val Val Leu Pro Arg Gly Lys Ser Leu Asp Gln Cys Val
      35           40           45
Glu Thr Leu Gln Lys Gln Thr Arg Val Gly Lys Ala Gly Thr Asn Lys
      50           55           60
Pro Pro Arg Cys Arg Gly Arg Gly Ala Arg Pro Gly Gly Arg Pro Ala
 65           70           75           80
Pro Arg Asn Val Phe Asp Phe Leu Asn Glu Lys Leu Gln Gly Gln Ala
      85           90           95
Pro Gly Ala Leu Gln Ala Gly Arg Pro Gln

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100

105

<210> 5609

<211> 1843

<212> DNA

<213> Homo sapiens

<400> 5609

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120
tttaacattt cagtccattc acttttttta aaataaaaaat aggacaaatt attcaattac
180
ttgtctcaat ttaacaatct tgaaaaagac tggaaggtag cctacagtgt tcagttgaca
240
taaaaataga cccgtattga tcatacaaat ctatcatgag aagttaccca gtgagagtga
300
gttattgtaa ttctgaatgt actcatcgtg ttctctactt ctacagaagc atcctcagtgt
360
agttgtattg tgcgagaaaa tgacaccctt gcccacatca ctctccattc catagaggga
420
cacaacccta tctagccaaa ccagaagaa cgcaggcgct tacacaactt ttctcgga
480
gtcgagaaaa tccaaaagtg ggctttgggc ttaccttaaa taggaatgga atgtaccact
540
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600
aatgaggatg gcggaggaag aggagtgggt actgaaggga ggtggtgcat aataagtga
660
cgagctacac aaagctcgag ctacacaaag ctacaggctcc acgggcctcg ccttggtccc
720
cagggatgct ctgcagccag cgggcggatg acctgaggtc gggcctgggc ctgtcccttt
780
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840
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1020
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1080
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1200
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1260
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1320
ccaatgcccc ggagaggggtc agagcacatg tgctctggtg gttgtcaaat ctctcaccat
1380

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 1500
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 1560
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 1620
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 1680
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 1740
 aantatagtt ttagaatata gtctgatatg acaaagtagg gatttttaaa gcctaacatt
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 1843

<210> 5610

<211> 153

<212> PRT

<213> Homo sapiens

<400> 5610

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Phe	Thr	Ala	Cys	Ser	Ser	Arg	Val	Gln	Met	Ala	Cys	Ile	Cys	Ala
		20						25				30		
Phe	Thr	Gly	Arg	Gln	Asp	His	Thr	Ser	Leu	Pro	His	Trp	Ala	Cys
		35				40					45			
Leu	Leu	Val	Asp	Ser	Cys	Met	Gln	Glu	Ala	Val	Met	Gly	Ser	Leu
		50				55					60			
Ile	Pro	Gln	Cys	Gly	Asn	Gly	Pro	Leu	Arg	Leu	Val	Leu	Arg	Val
65					70				75				80	
Gly	Ala	Gln	Ser	Trp	Val	Gly	Gly	Cys	Trp	Trp	Glu	Val	Arg	Asn
				85					90				95	
Phe	Trp	Leu	Pro	Ser	Gly	Gln	Leu	Pro	Thr	Ala	Leu	Thr	Trp	Glu
			100					105					110	
Asp	Ala	His	Arg	Gln	Asp	Ala	Leu	Gly	Tyr	Cys	Cys	Thr	Val	Leu
		115					120					125		
Glu	Ile	Phe	Ile	Gln	Pro	Thr	Arg	Phe	Asn	Arg	Ser	Leu	Gly	Ser
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<210> 5611

<211> 1152

<212> DNA

<213> Homo sapiens

<400> 5611

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 120

cgggtcctgg cgcctcagag cccggcccag gccgcggaac ggtgatgctc gggccggacg
 180
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 240
 gcagagaccc gtggattgct gtgccctgcc ctccggacct ggatcatgaa ggtgttgagg
 300
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 360
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 420
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 480
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 660
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 720
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 780
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 840
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 900
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 960
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 1020
 attgactccc agaacaacca gtatatattg accaagccca gagattcaac catcccacgt
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 1140
 tggcgatgta ca
 1152

<210> 5612

<211> 289

<212> PRT

<213> Homo sapiens

<400> 5612

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 20 25 30
 Ile Lys Leu His Arg Gly Arg Gly Val Ala Ala Met Gln Ser Arg Gln
 35 40 45
 Trp Val Arg Asp Ser Cys Arg Lys Leu Ser Gly Leu Leu Arg Gln Lys
 50 55 60
 Asn Ala Val Leu Asn Lys Leu Lys Thr Ala Ile Gly Ala Val Glu Lys
 65 70 75 80
 Asp Val Gly Leu Ser Asp Glu Glu Lys Leu Phe Gln Val His Thr Phe

85										90										95																											
Glu	Ile	Phe	Gln	Lys	Glu	Leu	Asn	Glu	Ser	Glu	Asn	Ser	Val	Phe	Gln	Glu	Ile	Phe	Gln	Lys	Glu	Leu	Asn	Glu	Ser	Glu	Asn	Ser	Val	Phe	Gln	Glu	Ile	Phe	Gln	Lys	Glu	Leu	Asn	Glu	Ser	Glu	Asn	Ser	Val	Phe	Gln
100										105										110																											
Ala	Val	Tyr	Gly	Leu	Gln	Arg	Ala	Leu	Gln	Gly	Asp	Tyr	Lys	Asp	Val	Ala	Val	Tyr	Gly	Leu	Gln	Arg	Ala	Leu	Gln	Gly	Asp	Tyr	Lys	Asp	Val	Ala	Val	Tyr	Gly	Leu	Gln	Arg	Ala	Leu	Gln	Gly	Asp	Tyr	Lys	Asp	Val
115										120										125																											
Val	Asn	Met	Lys	Glu	Ser	Ser	Arg	Gln	Arg	Leu	Glu	Ala	Leu	Arg	Glu	Val	Asn	Met	Lys	Glu	Ser	Ser	Arg	Gln	Arg	Leu	Glu	Ala	Leu	Arg	Glu	Val	Asn	Met	Lys	Glu	Ser	Ser	Arg	Gln	Arg	Leu	Glu	Ala	Leu	Arg	Glu
130										135										140																											
Ala	Ala	Ile	Lys	Glu	Glu	Thr	Glu	Tyr	Met	Glu	Leu	Leu	Ala	Ala	Glu	Ala	Ala	Ile	Lys	Glu	Glu	Thr	Glu	Tyr	Met	Glu	Leu	Leu	Ala	Ala	Glu	Ala	Ala	Ile	Lys	Glu	Glu	Thr	Glu	Tyr	Met	Glu	Leu	Leu	Ala	Ala	Glu
145										150										155																											
Lys	His	Gln	Val	Glu	Ala	Leu	Lys	Asn	Met	Gln	His	Gln	Asn	Gln	Ser	Lys	His	Gln	Val	Glu	Ala	Leu	Lys	Asn	Met	Gln	His	Gln	Asn	Gln	Ser	Lys	His	Gln	Val	Glu	Ala	Leu	Lys	Asn	Met	Gln	His	Gln	Asn	Gln	Ser
165										170										175																											
Leu	Ser	Met	Leu	Asp	Glu	Ile	Leu	Glu	Asp	Val	Arg	Lys	Ala	Ala	Asp	Leu	Ser	Met	Leu	Asp	Glu	Ile	Leu	Glu	Asp	Val	Arg	Lys	Ala	Ala	Asp	Leu	Ser	Met	Leu	Asp	Glu	Ile	Leu	Glu	Asp	Val	Arg	Lys	Ala	Ala	Asp
180										185										190																											
Arg	Leu	Glu	Glu	Glu	Ile	Glu	Glu	His	Ala	Phe	Asp	Asp	Asn	Lys	Ser	Arg	Leu	Glu	Glu	Glu	Ile	Glu	Glu	His	Ala	Phe	Asp	Asp	Asn	Lys	Ser	Arg	Leu	Glu	Glu	Glu	Ile	Glu	Glu	His	Ala	Phe	Asp	Asp	Asn	Lys	Ser
195										200										205																											
Val	Lys	Gly	Val	Asn	Phe	Glu	Ala	Val	Leu	Arg	Val	Glu	Glu	Glu	Glu	Val	Lys	Gly	Val	Asn	Phe	Glu	Ala	Val	Leu	Arg	Val	Glu	Glu	Glu	Glu	Val	Lys	Gly	Val	Asn	Phe	Glu	Ala	Val	Leu	Arg	Val	Glu	Glu	Glu	Glu
210										215										220																											
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245										250										255																											
Lys	Pro	Arg	Asp	Ser	Thr	Ile	Pro	Arg	Ala	Asp	His	His	Phe	Ile	Lys	Lys	Pro	Arg	Asp	Ser	Thr	Ile	Pro	Arg	Ala	Asp	His	His	Phe	Ile	Lys	Lys	Pro	Arg	Asp	Ser	Thr	Ile	Pro	Arg	Ala	Asp	His	His	Phe	Ile	Lys
260										265										270																											
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<212> DNA
<213> Homo sapiens
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420
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480
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<211> 242

<212> PRT

<213> Homo sapiens

<400> 5614

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		20					25					30			
Leu	Arg	Lys	Phe	Arg	Glu	Leu	His	Leu	Met	Arg	Asn	Glu	Ala	Arg	Lys
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Leu	Asn	His	Gln	Glu	Val	Val	Glu	Glu	Asp	Lys	Arg	Leu	Lys	Leu	Pro
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Ala	Asn	Trp	Glu	Ala	Lys	Lys	Ala	Arg	Leu	Glu	Trp	Glu	Leu	Lys	Glu
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Glu	Glu	Lys	Lys	Lys	Glu	Cys	Ala	Ala	Arg	Gly	Glu	Asp	Tyr	Glu	Lys

	85		90		95
Val Lys Leu	Leu Glu Ile Ser Ala	Glu Asp Ala Glu Arg Trp	Glu Arg		
	100	105	110		
Lys Lys Lys	Arg Lys Asn Pro Asp	Leu Gly Phe Ser Asp	Tyr Ala Ala		
	115	120	125		
Ala Gln Leu	Arg Gln Tyr His Arg	Leu Thr Lys Gln	Ile Lys Pro Asp		
	130	135	140		
Met Glu Thr	Tyr Glu Arg Leu Arg	Glu Lys His Gly	Glu Glu Phe Phe		
	145	150	155	160	
Pro Thr Ser	Asn Ser Leu Leu His	Gly Thr His Val	Pro Ser Thr Glu		
	165	170	175		
Glu Ile Asp	Arg Met Val Ile Asp	Leu Glu Lys Gln	Ile Glu Lys Arg		
	180	185	190		
Asp Lys Tyr	Ser Arg Arg Arg Pro	Tyr Asn Asp Asp	Ala Asp Ile Asp		
	195	200	205		
Tyr Ile Asn	Glu Arg Asn Ala Lys	Phe Asn Lys Lys	Ala Glu Arg Phe		
	210	215	220		
Tyr Gly Lys	Tyr Thr Ala Glu Ile	Lys Gln Asn Leu	Glu Arg Gly Thr		
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<210> 5615

<211> 1522

<212> DNA

<213> Homo sapiens

<400> 5615

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<210> 5616

<211> 507

<212> PRT

<213> Homo sapiens

<400> 5616

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Gln Gln Gln Gln Gln Gly Val Leu Pro Gln Thr Val Pro Ser Gln Pro
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Ser Ser Ser Thr Val Pro Pro Pro His Arg Pro Leu Tyr Gln Pro
50 55 60
Met Gln Pro His Pro Gln His Leu Ala Ser Met Gly Phe Asp Pro Arg
65 70 75 80
Trp Leu Met Met Gln Ser Tyr Met Asp Pro Arg Met Met Ser Gly Arg
85 90 95
Pro Ala Met Asp Ile Pro Pro Ile His Pro Gly Met Ile Pro Pro Lys
100 105 110
Pro Leu Met Arg Arg Asp Gln Met Glu Gly Ser Pro Asn Ser Ser Glu
115 120 125
Ser Phe Glu His Ile Ala Arg Ser Ala Arg Asp His Ala Ile Ser Leu
130 135 140
Ser Glu Pro Arg Met Leu Trp Gly Ser Asp Pro Tyr Pro His Ala Glu
145 150 155 160
Pro Gln Gln Ala Thr Thr Pro Lys Ala Thr Glu Glu Pro Glu Asp Val

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Arg Ser Glu Ala Ala Leu Asp Gln Glu Gln Ile Thr Ala Ala Tyr Ser
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210          215          220
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225          230          235
Glu Ala Pro Asp Gln Lys Thr Leu Ser Thr Pro Gln Glu Glu Arg Ile
245          250          255
Ser Ala Val Glu Ser Gln Pro Ser Arg Lys Arg Ser Val Ser His Gly
260          265          270
Ser Asn His Thr Gln Lys Pro Asp Glu Gln Arg Ser Glu Pro Ser Ala
275          280          285
Gly Ile Pro Lys Val Thr Ser Arg Cys Ile Asp Ser Lys Glu Pro Ile
290          295          300
Glu Arg Pro Glu Glu Lys Pro Lys Lys Glu Gly Phe Ile Arg Ser Ser
305          310          315
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325          330          335
Trp Gly Pro Arg Pro Ser Ser Asn Arg Arg Glu Glu Val Asn Asp Arg
340          345          350
Pro Val Arg Arg Ser Gly Pro Ile Lys Lys Pro Val Leu Arg Asp Met
355          360          365
Lys Glu Glu Arg Glu Gln Arg Lys Glu Lys Glu Gly Glu Lys Ala Glu
370          375          380
Lys Val Thr Glu Lys Val Val Val Lys Pro Glu Lys Thr Glu Lys Lys
385          390          395
Asp Leu Pro Pro Pro Pro Pro Pro Gln Pro Pro Ala Pro Ile Gln
405          410          415
Pro Gln Ser Val Pro Pro Pro Ile Gln Pro Glu Ala Glu Lys Phe Pro
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435          440          445
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<210> 5617

<211> 3480

<212> DNA

<213> Homo sapiens

<400> 5617

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<210> 5618

<211> 1003

<212> PRT

<213> Homo sapiens

<400> 5618

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			20					25					30		
Thr	Thr	Pro	Lys	Ser	Phe	Leu	Glu	Gln	Ile	Ser	Leu	Phe	Lys	Asn	Leu
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Leu	Lys	Lys	Lys	Gln	Asn	Glu	Val	Ser	Glu	Lys	Lys	Glu	Arg	Leu	Val
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Asn	Gly	Ile	Gln	Lys	Leu	Lys	Thr	Thr	Ala	Ser	Gln	Val	Gly	Asp	Leu
65					70					75				80	
Lys	Ala	Arg	Leu	Ala	Ser	Gln	Glu	Ala	Glu	Leu	Gln	Leu	Arg	Asn	His
			85						90					95	
Asp	Ala	Glu	Ala	Leu	Ile	Thr	Lys	Ile	Gly	Leu	Gln	Thr	Glu	Lys	Val
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Ser	Arg	Glu	Lys	Thr	Ile	Ala	Asp	Ala	Glu	Glu	Arg	Lys	Val	Thr	Ala
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Ile	Gln	Thr	Glu	Val	Phe	Gln	Lys	Gln	Arg	Glu	Cys	Glu	Ala	Asp	Leu
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			165						170					175	
Ile	Ala	Val	Thr	Asn	Val	Thr	Ala	Ala	Val	Met	Val	Leu	Leu	Ala	Pro
	180						185						190		
Arg	Gly	Arg	Val	Pro	Lys	Asp	Arg	Ser	Trp	Lys	Ala	Ala	Lys	Val	Phe
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Met	Gly	Lys	Val	Asp	Asp	Phe	Leu	Gln	Ala	Leu	Ile	Asn	Tyr	Asp	Lys
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Glu	His	Ile	Pro	Glu	Asn	Cys	Leu	Lys	Val	Val	Asn	Glu	His	Tyr	Leu
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Lys	Asp	Pro	Glu	Phe	Asn	Pro	Asn	Leu	Ile	Arg	Thr	Lys	Ser	Phe	Ala
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Ala	Ala	Gly	Leu	Cys	Ala	Trp	Val	Ile	Asn	Ile	Ile	Lys	Phe	Tyr	Glu
		260					265						270		
Val	Tyr	Cys	Asp	Val	Glu	Pro	Lys	Arg	Gln	Ala	Leu	Ala	Gln	Ala	Asn
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Leu	Val	Val	Ser	Ala	Asn	Tyr	Asp	Ile	Glu	Lys	Ser	Glu	Lys	Ile	Arg
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Trp	Gly	Gln	Ser	Ile	Lys	Ser	Phe	Glu	Ala	Gln	Glu	Lys	Thr	Leu	Cys
			325					330						335	
Gly	Asp	Val	Leu	Leu	Thr	Ala	Ala	Phe	Val	Ser	Tyr	Val	Gly	Pro	Phe

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Ser Met Leu Thr Asp Asp Ala Thr Ile Ala Trp Asn Asn Glu Gly
385      390      395      400
Leu Pro Ser Asp Arg Met Ser Thr Glu Asn Ala Ala Ile Leu Thr His
      405      410      415
Cys Glu Arg Trp Pro Leu Val Ile Asp Pro Gln Gln Gln Gly Ile Lys
      420      425      430
Trp Ile Lys Asn Lys Tyr Gly Met Asp Leu Lys Val Thr His Leu Gly
      435      440      445
Gln Lys Gly Phe Leu Asn Ala Ile Glu Thr Ala Leu Ala Phe Gly Asp
      450      455      460
Val Ile Leu Ile Glu Asn Leu Glu Glu Thr Ile Asp Pro Val Leu Asp
465      470      475      480
Pro Leu Leu Gly Arg Asn Thr Ile Lys Lys Gly Lys Tyr Ile Arg Ile
      485      490      495
Gly Asp Lys Glu Cys Glu Phe Asn Lys Asn Phe Arg Leu Ile Leu His
      500      505      510
Thr Lys Leu Ala Asn Pro His Tyr Lys Pro Glu Leu Gln Ala Gln Thr
      515      520      525
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Leu Ala Glu Val Val Ser Ile Glu Arg Pro Asp Leu Glu Lys Leu Lys
545      550      555      560
Leu Val Leu Thr Lys His Gln Asn Asp Phe Lys Ile Glu Leu Lys Tyr
      565      570      575
Leu Glu Asp Asp Leu Leu Leu Arg Leu Ser Ala Ala Glu Gly Ser Phe
      580      585      590
Leu Asp Asp Thr Lys Leu Val Glu Arg Leu Glu Ala Thr Lys Thr Thr
      595      600      605
Val Ala Glu Ile Glu His Lys Val Ile Glu Ala Lys Glu Asn Glu Arg
      610      615      620
Lys Ile Asn Glu Ala Arg Glu Cys Tyr Arg Pro Val Ala Ala Arg Ala
625      630      635      640
Ser Leu Leu Tyr Phe Val Ile Asn Asp Leu Gln Lys Ile Asn Pro Leu
      645      650      655
Tyr Gln Phe Ser Leu Lys Ala Phe Asn Val Leu Phe His Arg Ala Ile
      660      665      670
Glu Gln Ala Asp Lys Val Glu Asp Met Gln Gly Arg Ile Ser Ile Leu
      675      680      685
Met Glu Ser Ile Thr His Ala Val Phe Leu Tyr Thr Ser Gln Ala Leu
      690      695      700
Phe Glu Lys Asp Lys Leu Thr Phe Leu Ser Gln Met Ala Phe Gln Ile
705      710      715      720
Leu Leu Arg Lys Lys Glu Ile Asp Pro Leu Glu Leu Asp Phe Leu Leu
      725      730      735
Arg Phe Thr Val Glu His Thr His Leu Ser Pro Val Asp Phe Leu Thr
      740      745      750
Ser Gln Ser Trp Ser Ala Ile Lys Ala Ile Ala Val Met Glu Glu Phe
      755      760      765
Arg Gly Ile Asp Arg Asp Val Glu Gly Ser Ala Lys Gln Trp Arg Lys

```

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      770              775              780
Trp Val Glu Ser Glu Cys Pro Glu Lys Glu Lys Leu Pro Gln Glu Trp
785              790              795
Lys Lys Lys Ser Leu Ile Gln Lys Leu Ile Leu Arg Ala Met Arg
      805              810              815
Pro Asp Arg Met Thr Tyr Ala Leu Arg Asn Phe Val Glu Glu Lys Leu
      820              825              830
Gly Ala Lys Tyr Val Glu Arg Thr Arg Leu Asp Leu Val Lys Ala Phe
      835              840              845
Glu Glu Ser Ser Pro Ala Thr Pro Ile Phe Phe Ile Leu Ser Pro Gly
      850              855              860
Val Asp Ala Leu Lys Asp Leu Glu Ile Leu Gly Lys Arg Leu Gly Phe
      865              870              875
Thr Ile Asp Ser Gly Lys Phe His Asn Val Ser Leu Gly Gln Gly Gln
      885              890              895
Glu Thr Val Ala Glu Val Ala Leu Glu Lys Ala Ser Lys Gly Gly His
      900              905              910
Trp Val Ile Leu Gln Asn Val His Leu Val Ala Lys Trp Leu Gly Thr
      915              920              925
Leu Glu Lys Leu Leu Glu Arg Phe Ser Gln Gly Ser His Arg Asp Tyr
      930              935              940
Arg Val Phe Met Ser Ala Glu Ser Ala Pro Thr Pro Asp Glu His Ile
      945              950              955
Ile Pro Gln Gly Leu Leu Glu Asn Ser Ile Lys Ile Thr Asn Glu Pro
      965              970              975
Pro Thr Gly Met Leu Ala Asn Leu His Ala Ala Leu Tyr Asn Phe Asp
      980              985              990
Gln Val Arg Lys Arg Ser Arg Leu Gly Arg Gln
      995              1000

```

<210> 5619

<211> 1219

<212> DNA

<213> Homo sapiens

<400> 5619

```

aagccggaga gctggagcct tgaagccacc ccggtcaaag gatgctgagt ccggagcgcc
60
tagccctacc ggactacgag tatctggctc agcgacatgt cctcacctac atggaggatg
120
cagtgtgcc a gctgctagaa aacaggggaag atattagcca atatggaatt gccaggttct
180
tcaatgaata ttttaacagt gtatgccagg gaacacacat tctctttcga gaattcagct
240
tcgtccaagc cccccccac aatagggtat catttttacg ggccttctgg agatgcttcc
300
gaactgtggg caaaaatggc gatttgctga ccatgaaaga atatcactgt ttgctgcaat
360
tactgtgtcc tgatttcccg ctggagctca ctcaaaaagc agccaggatt gtgctcatgg
420
acgatgccat ggactgcttg atgtcttttt cagatttcct ctttgcttc cagatccagt
480
tttactactc agaattcctg gacagtgtgg ctgccatcta tgaggacctg ctgtcaggca
540

```

agaaccccaa cacagtgatt gtgccgacgt cgtccagtg gacgaccgc caacgacctg
 600
 ccttggggcg ggcgggcacg ctggaggggc tggaggcgtc gctgttctac cagtgtctgg
 660
 aaaacctgtg tgatcggcac aagtacagct gccaccccc agcacttgtc aaagaggccc
 720
 tcagcaatgt tcagagactg accttctatg gattcctcat ggctctctca aagcaccgtg
 780
 gaatcaacca agccctcggg aagtcagagc taagcagcgg tcagcctctc ctgccgcaca
 840
 acacagggag cagctggcct ctgttagcaa cacggctcca gaggggaagg ggcataacca
 900
 tctctgcctt gacttcccag ggccggactc aatcccaggg agcaggaata tggcgacaaa
 960
 acatggctct tacacattcc catggtaggg gacagccctc ctcgcttgca gccctgcccc
 1020
 aacatgaaac cacctcccca tagcagaagc gccaccccc tcctcagaga acccagctc
 1080
 tgctttgggg agcagcctgc aggtcgggca gacacaggac tatttactca gtgacgctag
 1140
 agattatata tcagagagac ctgaatccca ttataaaca aggcaaagggt gtgtctgcgg
 1200
 agaccttttt tccaagctg
 1219

<210> 5620

<211> 333

<212> PRT

<213> Homo sapiens

<400> 5620

Met	Leu	Ser	Pro	Glu	Arg	Leu	Ala	Leu	Pro	Asp	Tyr	Glu	Tyr	Leu	Ala
1				5					10					15	
Gln	Arg	His	Val	Leu	Thr	Tyr	Met	Glu	Asp	Ala	Val	Cys	Gln	Leu	Leu
			20					25					30		
Glu	Asn	Arg	Glu	Asp	Ile	Ser	Gln	Tyr	Gly	Ile	Ala	Arg	Phe	Phe	Thr
			35				40					45			
Glu	Tyr	Phe	Asn	Ser	Val	Cys	Gln	Gly	Thr	His	Ile	Leu	Phe	Arg	Glu
			50			55				60					
Phe	Ser	Phe	Val	Gln	Ala	Thr	Pro	His	Asn	Arg	Val	Ser	Phe	Leu	Arg
65					70				75					80	
Ala	Phe	Trp	Arg	Cys	Phe	Arg	Thr	Val	Gly	Lys	Asn	Gly	Asp	Leu	Leu
			85					90					95		
Thr	Met	Lys	Glu	Tyr	His	Cys	Leu	Leu	Gln	Leu	Leu	Cys	Pro	Asp	Phe
			100				105						110		
Pro	Leu	Glu	Leu	Thr	Gln	Lys	Ala	Ala	Arg	Ile	Val	Leu	Met	Asp	Asp
			115				120					125			
Ala	Met	Asp	Cys	Leu	Met	Ser	Phe	Ser	Asp	Phe	Leu	Phe	Ala	Phe	Gln
			130			135				140					
Ile	Gln	Phe	Tyr	Tyr	Ser	Glu	Phe	Leu	Asp	Ser	Val	Ala	Ala	Ile	Tyr
145					150				155					160	
Glu	Asp	Leu	Leu	Ser	Gly	Lys	Asn	Pro	Asn	Thr	Val	Ile	Val	Pro	Thr
					165				170					175	
Ser	Ser	Ser	Gly	Gln	His	Arg	Gln	Arg	Pro	Ala	Leu	Gly	Gly	Ala	Gly

```

      180              185              190
Thr Leu Glu Gly Val Glu Ala Ser Leu Phe Tyr Gln Cys Leu Glu Asn
      195              200              205
Leu Cys Asp Arg His Lys Tyr Ser Cys Pro Pro Pro Ala Leu Val Lys
      210              215              220
Glu Ala Leu Ser Asn Val Gln Arg Leu Thr Phe Tyr Gly Phe Leu Met
      225              230              235              240
Ala Leu Ser Lys His Arg Gly Ile Asn Gln Ala Leu Gly Lys Ser Glu
      245              250              255
Leu Ser Ser Arg Gln Pro Leu Leu Pro His Asn Thr Gly Ser Ser Trp
      260              265              270
Pro Leu Leu Ala Thr Arg Leu Gln Arg Gly Arg Gly Ile Thr Ile Ser
      275              280              285
Ala Leu Thr Ser Gln Gly Arg Thr Gln Ser Gln Gly Ala Gly Ile Trp
      290              295              300
Arg Gln Asn Met Ala Leu Thr His Ser His Gly Arg Gly Gln Pro Ser
      305              310              315              320
Leu Pro Ala Ala Leu Pro Gln His Glu Thr Thr Ser Pro
      325              330

```

<210> 5621

<211> 456

<212> DNA

<213> Homo sapiens

<400> 5621

```

tttttgtgaa atagaattta ttgtggctct gattatgtac acgtgagatg gcctggctgg
60
gccggcgccggg ctcacatggt ttgtacaata aatacatctg tggggcgggc tctccgcagc
120
cggggaagggc caccgccacg gttcagtcga gcttcggggc tcccagcttc atggggccct
180
tgggccacctt cctctcgggc ggtttggcct ccattctccc ccgccgtcc tcgcgttct
240
tccggggccag ctcagccttg acctgtcctg ggtgtctggga cgtgcagaca gggtagcgaa
300
gggggtcgccc ttgtcgcttg actctggggc accccagtta tactcgctgg ccagccgtgt
360
accgtcagga ggtggctcct gggagcttgg ctgaaccctg ggcggtggcc cttcccggtc
420
gcggagagcc cgcgccacag atgtatttat tgtaca
456

```

<210> 5622

<211> 82

<212> PRT

<213> Homo sapiens

<400> 5622

```

Met Ala Trp Leu Gly Arg Pro Gly Ser His Gly Leu Tyr Asn Lys Tyr
1      5      10      15
Ile Cys Gly Ala Gly Ser Pro Gln Pro Gly Arg Ala Thr Ala Thr Val
20      25      30
Gln Ser Ser Phe Arg Ala Pro Ser Phe Met Gly Pro Leu Ala Thr Phe

```

```

          35              40              45
Leu Ser Ala Arg Leu Ala Ser Ile Ser Arg Arg Arg Ser Ser Arg Phe
          50              55              60
Phe Arg Ala Ser Ser Ala Leu Thr Cys Pro Gly Cys Trp Asp Val Gln
65              70              75              80
Thr Gly

```

<210> 5623
 <211> 357
 <212> DNA
 <213> Homo sapiens

```

<400> 5623
nctggaagaa ctcgtcatgc tctttgtagc gtggtgcttc tgttgcacac aggacaactt
60
gcctttgatg attttcaaga gattttgct atgatgtggc aaaagtatgc aggaagcagg
120
cggtcaatgc ctctgggagc aaggatcctt ttccacggtg tgttctatgc cgggggcttt
180
gccattgtgt attacctcat tcaaaagttt cattccaggg ctttatatta caagttggca
240
gtggagcagc tgcagagcca tcccgaggca caggaagctc tgggccctcc tctcaacatc
300
cattatctca agctcatcga cagggaanaac ttcgtggaca ttgttgatgc caagttg
357

```

<210> 5624
 <211> 88
 <212> PRT
 <213> Homo sapiens

```

<400> 5624
Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly Ala
1          5          10          15
Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile Val
          20          25          30
Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys Leu
          35          40          45
Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu Gly
          50          55          60
Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn Phe
65          70          75          80
Val Asp Ile Val Asp Ala Lys Leu
          85

```

<210> 5625
 <211> 1017
 <212> DNA
 <213> Homo sapiens

```

<400> 5625
gccgactcgt ggtacctggc gcttctgggc ttcgtgagc acttccgcac ttccagcccg
60

```

```

ccccaaatcc gcctgtgcgt gcactgcctg caggccgtgt tccccctcaa gccgcccag
120
cgcatcgagg cccgtacaca cctgcagctg ggctccgttc tctatcacca caccaagaac
180
agcgagcagg cgcgcagcca cctggagaag gcgtgggtga tatcacagca aatccccacg
240
ttcgaagatg ttaaatattg agcagcaagt ctgttgtctg aattgtactg tcaagagaat
300
tccgttgatg cagcaaagcc gctgctgcgg aaggcgatcc agatctcaca gcagacccca
360
tattggcact gccgctgct cttccagctc gctcaactgc acacgcttga gaaggacctg
420
gtgtcggcct gtgacctcct ggggtgtagg gccgagtag cccgggtggg gggatctgaa
480
tacacacggg cgctgttcct cctcagcaag gggatgtctg tgctgatgga gcgaaagctg
540
caggaggtgc acccgctgct gaccctctgc gggcagatcg tggagaactg gcaggggaac
600
cccattccaga aggagtcgct gcgtgtcttc ttctgggtgc tccagggtcac ccactatctg
660
gatgccgggc aggtgaagag cgtgaagccg tgtctgaagc agctgcagca gtgcatccag
720
accatctcca cactgcacga tgatgagatc ctgccacga accccgctga cctcttccac
780
tggctgcccc aggagcacat gtgtgtgctt gtctacctgg tgactgtgat gcactccatg
840
caggccggct acctggagaa ggcgcagaag tacacggaca aggccctcat gcagctggag
900
aagctcaaga tgctggactg cagccccatc ctgtcatcct tccaagtgat cctgctggag
960
cacatcatca tgtgccgcct tgtcacgggt cacaaggcca cggcgtgca ggagatc
1017

```

<210> 5626

<211> 339

<212> PRT

<213> Homo sapiens

<400> 5626

```

Ala Asp Ser Trp Tyr Leu Ala Leu Leu Gly Phe Ala Glu His Phe Arg
 1           5           10           15
Thr Ser Ser Pro Pro Lys Ile Arg Leu Cys Val His Cys Leu Gln Ala
      20           25           30
Val Phe Pro Phe Lys Pro Pro Gln Arg Ile Glu Ala Arg Thr His Leu
      35           40           45
Gln Leu Gly Ser Val Leu Tyr His His Thr Lys Asn Ser Glu Gln Ala
      50           55           60
Arg Ser His Leu Glu Lys Ala Trp Leu Ile Ser Gln Gln Ile Pro Gln
      65           70           75           80
Phe Glu Asp Val Lys Phe Glu Ala Ala Ser Leu Leu Ser Glu Leu Tyr
      85           90           95
Cys Gln Glu Asn Ser Val Asp Ala Ala Lys Pro Leu Leu Arg Lys Ala
      100          105          110
Ile Gln Ile Ser Gln Gln Thr Pro Tyr Trp His Cys Arg Leu Leu Phe

```



```

      115              120              125
Gln Leu Ala Gln Leu His Thr Leu Glu Lys Asp Leu Val Ser Ala Cys
130              135              140
Asp Leu Leu Gly Val Gly Ala Glu Tyr Ala Arg Val Val Gly Ser Glu
145              150              155              160
Tyr Thr Arg Ala Leu Phe Leu Leu Ser Lys Gly Met Leu Leu Leu Met
      165              170              175
Glu Arg Lys Leu Gln Glu Val His Pro Leu Leu Thr Leu Cys Gly Gln
      180              185              190
Ile Val Glu Asn Trp Gln Gly Asn Pro Ile Gln Lys Glu Ser Leu Arg
      195              200              205
Val Phe Phe Leu Val Leu Gln Val Thr His Tyr Leu Asp Ala Gly Gln
      210              215              220
Val Lys Ser Val Lys Pro Cys Leu Lys Gln Leu Gln Gln Cys Ile Gln
225              230              235              240
Thr Ile Ser Thr Leu His Asp Asp Glu Ile Leu Pro Ser Asn Pro Ala
      245              250              255
Asp Leu Phe His Trp Leu Pro Lys Glu His Met Cys Val Leu Val Tyr
      260              265              270
Leu Val Thr Val Met His Ser Met Gln Ala Gly Tyr Leu Glu Lys Ala
      275              280              285
Gln Lys Tyr Thr Asp Lys Ala Leu Met Gln Leu Glu Lys Leu Lys Met
      290              295              300
Leu Asp Cys Ser Pro Ile Leu Ser Ser Phe Gln Val Ile Leu Leu Glu
305              310              315              320
His Ile Ile Met Cys Arg Leu Val Thr Gly His Lys Ala Thr Ala Leu
      325              330              335
Gln Glu Ile

```

<210> 5627

<211> 1401

<212> DNA

<213> Homo sapiens

<400> 5627

```

nctctcacac tgtggaattc tctctatcag cctcaaagtc cagatttggg aagggagtct
60
cagcgagggg cagcagctgg cccaaccggg aggcagagcg gcaactgaac tctagccgga
120
aagagccagg gttatgtgca catgggaggt ggggaggaca ggggctgtat gtgacctca
180
catctgttcc tcgcgcccc gatggcttct gctgcctgct ccatggagcc catcgacagc
240
tttgagctcc tggatctcct gtttgaccgg caggacggca tcttgagaca cgtggagctg
300
ggcgagggct ggggtcacgt caaggaccag gtccctgccaa accccgactc tgacgacttc
360
ctcagctcca tcttgggctc tggagactca ctgccagct cccactctgt gtccccgaa
420
ggcagtgata gtggcatctc cgaagacctc ccctccgacc cccaggacac ccctccacgc
480
agcggaccag ccacctcccc cgccggctgc catcctgccc agcctggcaa ggggacctgc
540

```

ctctcctatc atcctggcaa ctcttgctcc accacaaccc caggggccagt gatccaacaa
 600
 cagcatcacc tgggggcttc ctacctcctg cgacctgggg ctggggcactg tcaggagctg
 660
 gtgctcaccg aggatgagaa gaagctgctg gctaaagaag gcatcacctc gccactcag
 720
 ctgccccctca ctaagtacga ggagcgagtg ctgaaaaaaa tccgcgggaa aatccggaac
 780
 aagcagtcgg cgcaagaaag caggaagaag aagaaggaat atatcgatgg cctggagact
 840
 cggtcctgtt gctgtccttt gccctcatca tctctccctc catcagccct tttggcccca
 900
 acaaaaaccga gagccctggg gactttgctg ctgtacgagt gttctccaga actttgcaca
 960
 acgatgtctc ctcccgctg gctgtgtgat ctgtgccagg ctccgaggcc ccaggaccct
 1020
 gacccgaggc tgacacaacc cgagaagagt ctccaggaag ccccggggca gactggggct
 1080
 tccaggacac cgcaacctg accaattcga cggaggagct ggacaacgcc accctgggtc
 1140
 tgagggaatg aacagagggg ctggggccagg tcgccctgct ggactgggtg ggcctggggc
 1200
 cgagcactgg ctcaggacgt gcagggtctg aggcggcggg agacgagctg tgagcccccac
 1260
 caggactatg ctcccgaggc cctctgccca ggggtgcctt ggggatgctg cactggggcag
 1320
 ctaccacact ggggatggga cgtgaggcca agacccacgc agagatgcca gaatggggga
 1380
 ggcacagctc atagccacac a
 1401

<210> 5628

<211> 299

<212> PRT

<213> Homo sapiens

<400> 5628

Met	Ala	Ser	Ala	Ala	Cys	Ser	Met	Asp	Pro	Ile	Asp	Ser	Phe	Glu	Leu
1			5						10					15	
Leu	Asp	Leu	Leu	Phe	Asp	Arg	Gln	Asp	Gly	Ile	Leu	Arg	His	Val	Glu
		20						25					30		
Leu	Gly	Glu	Gly	Trp	Gly	His	Val	Lys	Asp	Gln	Val	Leu	Pro	Asn	Pro
		35				40					45				
Asp	Ser	Ser	Asp	Phe	Leu	Ser	Ser	Ile	Leu	Gly	Ser	Gly	Asp	Ser	Leu
	50				55						60				
Pro	Ser	Ser	Pro	Leu	Trp	Ser	Pro	Glu	Gly	Ser	Asp	Ser	Gly	Ile	Ser
	65			70					75				80		
Glu	Asp	Leu	Pro	Ser	Asp	Pro	Gln	Asp	Thr	Pro	Pro	Arg	Ser	Gly	Pro
			85						90				95		
Ala	Thr	Ser	Pro	Ala	Gly	Cys	His	Pro	Ala	Gln	Pro	Gly	Lys	Gly	Pro
		100					105					110			
Cys	Leu	Ser	Tyr	His	Pro	Gly	Asn	Ser	Cys	Ser	Thr	Thr	Thr	Pro	Gly
		115					120				125				
Pro	Val	Ile	Gln	Gln	Gln	His	His	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	Arg

```

      130              135              140
Pro Gly Ala Gly His Cys Gln Glu Leu Val Leu Thr Glu Asp Glu Lys
145              150              155              160
Lys Leu Leu Ala Lys Glu Gly Ile Thr Leu Pro Thr Gln Leu Pro Leu
      165              170              175
Thr Lys Tyr Glu Glu Arg Val Leu Lys Lys Ile Arg Arg Lys Ile Arg
      180              185              190
Asn Lys Gln Ser Ala Gln Glu Ser Arg Lys Lys Lys Lys Glu Tyr Ile
      195              200              205
Asp Gly Leu Glu Thr Arg Ser Cys Cys Cys Pro Leu Pro Ser Ser Ser
      210              215              220
Ser Pro Pro Ser Ala Leu Leu Ala Pro Thr Lys Pro Arg Ala Leu Gly
225              230              235              240
Thr Leu Arg Leu Tyr Glu Cys Ser Pro Glu Leu Cys Thr Thr Met Leu
      245              250              255
Pro Pro Ala Trp Leu Leu Met Leu Cys Gln Ala Pro Arg Pro Gln Asp
      260              265              270
Pro Asp Pro Arg Leu Thr Gln Pro Glu Lys Ser Leu Gln Glu Ala Pro
      275              280              285
Gly Gln Thr Gly Ala Ser Arg Thr Pro Arg Thr
      290              295

```

<210> 5629

<211> 428

<212> DNA

<213> Homo sapiens

<400> 5629

```

gtgcacgacc ccactgaatc atcccacaac catggatggg agacacactc agtctccttt
60
aacagaagat aaagctgggg cttacagaga atgtacaact tggcccaggg cacaccagtt
120
agccatcagg ggcagngctg ctattcaggt ctgggactgt gggactccag agcccatggt
180
ttttacgagg atgccatact gccacaatgg atggtgtctt tatctctga tatatgattg
240
tgtgttggga ggcgtggggg ggcagctgga agaatggaga ggcataattg tggaggatct
300
tccccattc tctgtaccc tctcttggag ctcccagttc catctgagaa attatctact
360
ctgagaaatc gtcacaacac agcatggttg tgagtgcagt ggcagaagcc tgtgacctgt
420
tgtatggg
428

```

<210> 5630

<211> 110

<212> PRT

<213> Homo sapiens

<400> 5630

```

Met Asp Gly Arg His Thr Gln Ser Pro Leu Thr Glu Asp Lys Ala Gly
1          5          10          15
Ala Tyr Arg Glu Cys Thr Thr Trp Pro Arg Ala His Gln Leu Ala Ile

```


1	5	10	15
Ala Gly Ala Gly Ala Gly His Leu Thr Pro Gln Ala Ser Pro Thr Ser			
	20	25	30
Glu Leu Pro Thr Ala Lys Thr Pro Gly Glu Ala Gly Arg Gly Gly Val			
	35	40	45
Arg Gly Lys Glu Gly Leu Cys Glu Ser Lys Pro His Pro Gln Ser Arg			
	50	55	60
Ala Glu Thr Gln Val Cys Lys Ser His Pro Pro Pro Thr Ser Ser Ser			
	65	70	75
Phe Glu Ala Ser Ser Thr Arg Gly Arg Ala Gly Ala Ala Gln Arg Pro			
	85	90	95
Glu Lys Gly Lys Pro His Arg Arg Lys Leu Lys Ala Ser Val Pro Cys			
	100	105	110
Val Ser Ala Glu Arg Val Asn Gly Pro Lys Gly Ser Ser Leu Gln Thr			
	115	120	125
Ala Arg Ile His Pro Thr Gly Gly His Arg Thr Arg Pro Gly Pro Ser			
	130	135	140
Ala Ser Val Pro Val Gln Pro Thr Pro Val Gln Pro Gly Ala Leu Ser			
	145	150	155
Asp Leu Thr Thr Arg Val Pro Ser Thr Cys Val His Thr Gln Met Gln			
	165	170	175
Glu Arg Thr His Thr Thr Val			
	180		

<210> 5633

<211> 2181

<212> DNA

<213> Homo sapiens

<400> 5633

gccaatgtcc ctgtggccac tcagctgaga ccgaggcgca cctgggcagc tgcgggtgtc
60
tgtaacctcc gtgtcccaca tagatgccag gctctgcttc tegtgttctg gaggtcatta
120
gtcaattgta tgtggtgctg tctgtcctcc tgattgcaga ggaggaagga accccctaaa
180
tgagcgggtt ctgagtgtg gggccgctgg tctgctctgc ctggtgggat tctccagtgc
240
tggttctatc tgtgccccag cccactctc accaacaagg agggcgtaga aatgacaagg
300
aatccatccc tagagttcac aggagatcta gggcagagtt tccaagctgc agctgctctg
360
gccctgtgtg agctgtgtgt ctgaggaagc cccaggctga ggtagctacc aggcggaggc
420
tgggttttga ggcctccaca tcaggaatt gagcggtagg ggtttcagcc ttcacgttgg
480
tcgcgcact gtatgggaag tggggtctgg ggtctgcttg cccagtctca ccgtcctctt
540
cctcccaaaa gccgcctgga taaggggctg gccgcactgg tcggggagcg tggcgcggat
600
ctgggtgtga tcgagggcat gggccgtgct gtccacacaa actaccacgc agccctgcgc
660
tgcgagagcc tcaagctggc cgatcatcaag aacgcgtggc tggccgagcg gctggggcgg
720

cggtctttca ggcctatctt caagtacgag gtcccagccg agtgaggcgc tgcagctgcc
780
ggactcttct gcttgtcact tgtccgagtg gcttcagaga ttaaaggggc cccctcataa
840
atgtgcctta attttcgag ataacagggg gaatagacat ctttttgga gtcttcccc
900
ttgtcagggg gctactcctt agagggacag aggtcctcct ggctgcaac tcaggccccg
960
ccctgaacga cgtgaccac agcagagccc tcatcgtggc agagcgtatt gcgggcatgg
1020
accctgaccg tgcgcagcct gctggacacc agggagcact gtctgaacga gttcaacttc
1080
ccggatccct actccaaagt gaagcagcgg gagaatggcg tggcgctgag gtgcttcccc
1140
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<210> 5634

<211> 289

<212> PRT

<213> Homo sapiens

<400> 5634

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Phe Asn Phe Pro Asp Pro Tyr Ser Lys Val Lys Gln Arg Glu Asn Gly
          35          40          45
Val Ala Leu Arg Cys Phe Pro Gly Val Val Arg Ser Leu Asp Ala Leu
50          55          60
Gly Trp Glu Glu Arg Gln Leu Ala Leu Val Lys Gly Leu Leu Ala Gly
65          70          75          80
Asn Val Phe Asp Trp Gly Ala Lys Ala Val Ser Ala Val Leu Glu Ser
          85          90          95
Asp Pro Tyr Phe Gly Phe Glu Glu Ala Lys Arg Lys Leu Gln Glu Arg
100          105          110
Pro Trp Leu Val Asp Ser Tyr Ser Glu Trp Leu Gln Arg Leu Lys Gly
115          120          125
Pro Pro His Lys Cys Ala Leu Ile Phe Ala Asp Asn Ser Gly Ile Asp
130          135          140
Ile Ile Leu Gly Val Phe Pro Phe Val Arg Glu Leu Leu Leu Arg Gly
145          150          155          160
Thr Glu Val Ile Leu Ala Cys Asn Ser Gly Pro Ala Leu Asn Asp Val
165          170          175
Thr His Ser Glu Ser Leu Ile Val Ala Glu Arg Ile Ala Gly Met Asp
180          185          190
Pro Val Val His Ser Ala Leu Gln Glu Glu Arg Leu Leu Leu Val Gln
195          200          205
Thr Gly Ser Ser Ser Pro Cys Leu Asp Leu Ser Arg Leu Asp Lys Gly
210          215          220
Leu Ala Ala Leu Val Arg Glu Arg Gly Ala Asp Leu Val Val Ile Glu
225          230          235          240
Gly Met Gly Arg Ala Val His Thr Asn Tyr His Ala Ala Leu Arg Cys
245          250          255
Glu Ser Leu Lys Leu Ala Val Ile Lys Asn Ala Trp Leu Ala Glu Arg
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<210> 5635

<211> 614

<212> DNA

<213> Homo sapiens

<400> 5635

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<210> 5636

<211> 204

<212> PRT

<213> Homo sapiens

<400> 5636

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		35				40						45			
Leu	Ala	Cys	Gln	Ile	Tyr	Glu	Asn	Asn	Pro	Gln	Leu	Lys	Glu	Ser	Leu
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65				70						75				80	
His	Tyr	Ala	Ala	Arg	His	Gly	Met	Asn	Lys	Ile	Leu	Gly	Asp	Asp	Phe
				85				90					95		
Arg	Arg	Ala	Asp	Cys	Leu	Gln	Met	Ile	Leu	Lys	Trp	Lys	Gly	Ala	Lys
		100						105				110			
Leu	Asp	Gln	Gly	Glu	Tyr	Glu	Arg	Ala	Ala	Ile	Asp	Ala	Val	Asp	Asn
	115					120					125				
Lys	Lys	Asn	Thr	Pro	Leu	His	Tyr	Ala	Ala	Ala	Ser	Gly	Met	Lys	Ala
	130					135					140				
Cys	Val	Glu	Lys	His	Gly	Gly	Asp	Leu	Phe	Ala	Glu	Asn	Glu	Asn	Lys
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Asp	Thr	Pro	Cys	Asp	Cys	Ala	Glu	Lys	Gln	His	His	Lys	Asp	Leu	Ala
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<210> 5637

<211> 825

<212> DNA

<213> Homo sapiens

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<210> 5638

<211> 132

<212> PRT

<213> Homo sapiens

<400> 5638

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Leu	Asn	Ile	Asn	Lys	Ser	Asp	Ser	His	Ser	Pro	Thr	Val	Leu	Ala	Ser
			20					25						30	
Leu	Thr	Gly	Ala	Arg	Trp	Phe	Cys	Asp	Pro	Ser	Gln	Ala	His	Ala	Pro
		35					40					45			
Leu	Ala	Gly	Arg	Leu	Ala	Arg	Ala	Pro	Leu	Trp	Leu	Ala	Cys	Gly	Asp
		50				55					60				
Thr	Trp	Ala	Leu	Leu	His	Val	Pro	Thr	Arg	Ala	Val	Ala	Gly	Ser	Lys
		65			70				75					80	
Glu	Ala	Gln	Pro	Arg	Pro	Ala	Cys	Val	Asp	Pro	Ala	Gly	Leu	Arg	Ala
			85						90					95	
Pro	Glu	Leu	Leu	Thr	Val	Ser	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Arg	Arg
			100					105						110	
Pro	Pro	Ser	Ser	Cys	Pro	Ala	Trp	Asp	Pro	Ser	Ala	Val	Cys	Leu	Leu
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130

<210> 5639

<211> 2433

<212> DNA

<213> Homo sapiens

<400> 5639

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<210> 5640

<211> 540

<212> PRT

<213> Homo sapiens

<400> 5640

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			20					25					30		
Ala	Ser	Ala	Pro	Gln	Glu	Lys	Leu	Ser	Ser	Glu	Val	Glu	Asp	Pro	Pro
			35				40					45			
Pro	Tyr	Leu	Met	Met	Asp	Glu	Leu	Leu	Gly	Arg	Gln	Arg	Lys	Val	Tyr
			50			55					60				
Leu	Glu	Thr	Tyr	Gly	Cys	Gln	Met	Asn	Val	Asn	Asp	Thr	Glu	Ile	Ala
					70				75					80	
Trp	Ser	Ile	Leu	Gln	Lys	Ser	Gly	Tyr	Leu	Arg	Pro	Val	Thr	Ser	Lys

			85				90				95				
Ala	Asp	Val	Ile	Leu	Leu	Val	Thr	Cys	Ser	Ile	Arg	Glu	Lys	Ala	Glu
			100					105				110			
Gln	Thr	Ile	Trp	Asn	Arg	Leu	His	Gln	Leu	Lys	Ala	Leu	Lys	Thr	Arg
			115					120				125			
Arg	Pro	Arg	Ser	Arg	Val	Pro	Leu	Arg	Ile	Gly	Ile	Leu	Gly	Cys	Met
			130					135				140			
Ala	Glu	Arg	Leu	Lys	Glu	Glu	Ile	Leu	Asn	Arg	Glu	Lys	Met	Val	Asp
			145					150			155			160	
Ile	Leu	Ala	Gly	Pro	Asp	Ala	Tyr	Arg	Asp	Leu	Pro	Arg	Leu	Leu	Ala
			165					170					175		
Val	Ala	Glu	Ser	Gly	Gln	Gln	Ala	Ala	Asn	Val	Leu	Leu	Ser	Leu	Asp
			180					185					190		
Glu	Thr	Tyr	Ala	Asp	Val	Met	Pro	Val	Gln	Thr	Ser	Ala	Ser	Ala	Thr
			195					200				205			
Ser	Ala	Phe	Val	Ser	Ile	Met	Arg	Gly	Cys	Asp	Asn	Met	Cys	Ser	Tyr
			210					215				220			
Cys	Ile	Val	Pro	Phe	Thr	Arg	Gly	Arg	Glu	Arg	Ser	Arg	Pro	Ile	Ala
			225					230				235		240	
Ser	Ile	Leu	Glu	Glu	Val	Lys	Lys	Leu	Ser	Glu	Gln	Gly	Leu	Lys	Glu
			245					250					255		
Val	Thr	Leu	Leu	Gly	Gln	Asn	Val	Asn	Ser	Phe	Arg	Asp	Asn	Ser	Glu
			260					265					270		
Val	Gln	Phe	Asn	Ser	Ala	Val	Pro	Thr	Asn	Leu	Ser	Arg	Gly	Phe	Thr
			275					280					285		
Thr	Asn	Tyr	Lys	Thr	Lys	Gln	Gly	Gly	Leu	Arg	Phe	Ala	His	Leu	Leu
			290					295				300			
Asp	Gln	Val	Ser	Arg	Val	Asp	Pro	Glu	Met	Arg	Ile	Arg	Phe	Thr	Ser
			305					310				315		320	
Pro	His	Pro	Lys	Asp	Phe	Pro	Asp	Glu	Val	Leu	Gln	Leu	Ile	His	Glu
			325					330					335		
Arg	Asp	Asn	Ile	Cys	Lys	Gln	Ile	His	Leu	Pro	Ala	Gln	Ser	Gly	Ser
			340					345					350		
Ser	Arg	Val	Leu	Glu	Ala	Met	Arg	Arg	Gly	Tyr	Ser	Arg	Glu	Ala	Tyr
			355					360				365			
Val	Glu	Leu	Val	His	His	Ile	Arg	Glu	Ser	Ile	Pro	Gly	Val	Ser	Leu
			370					375				380			
Ser	Ser	Asp	Phe	Ile	Ala	Gly	Phe	Cys	Gly	Glu	Thr	Glu	Glu	Asp	His
			385					390				395		400	
Val	Gln	Thr	Val	Ser	Leu	Leu	Arg	Glu	Val	Gln	Tyr	Asn	Met	Gly	Phe
			405					410					415		
Leu	Phe	Ala	Tyr	Ser	Met	Arg	Gln	Lys	Thr	Arg	Ala	Tyr	His	Arg	Leu
			420					425				430			
Lys	Asp	Asp	Val	Pro	Glu	Glu	Val	Lys	Leu	Arg	Arg	Leu	Glu	Glu	Leu
			435					440				445			
Ile	Thr	Ile	Phe	Arg	Glu	Glu	Ala	Thr	Lys	Ala	Asn	Gln	Thr	Ser	Val
			450					455				460			
Gly	Cys	Thr	Gln	Leu	Val	Leu	Val	Glu	Gly	Leu	Ser	Lys	Arg	Ser	Ala
			465					470				475		480	
Thr	Asp	Leu	Cys	Gly	Arg	Asn	Asp	Gly	Asn	Leu	Lys	Val	Ile	Phe	Pro
			485					490					495		
Asp	Ala	Glu	Met	Glu	Asp	Val	Asn	Asn	Pro	Gly	Leu	Arg	Val	Arg	Ala
			500					505				510			
Gln	Pro	Gly	Asp	Tyr	Val	Leu	Val	Lys	Ile	Thr	Xaa	Gln	Pro	Val	Leu

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<210> 5641
<211> 293
<212> DNA
<213> Homo sapiens

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<210> 5642
<211> 87
<212> PRT
<213> Homo sapiens

<400> 5642
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20 25 30
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35 40 45
Ala Gly Ala Pro Leu Ala Ser Leu Glu Ser Gln Val Arg Arg Ala Asp
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Thr Ser Arg Asn Ser Ser Gln Cys Ser Arg Ser Leu Gly Arg Pro Thr
65 70 75 80
Ser Pro Leu His Pro Thr Ala
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<210> 5643
<211> 1218
<212> DNA
<213> Homo sapiens

<400> 5643
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<210> 5644

<211> 202

<212> PRT

<213> Homo sapiens

<400> 5644

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 35 40 45
 Asp Val Asp His Pro Gly Glu Ala Asp Ser Val Leu Arg Gly Ser Ser
 50 55 60
 Gln Val Gln Ala Arg Gly Arg Ala Leu Asn Ile Val Asp Gln Glu Gly
 65 70 75 80
 Ser Leu Leu Gly Lys Gly Glu Thr Gln Gly Leu Leu Thr Ala Lys Gly
 85 90 95
 Gly Val Gly Lys Leu Val Thr Leu Arg Asn Val Ser Thr Lys Lys Ile

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          100              105              110
Pro Thr Val Asn Arg Ile Thr Pro Lys Thr Gln Gly Thr Asn Gln Ile
          115              120              125
Gln Lys Asn Thr Pro Ser Pro Asp Val Thr Leu Gly Thr Asn Pro Gly
          130              135              140
Thr Glu Asp Ile Gln Phe Pro Ile Gln Lys Ile Pro Leu Gly Leu Asp
          145              150              155              160
Leu Lys Asn Leu Arg Leu Pro Arg Arg Lys Met Ser Phe Asp Ile Ile
          165              170              175
Asp Lys Ser Asp Val Phe Ser Arg Phe Gly Ile Glu Ile Ile Lys Trp
          180              185              190
Ala Gly Phe His Thr Ile Lys Leu Asp Tyr
          195              200

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<210> 5645
 <211> 156
 <212> DNA
 <213> Homo sapiens

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<400> 5645
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cttcagatca gtttcccctc tcccaggcaa gaggacacga gcaactggcaa gttcacctgc
120
aaagtccccg gctctacta ctttgtctac caccg
156

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<210> 5646
 <211> 52
 <212> PRT
 <213> Homo sapiens

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<400> 5646
Pro Arg Pro Ser Arg Arg Arg Asn Cys Arg Trp Ala Val Phe Gly Leu
1      5      10      15
Ala Gln Arg Cys Pro Gln Ile Ser Phe Pro Ser Pro Arg Gln Glu Asp
20     25     30
Thr Ser Thr Gly Lys Phe Thr Cys Lys Val Pro Gly Leu Tyr Tyr Phe
35     40     45
Val Tyr His Ala
50

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<210> 5647
 <211> 150
 <212> DNA
 <213> Homo sapiens

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<400> 5647
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aggcccaagg gggagccagg aatcccagcc attcccggga tccgaggacc caaagggcag
120
aagggagaac ccggttacc cggccatccn
150

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<210> 5648
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 5648
 Pro Met Gly Pro Gly Thr Leu Ala Phe Pro Gly Gly Pro Met Gly Pro
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 Phe Phe Pro Gly Arg Pro Lys Gly Glu Pro Gly Ile Pro Ala Ile Pro
 20 25 30
 Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu Pro Gly
 35 40 45
 His Pro
 50

<210> 5649
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 5649
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 aaccgcctgg tccctcggat cgcgccccagc ccagactcgg actcggacac agactcggag
 120
 gacccgagtc tccggcgag cgcggggcgcc ttgctccgct cgcaggtcat ccacagcggg
 180
 cacttcattg tgctcgcgc gcacagcgac tcgctgcccc ggcggcgcgca ccaggagggt
 240
 ccgtggggcc ctccgacttc gggccgcgca gtatcgaccc cacactcaca cgccctcttcg
 300
 agtgcttgag cctggcctac agtggcaagc tggggctctcc caagt
 345

<210> 5650
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 5650
 Met Ala Val Ala Ala Ala Thr Ala Trp Ser Leu Gly Ser Arg Pro Ala
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 Gln Thr Arg Thr Arg Thr Gln Thr Arg Arg Thr Arg Val Ser Gly Ala
 20 25 30
 Ala Arg Ala Ala Cys Ser Ala Arg Arg Ser Ser Thr Ala Val Thr Ser
 35 40 45
 Trp Cys Arg Arg Arg Thr Ala Thr Arg Cys Pro Gly Gly Ala Thr Arg
 50 55 60
 Arg Val Arg Gly Ala Leu Arg Leu Arg Ala Ala Gln Tyr Arg Pro His
 65 70 75 80
 Thr His Thr Pro Leu Arg Val Leu Glu Pro Gly Leu Gln Trp Gln Ala
 85 90 95
 Gly Val Ser Gln

100

<210> 5651
 <211> 615
 <212> DNA
 <213> Homo sapiens

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 ctgcgccatga agagccgctt tagcaccatt gacctccgcg ccgtactcgc ggagctgaat
 180
 gctagcttgc taggaatgag agtaaacaaat gtttatgatg tggataataa gacatacctt
 240
 attcgtcttc aaaaaccgga cttaaagct acacttttac ttgaatctgg catacaaatt
 300
 catacaacag aatttgagtgc gcctaagaat atgatgcgct ctagttttgc catgaagtgc
 360
 cgaaaacatt tgaagagtcg gagattagtc agtgcaaaac agcttggtgt ggatagaatt
 420
 gtagattttc aatttggaag tgatgaagct gcttaccatt taatcattga gctctatgat
 480
 agggggaaca ttgttcttac agattatgag tacgtaattt taaatattct aagggttcga
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 600
 agagctgctg aacct
 615

<210> 5652
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 5652
 Met Lys Ser Arg Phe Ser Thr Ile Asp Leu Arg Ala Val Leu Ala Glu
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 Leu Asn Ala Ser Leu Leu Gly Met Arg Val Asn Asn Val Tyr Asp Val
 20 25 30
 Asp Asn Lys Thr Tyr Leu Ile Arg Leu Gln Lys Pro Asp Phe Lys Ala
 35 40 45
 Thr Leu Leu Leu Glu Ser Gly Ile Gln Ile His Thr Thr Glu Phe Glu
 50 55 60
 Trp Pro Lys Asn Met Met Pro Ser Ser Phe Ala Met Lys Cys Arg Lys
 65 70 75 80
 His Leu Lys Ser Arg Arg Leu Val Ser Ala Lys Gln Leu Gly Val Asp
 85 90 95
 Arg Ile Val Asp Phe Gln Phe Gly Ser Asp Glu Ala Ala Tyr His Leu
 100 105 110
 Ile Ile Glu Leu Tyr Asp Arg Gly Asn Ile Val Leu Thr Asp Tyr Glu
 115 120 125
 Tyr Val Ile Leu Asn Ile Leu Arg Phe Arg Thr Asp Glu Ala Asp Asp

130	135	140
Val Lys Phe Ala Val Arg Glu Arg Tyr Pro Leu Asp His Ala Arg Ala		
145	150	155
Ala Glu Pro		

<210> 5653
 <211> 1439
 <212> DNA
 <213> Homo sapiens

<400> 5653
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 cacettctgt ggccacacgt ccaaaaccaa tcaggtcaac tcggcggtg tgctgctgag
 120
 gttgcaggtg aacttgccag tgctcgtgtc ataattctcc tcggggttgg tgaggaccgc
 180
 gttgaactctg atcaggctgt tgggtgcagg gggctgtgg gtctgccag tgaccactca
 240
 gacaccgtgt cctcttgctt gggagagggg aagcagatct gaggacatct ctgtgccagg
 300
 ccagaaaccg cccacctgca ggtgaggccc ggaccctgc ccagttcctt ctccgggatg
 360
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 420
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 600
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 720
 ttcacgttca ctgcgcagac ccaccagccc cctgcaccca acagcctgat cagattcaac
 780
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 1260

catgggttct ctccttcctc tgaacttctt taggagtcac tgctgtgtg gttcctggga
 1320
 cacttaacca atgcctcttg gtaactgccaat tctttttttt ttttttcaag tattggaagg
 1380
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 1439

<210> 5654
 <211> 245
 <212> PRT
 <213> Homo sapiens

<400> 5654
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 Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
 35 40 45
 Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
 50 55 60
 Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
 65 70 75 80
 Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
 85 90 95
 Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly Glu Glu Gly
 100 105 110
 Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr Arg Gln Thr
 115 120 125
 His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn Ala Val Leu
 130 135 140
 Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys Phe Thr Cys
 145 150 155 160
 Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser His Thr Ala
 165 170 175
 Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val Val Thr Phe
 180 185 190
 Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly Gly Val Leu
 195 200 205
 Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu Ala Val Asn Asp Tyr
 210 215 220
 Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe Ser Gly Phe
 225 230 235 240
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 245

<210> 5655
 <211> 3810
 <212> DNA
 <213> Homo sapiens

<400> 5655
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 420
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 480
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<210> 5656

<211> 987

<212> PRT

<213> Homo sapiens

<400> 5656

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			20					25					30		
Ala	Glu	Val	Arg	Arg	Glu	Trp	Ala	Lys	Tyr	Met	Glu	Val	His	Glu	Lys
		35					40				45				
Ala	Ser	Phe	Thr	Asn	Ser	Glu	Leu	His	Arg	Ala	Met	Asn	Leu	His	Val
	50				55					60					
Gly	Asn	Leu	Arg	Leu	Leu	Ser	Gly	Pro	Leu	Asp	Gln	Val	Arg	Ala	Ala
65					70				75					80	
Leu	Pro	Thr	Pro	Ala	Leu	Ser	Pro	Glu	Asp	Lys	Ala	Val	Leu	Gln	Asn
			85					90					95		
Leu	Lys	Arg	Ile	Leu	Ala	Lys	Val	Gln	Glu	Met	Arg	Asp	Gln	Arg	Val
		100					105						110		
Ser	Leu	Glu	Gln	Gln	Leu	Arg	Glu	Leu	Ile	Gln	Lys	Asp	Asp	Ile	Thr
	115						120					125			
Ala	Ser	Leu	Val	Thr	Thr	Asp	His	Ser	Glu	Met	Lys	Lys	Leu	Phe	Glu
	130				135					140					
Glu	Gln	Leu	Lys	Lys	Tyr	Asp	Gln	Leu	Lys	Val	Tyr	Leu	Glu	Gln	Asn
145					150				155					160	
Leu	Ala	Ala	Gln	Asp	Arg	Val	Leu	Cys	Ala	Leu	Thr	Glu	Ala	Asn	Val
			165				170						175		
Gln	Tyr	Ala	Ala	Val	Arg	Arg	Val	Leu	Ser	Asp	Leu	Asp	Gln	Lys	Trp
		180					185						190		
Asn	Ser	Thr	Leu	Gln	Thr	Leu	Val	Ala	Ser	Tyr	Glu	Ala	Tyr	Glu	Asp
	195					200					205				
Leu	Met	Lys	Lys	Ser	Gln	Glu	Gly	Arg	Asp	Phe	Tyr	Ala	Asp	Leu	Glu
	210					215					220				
Ser	Lys	Val	Ala	Ala	Leu	Leu	Glu	Arg	Thr	Gln	Ser	Thr	Cys	Gln	Ala

225	230										235					240			
Arg	Glu	Ala	Ala	Arg	Gln	Gln	Leu	Leu	Asp	Arg	Glu	Leu	Lys	Lys	Lys				
				245											255				
Pro	Pro	Pro	Arg	Pro	Thr	Ala	Pro	Lys	Pro	Leu	Leu	Pro	Arg	Arg	Glu				
				260											270				
Glu	Ser	Glu	Ala	Val	Glu	Ala	Gly	Asp	Pro	Pro	Glu	Glu	Leu	Arg	Ser				
				275											285				
Leu	Pro	Pro	Asp	Met	Val	Ala	Gly	Pro	Arg	Leu	Pro	Asp	Thr	Phe	Leu				
				290											300				
Gly	Ser	Ala	Thr	Pro	Leu	His	Phe	Pro	Pro	Ser	Pro	Phe	Pro	Ser	Ser				
				305											315				
Thr	Gly	Pro	Gly	Pro	His	Tyr	Leu	Ser	Gly	Pro	Leu	Pro	Pro	Gly	Thr				
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Tyr	Ser	Gly	Pro	Thr	Gln	Leu	Ile	Gln	Pro	Arg	Ala	Pro	Gly	Pro	His				
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Ala	Met	Pro	Val	Ala	Pro	Gly	Pro	Ala	Leu	Tyr	Pro	Ala	Pro	Ala	Tyr				
				355											365				
Thr	Pro	Glu	Leu	Gly	Leu	Val	Pro	Arg	Ser	Ser	Pro	Gln	His	Gly	Val				
				370											380				
Val	Ser	Ser	Pro	Tyr	Val	Gly	Val	Gly	Pro	Ala	Pro	Pro	Val	Ala	Gly				
				385											395				
Leu	Pro	Ser	Ala	Pro	Pro	Pro	Gln	Phe	Ser	Gly	Pro	Glu	Leu	Ala	Met				
				400											410				
Ala	Val	Arg	Pro	Ala	Thr	Thr	Thr	Val	Asp	Ser	Ile	Gln	Ala	Pro	Ile				
				420											430				
Pro	Ser	His	Thr	Ala	Pro	Arg	Pro	Asn	Pro	Thr	Pro	Ala	Pro	Pro	Pro				
				435											445				
Pro	Cys	Phe	Pro	Val	Pro	Pro	Pro	Gln	Pro	Leu	Pro	Thr	Pro	Tyr	Thr				
				450											460				
Tyr	Pro	Ala	Gly	Ala	Lys	Gln	Pro	Ile	Pro	Ala	Gln	His	His	Phe	Ser				
				465											475				
Ser	Gly	Ile	Pro	Thr	Gly	Phe	Pro	Ala	Pro	Arg	Ile	Gly	Pro	Gln	Pro				
				480											490				
Gln	Pro	His	Pro	Gln	Pro	His	Pro	Ser	Gln	Ala	Phe	Gly	Pro	Gln	Pro				
				500											510				
Pro	Gln	Gln	Pro	Leu	Pro	Leu	Gln	His	Pro	His	Leu	Phe	Pro	Pro	Gln				
				515											525				
Ala	Pro	Gly	Leu	Leu	Pro	Gln	Ser	Pro	Tyr	Pro	Tyr	Ala	Pro	Gln					
				530											540				
Pro	Gly	Val	Leu	Gly	Gln	Pro	Pro	Pro	Pro	Leu	His	Thr	Gln	Leu	Tyr				
				545											555				
Pro	Gly	Pro	Ala	Gln	Asp	Pro	Leu	Pro	Ala	His	Ser	Gly	Ala	Leu	Pro				
				565											570				
Phe	Pro	Ser	Pro	Gly	Pro	Pro	Gln	Pro	Pro	His	Pro	Pro	Leu	Ala	Tyr				
				580											590				
Gly	Pro	Ala	Pro	Ser	Thr	Arg	Pro	Met	Gly	Pro	Gln	Ala	Ala	Pro	Leu				
				595											605				
Thr	Ile	Arg	Gly	Pro	Ser	Ser	Ala	Gly	Gln	Ser	Thr	Pro	Ser	Pro	His				
				610											620				
Leu	Val	Pro	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Pro	Gly	Pro	Val	Pro	Pro				
				625											635				
Arg	Pro	Pro	Ala	Ala	Glu	Pro	Pro	Pro	Cys	Leu	Arg	Arg	Gly	Ala	Ala				
				640											650				
Ala	Ala	Asp	Leu	Leu	Ser	Ser	Ser	Pro	Glu	Ser	Gln	His	Gly	Gly	Thr				
				645											655				

660
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 675 680 685
 Ala Ala Glu Gly Arg Arg Pro Gln Ala Leu Arg Leu Ile Glu Arg Asp
 690 695 700
 Pro Tyr Glu His Pro Glu Arg Leu Arg Gln Leu Gln Gln Glu Leu Glu
 705 710 715 720
 Ala Phe Arg Gly Gln Leu Gly Asp Val Gly Ala Leu Asp Thr Val Trp
 725 730 735
 Arg Glu Leu Gln Asp Ala Gln Glu His Asp Ala Arg Gly Arg Ser Ile
 740 745 750
 Ala Ile Ala Arg Cys Tyr Ser Leu Lys Asn Arg His Gln Asp Val Met
 755 760 765
 Pro Tyr Asp Ser Asn Arg Val Val Leu Arg Ser Gly Lys Asp Asp Tyr
 770 775 780
 Ile Asn Ala Ser Cys Val Glu Gly Leu Ser Pro Tyr Cys Pro Pro Leu
 785 790 795 800
 Val Ala Thr Gln Ala Pro Leu Pro Gly Thr Ala Ala Asp Phe Trp Leu
 805 810 815
 Met Val His Glu Gln Lys Val Ser Val Ile Val Met Leu Val Ser Glu
 820 825 830
 Ala Glu Met Glu Lys Gln Lys Val Ala Arg Tyr Phe Pro Thr Glu Arg
 835 840 845
 Gly Gln Pro Met Val His Gly Ala Leu Ser Leu Ala Leu Ser Ser Val
 850 855 860
 Arg Ser Thr Glu Thr His Val Glu Arg Val Leu Ser Leu Gln Phe Arg
 865 870 875 880
 Asp Gln Ser Leu Lys Arg Ser Leu Val His Leu His Phe Pro Thr Trp
 885 890 895
 Pro Glu Leu Gly Leu Pro Asp Ser Pro Ser Asn Leu Leu Arg Phe Ile
 900 905 910
 Gln Glu Val His Ala His Tyr Leu His Gln Arg Pro Leu His Thr Pro
 915 920 925
 Ile Ile Val His Cys Ser Ser Gly Val Gly Arg Thr Gly Ala Phe Ala
 930 935 940
 Leu Leu Tyr Ala Ala Val Gln Glu Val Glu Ala Gly Asn Gly Ile Pro
 945 950 955 960
 Glu Leu Pro Gln Leu Val Arg Arg Met Arg Gln Gln Arg Lys His Met
 965 970 975
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<210> 5657

<211> 1020

<212> DNA

<213> Homo sapiens

<400> 5657

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 120
 gctcgggct atgggacca gaacattcga ctgagccggg atgccgtgaa ggacttcgac
 180

tgctgtgtgc tctccctgca gccttgccac gatcctgttg tcaccccaga tggctacctg
 240
 tatgagcgtg aggccatcct ggagtacatt ctgcaccaga agaaggagat tggccggcag
 300
 atgaaggcct acgagaagca gcggggcacc cggcgcgagg agcagaagga gcttcagcgg
 360
 gcggcctcgc aggaccatgt gcggggcttc ctggagaagg agtcgggtat cgtgagccgg
 420
 cccctcaacc ctttcacagc caaggccctc tcgggcacca gccagatga tgtccaacct
 480
 gggcccagtg tgggtcctcc aagtaaggac aaggacaaag tgctgccag cttctggatc
 540
 ccgtcgtcta cgcccgaagc caaggccacc aagctggaga agcgcgccg cacggtgacc
 600
 tgcccctatg caggggaagcc cctgcgcatg tcggacctga cggcgtgca cttcacaccg
 660
 ctacacagct ccgtggaccg cgtggggctc atcaccgcga gcgagcgcta cgtgtgtgac
 720
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 780
 gtggtcaccc tcgaatgctg ggagaagctg attcggaagg acatggtgga ccctgtgact
 840
 ggagacaaac tcacagaccg cgacatcatc gtgctgcagc gggcggttac cggcttcgcg
 900
 ggctccggag tgaagctgca agcggagaaa tcacggccgg tgatgcaggc ctgagtgtgt
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 1020

<210> 5658

<211> 301

<212> PRT

<213> Homo sapiens

<400> 5658

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His	Glu	Lys	Lys	Lys	Asp	Thr	Ala	Ala	Ser	Gly	Tyr	Gly	Thr	Gln	Asn
			20					25					30		
Ile	Arg	Leu	Ser	Arg	Asp	Ala	Val	Lys	Asp	Phe	Asp	Cys	Cys	Cys	Leu
		35					40					45			
Ser	Leu	Gln	Pro	Cys	His	Asp	Pro	Val	Val	Thr	Pro	Asp	Gly	Tyr	Leu
	50				55						60				
Tyr	Glu	Arg	Glu	Ala	Ile	Leu	Glu	Tyr	Ile	Leu	His	Gln	Lys	Lys	Glu
	65				70				75					80	
Ile	Ala	Arg	Gln	Met	Lys	Ala	Tyr	Glu	Lys	Gln	Arg	Gly	Thr	Arg	Arg
			85					90					95		
Glu	Glu	Gln	Lys	Glu	Leu	Gln	Arg	Ala	Ala	Ser	Gln	Asp	His	Val	Arg
			100					105					110		
Gly	Phe	Leu	Glu	Lys	Glu	Ser	Ala	Ile	Val	Ser	Arg	Pro	Leu	Asn	Pro
	115						120								
Phe	Thr	Ala	Lys	Ala	Leu	Ser	Gly	Thr	Ser	Pro	Asp	Asp	Val	Gln	Pro
	130					135					140				
Gly	Pro	Ser	Val	Gly	Pro	Pro	Ser	Lys	Asp	Lys	Asp	Lys	Val	Leu	Pro

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145          150          155          160
Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala Lys Ala Thr Lys Leu
165          170          175
Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met Ser Gly Lys Pro Leu
180          185          190
Arg Met Ser Asp Leu Thr Pro Val His Phe Thr Pro Leu Asp Ser Ser
195          200          205
Val Asp Arg Val Gly Leu Ile Thr Arg Ser Glu Arg Tyr Val Cys Ala
210          215          220
Val Thr Arg Asp Ser Leu Ser Asn Ala Thr Pro Cys Ala Val Leu Arg
225          230          235          240
Pro Ser Gly Ala Val Val Thr Leu Glu Cys Val Glu Lys Leu Ile Arg
245          250          255
Lys Asp Met Val Asp Pro Val Thr Gly Asp Lys Leu Thr Asp Arg Asp
260          265          270
Ile Ile Val Leu Gln Arg Gly Gly Thr Gly Phe Ala Gly Ser Gly Val
275          280          285
Lys Leu Gln Ala Glu Lys Ser Arg Pro Val Met Gln Ala
290          295          300

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<210> 5659

<211> 1263

<212> DNA

<213> Homo sapiens

<400> 5659

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120
tcagagaagg cttagatcta tgcattgggt gttattctca gatgcagaga tgtaaagtgc
180
atttttctct tctgttttca ggtcacatgt gccaat ttaa cgaacgggtgg aaagtcagaa
240
cttctgaaat caggaagcag caaatccaca ctaagcaca tatggacaga aagcagcaaa
300
gacttgctta tcagccgact cctgtcacag acttttcgtg gcaaagagaa tgatacagat
360
ttggacctga gatatgacac ccagaaacct tattctgagc aagacctctg ggactggctg
420
aggaactcca cagaccttca agagcctcgg ccagggcca agagaaggcc cattgttaaa
480
acgggcaagt ttaagaaaat gtttgatgag ggcgattttt attccaacat caaaacagtg
540
aagctgaacc tgttgataac tgggaaaatt gtagatcatg gcaatgggac atttagtggt
600
tatttcagcg ataattcaac tgggtcaaggg aatgtatctg tcagcttggt accccctaca
660
aaaatcgtgg aatttgactt ggcacaacaa accgtgattg atgccaaaga ttccaagtct
720
tttaattgtc gcattgaata tgaaaagggt gacaaggcta ccaagaacac actctgcaac
780
tatgaccctt caaaaacctg ttaccaggag caaacccaaa gtcatgtatc ctggctctgc
840

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tccaagccct ttaaggtgat ctgtatttac atttcctttt atagtagaca ttataaactg
 900
 gtacagaaaag tgtgcctctga ctacaactac cacagtgcaca caccttactt tcctcgggga
 960
 tgaaggtgaa catgggggtg agactgaagc ctgaggaatt aaaggtcata tgacaggggt
 1020
 gttacctcaa agaagaaggt cacatctgtt gcctggaatg tgtctacact gctgctcttg
 1080
 tcaactgggt gcaaaatata ctagtggaaa acactctgat gtaatttctg ccagtcagc
 1140
 ttcacccctc agtataattg taaatcatca cagattttga attcacacct gaagacatgc
 1200
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 1260
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 1263

<210> 5660

<211> 253

<212> PRT

<213> Homo sapiens

<400> 5660

Val Thr Cys Ala Asn Leu Thr Asn Gly Gly Lys Ser Glu Leu Leu Lys
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 Ser Gly Ser Ser Lys Ser Thr Leu Lys His Ile Trp Thr Glu Ser Ser
 20 25 30
 Lys Asp Leu Ser Ile Ser Arg Leu Leu Ser Gln Thr Phe Arg Gly Lys
 35 40 45
 Glu Asn Asp Thr Asp Leu Asp Leu Arg Tyr Asp Thr Pro Glu Pro Tyr
 50 55 60
 Ser Glu Gln Asp Leu Trp Asp Trp Leu Arg Asn Ser Thr Asp Leu Gln
 65 70 75 80
 Glu Pro Arg Pro Arg Ala Lys Arg Arg Pro Ile Val Lys Thr Gly Lys
 85 90 95
 Phe Lys Lys Met Phe Gly Trp Gly Asp Phe His Ser Asn Ile Lys Thr
 100 105 110
 Val Lys Leu Asn Leu Leu Ile Thr Gly Lys Ile Val Asp His Gly Asn
 115 120 125
 Gly Thr Phe Ser Val Tyr Phe Arg His Asn Ser Thr Gly Gln Gly Asn
 130 135 140
 Val Ser Val Ser Leu Val Pro Pro Thr Lys Ile Val Glu Phe Asp Leu
 145 150 155 160
 Ala Gln Gln Thr Val Ile Asp Ala Lys Asp Ser Lys Ser Phe Asn Cys
 165 170 175
 Arg Ile Glu Tyr Glu Lys Val Asp Lys Ala Thr Lys Asn Thr Leu Cys
 180 185 190
 Asn Tyr Asp Pro Ser Lys Thr Cys Tyr Gln Glu Gln Thr Gln Ser His
 195 200 205
 Val Ser Trp Leu Cys Ser Lys Pro Phe Lys Val Ile Cys Ile Tyr Ile
 210 215 220
 Ser Phe Tyr Ser Thr Asp Tyr Lys Leu Val Gln Lys Val Cys Pro Asp
 225 230 235 240
 Tyr Asn Tyr His Ser Asp Thr Pro Tyr Phe Pro Ser Gly

245

250

<210> 5661

<211> 578

<212> DNA

<213> Homo sapiens

<400> 5661

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 120
 ataaccagtg gcacggcaag gaccagcagc gaagcaccag ccactggccc cgacctcccc
 180
 caccaggagc ctgacgggca cttagacaca cacagtggcc tgagctccaa ctccagcatg
 240
 accacggggg agcttcagca gtactggcag aaccagaaa ggcgctggaa gcacgtcaaa
 300
 ctgctctttg agatcgcttc agctcgcatc gaggagagaa aagtctctaa gtttgtgatg
 360
 gggaaatcaa ggcctggaga gatgacttat ccagggtcac gtggcgagac agggacagca
 420
 ccagaaccag acccgagatg tccacgtcaa agtgacatgc tctgagaggc agcacacaca
 480
 gaataaacct gcattcaaat tccaggaagc tcttaggggt catccagctg ggccatgggg
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 578

<210> 5662

<211> 148

<212> PRT

<213> Homo sapiens

<400> 5662

Met Thr Leu Leu Pro Asp Pro Trp Thr His Thr Ala Leu Gly Thr Gly
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 Cys Leu Gly Ala Cys Lys Ser Arg Ala Pro Trp Glu Pro Trp Cys Met
 20 25 30
 Gly Pro Ile Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala
 35 40 45
 Thr Gly Pro Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr
 50 55 60
 His Ser Gly Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln
 65 70 75 80
 Gln Tyr Trp Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu
 85 90 95
 Phe Glu Ile Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe
 100 105 110
 Val Met Gly Lys Ser Arg Pro Gly Glu Met Thr Tyr Pro Gly Ser Arg
 115 120 125
 Gly Glu Thr Gly Thr Ala Pro Glu Pro Asp Pro Arg Cys Pro Arg Gln
 130 135 140
 Ser Asp Met Leu

145

<210> 5663

<211> 857

<212> DNA

<213> Homo sapiens

<400> 5663

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120
agacaggagg ctgccgtggt caagaagggc caagccttga agtctcacgg caccctctgt
180
ggtggaggta taaggctcag gggccaacta ctgggtcttg cagtcccat cgttgctgtg
240
ggctgtcttc accttcttta gttccttctg tagctcagac tcggccaacca caacctcctt
300
tggtctctcg taagagatga tcaggggtgca gttggcgtgg gcaaagctca gcaaggcgtc
360
atccagaggt agctggtgtc tatctagatc aggaatggag aacttcttgt agtactctct
420
gttggttgtt ctgacaatga tgcagcgctc cttctgtgtc acagagacac tatagacatc
480
cttaggatag gggagggttc gaatccgcca ctggaaactc atcttggtgt ccttcgcgat
540
gaagatagga ttggcattgc tttccttgat gagttcaggc cccaggttcc ctgctcctag
600
gggcgctggg tctcctactt caagctgcca ctggcccatg gctcccaggg cacttttacc
660
acgccacttt ctcaagaata gttcaactcg cttctcgtca tattcttcag ccatttctct
720
gocgtctggg aataaatagt gaaccttctc tctcccgctc tgcagcagcg cagtcttctg
780
ggctgtccgc agactctcca accagcccgt caccgccatc tttccctcgc taagcagcac
840
gccagccgc tgccatg
857

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<210> 5664

<211> 203

<212> PRT

<213> Homo sapiens

<400> 5664

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Met Ala Val Thr Gly Trp Leu Glu Ser Leu Arg Thr Ala Gln Lys Thr
1           5           10           15
Ala Leu Leu Gln Asp Gly Arg Arg Lys Val His Tyr Leu Phe Pro Asp
20           25           30
Gly Lys Glu Met Ala Glu Glu Tyr Asp Glu Lys Thr Ser Glu Leu Leu
35           40           45
Val Arg Lys Trp Arg Val Lys Ser Ala Leu Gly Ala Met Gly Gln Trp
50           55           60
Gln Leu Glu Val Gly Asp Pro Ala Pro Leu Gly Ala Gly Asn Leu Gly

```

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65          70          75          80
Pro Glu Leu Ile Lys Glu Ser Asn Ala Asn Pro Ile Phe Met Arg Lys
      85          90          95
Asp Thr Lys Met Ser Phe Gln Trp Arg Ile Arg Asn Leu Pro Tyr Pro
      100          105          110
Lys Asp Val Tyr Ser Val Ser Val Asp Gln Lys Glu Arg Cys Ile Ile
      115          120          125
Val Arg Thr Thr Asn Lys Lys Tyr Tyr Lys Lys Phe Ser Ile Pro Asp
      130          135          140
Leu Asp Arg His Gln Leu Pro Leu Asp Asp Ala Leu Leu Ser Phe Ala
      145          150          155          160
His Ala Asn Cys Thr Leu Ile Ile Ser Tyr Gln Lys Pro Lys Glu Val
      165          170          175          180
Val Val Ala Glu Ser Glu Leu Gln Lys Glu Leu Lys Lys Val Lys Thr
      185          190
Ala His Ser Asn Asp Gly Asp Cys Lys Thr Gln
      195          200

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<210> 5665

<211> 531

<212> DNA

<213> Homo sapiens

<400> 5665

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120
cagcgccct ctgaagtcac ttgcttcacg gaggtgttac tgtctgtgc tggacagagc
180
atgatggggg ctgcaagggc tccctcaaac cctggactec tccaacagag ggcctctggt
240
tgccaggctc agctctgccc tgcgtcgccc ccaggggcgt gggaggggtg ttaatcctgg
300
cccgggcctt cccgcaggt ggagcgctg tcgcacccgc tgcgcagca gcagtatgag
360
ctgtaccggg agcgctgct gcagcgatgc gagcgcgccc cggtgagca ggtgtgtac
420
cacggcacga cggcacgggc agtgccctgac atctgcgccc acgggttcaa ccgcagcttc
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531

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<210> 5666

<211> 79

<212> PRT

<213> Homo sapiens

<400> 5666

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Ser Trp Pro Gly Pro Ser Pro Gln Val Glu Arg Val Ser His Pro Leu
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Leu Gln Gln Gln Tyr Glu Leu Tyr Arg Glu Arg Leu Leu Gln Arg Cys
20          25          30
Glu Arg Arg Pro Val Glu Gln Val Leu Tyr His Gly Thr Thr Ala Pro

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35	40	45
Ala Val Pro Asp Ile Cys	Ala His Gly Phe Asn Arg Ser Phe Cys Gly	
50	55	60
Arg Asn Ala Thr Val Tyr	Gly Lys Gly Val Tyr Phe Ala Arg Arg	
65	70	75

<210> 5667
 <211> 858
 <212> DNA
 <213> Homo sapiens

<400> 5667
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 120
 tttgagaagt taagaatgat ttccaaggaa atccgccaag ttgttcgaat gacttctgct
 180
 aacatggacc cagctatgat gtttcgacag aggtcactga gtcaaggaag cacaaattca
 240
 aacatgctgg atgttcaggg aggtgctcac aaaaaaggg caccgcgcag ctctctgctt
 300
 aatggccaaga agctatatga ggatgcccaa atggcaagga aggtgaagca gtatctttcc
 360
 agtctcgatg tagagacaga tgaggagaag ttccagatga tgcattaca gntggagcct
 420
 gcatatggta cctgtgagta caagttttca tttatgtgac gctaaagagc acaacaaaat
 480
 aaaaacttat ttctctagaa ttatacctaa gtcccaagaa aattaacttt cactcacaaa
 540
 agattgctgg cataccttaa gcatcatgtg atccaattaa tcacagactg aatccccatcc
 600
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 660
 taattctttt aaaaactgga tcattataga ggaggctttc tgtttgagaa catttttata
 720
 ttcatcctta aagagtaaac ataagtggaa tttttacctc tttttatttc atggataata
 780
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 840
 aggtgccagt agtaaggt
 858

<210> 5668
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 5668
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 phe Pro Val Val Lys Lys Asp Met Thr Phe Leu His Glu Gly Asn Asp
 20 25 30
 Ser Lys Val Asp Gly Leu Val Asn Phe Glu Lys Leu Arg Met Ile Ser

35	40	45
Lys Glu Ile Arg Gln Val Val Arg Met Thr Ser Ala Asn Met Asp Pro		
50	55	60
Ala Met Met Phe Arg Gln Arg Ser Leu Ser Gln Gly Ser Thr Asn Ser		
65	70	75
Asn Met Leu Asp Val Gln Gly Gly Ala His Lys Lys Arg Ala Arg Arg		80
	85	90
Ser Ser Leu Leu Asn Ala Lys Lys Leu Tyr Glu Asp Ala Gln Met Ala		95
	100	105
Arg Lys Val Lys Gln Tyr Leu Ser Ser Leu Asp Val Glu Thr Asp Glu		110
	115	120
Glu Lys Phe Gln Met Met Ser Leu Gln Xaa Glu Pro Ala Tyr Gly Thr		125
	130	135
Cys Glu Tyr Lys Phe Ser Phe Met		140
145	150	

<210> 5669

<211> 1842

<212> DNA

<213> Homo sapiens

<400> 5669

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120
gccatgatgc gcagctccat agagaggggc aaatgggtct tcttcagaa ctgccacctg
180
gcaccaagct ggatgccagc cctagaacgc ctcacgagc acatcaaccc cgacaaggta
240
cacagggact tccgctctg gctcaccagc ctgccagca acaagttccc agtgtccatc
300
ctgcagaacg gctccaagat gaccattgag ccgccaacgc gtgtcagggc caacctgtg
360
aagtcctata gtacgtcttg tgaagacttc ctcaactcct gccacaaggc gatggagtcc
420
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480
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540
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600
acggcagggg agatcaatta cgggggcccgt gtcactgatg actgggaccg gcgctgcac
660
atgaacatct tggaggactt ctacaacctt gacgtgtctt ccctgagca cagctacagc
720
gcctcgggca tctaccacca gatcccgctt acctacgacc tccacggcta cctctcctac
780
atcaagagcc tccactcaa tgatgtgctt gagatcttgg gctgcatga caatgccaac
840
atcacctttg cccagaacga gacgttggcc ctccctgggca ccatcatcca gctgcaaccc
900
aatcatctt ctgcaggcag ccaggggccg gaggagatag tggaggacgt caccctaaac
960

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attctgctca aggtgctga gcctatcaac ttgcaatggg tgatggccaa gtacccagtg
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 1080
 ctgcagggtga tcacacagac actgcaagac ctactcaagg cactcaaggg gctggtagtg
 1140
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 1200
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 1320
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 1680
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 1842

<210> 5670

<211> 591

<212> PRT

<213> Homo sapiens

<400> 5670

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 Ala Glu Glu Met Lys Phe Ser Lys Lys Leu Ser Ala Ile Ser Leu Gly
 20 25 30
 Gln Gly Gln Gly Pro Arg Ala Glu Ala Met Met Arg Ser Ser Ile Glu
 35 40 45
 Arg Gly Lys Trp Val Phe Phe Gln Asn Cys His Leu Ala Pro Ser Trp
 50 55 60
 Met Pro Ala Leu Glu Arg Leu Ile Glu His Ile Asn Pro Asp Lys Val
 65 70 75 80
 His Arg Asp Phe Arg Leu Trp Leu Thr Ser Leu Pro Ser Asn Lys Phe
 85 90 95
 Pro Val Ser Ile Leu Gln Asn Gly Ser Lys Met Thr Ile Glu Pro Pro
 100 105 110
 Arg Gly Val Arg Ala Asn Leu Leu Lys Ser Tyr Ser Ser Leu Gly Glu
 115 120 125
 Asp Phe Leu Asn Ser Cys His Lys Val Met Glu Phe Lys Ser Leu Leu

130					135					140					
Leu	Ser	Leu	Cys	Leu	Phe	His	Gly	Asn	Ala	Leu	Glu	Arg	Arg	Lys	Phe
145					150					155					160
Gly	Pro	Leu	Gly	Phe	Asn	Ile	Pro	Tyr	Glu	Phe	Thr	Asp	Gly	Asp	Leu
				165					170						175
Arg	Ile	Cys	Ile	Ser	Gln	Leu	Lys	Met	Phe	Leu	Asp	Glu	Tyr	Asp	Asp
			180						185					190	
Ile	Pro	Tyr	Lys	Val	Leu	Lys	Tyr	Thr	Ala	Gly	Glu	Ile	Asn	Tyr	Gly
			195				200					205			
Gly	Arg	Val	Thr	Asp	Asp	Trp	Asp	Arg	Arg	Cys	Ile	Met	Asn	Ile	Leu
210						215					220				
Glu	Asp	Phe	Tyr	Asn	Pro	Asp	Val	Leu	Ser	Pro	Glu	His	Ser	Tyr	Ser
225					230					235					240
Ala	Ser	Gly	Ile	Tyr	His	Gln	Ile	Pro	Pro	Thr	Tyr	Asp	Leu	His	Gly
				245					250					255	
Tyr	Leu	Ser	Tyr	Ile	Lys	Ser	Leu	Pro	Leu	Asn	Asp	Met	Pro	Glu	Ile
			260				265						270		
Phe	Gly	Leu	His	Asp	Asn	Ala	Asn	Ile	Thr	Phe	Ala	Gln	Asn	Glu	Thr
			275				280					285			
Phe	Ala	Leu	Leu	Gly	Thr	Ile	Ile	Gln	Leu	Gln	Pro	Lys	Ser	Ser	Ser
290					295					300					
Ala	Gly	Ser	Gln	Gly	Arg	Glu	Glu	Ile	Val	Glu	Asp	Val	Thr	Gln	Asn
305					310					315					320
Ile	Leu	Leu	Lys	Val	Pro	Glu	Pro	Ile	Asn	Leu	Gln	Trp	Val	Met	Ala
			325						330					335	
Lys	Tyr	Pro	Val	Leu	Tyr	Glu	Glu	Ser	Met	Asn	Thr	Val	Leu	Val	Gln
			340					345					350		
Glu	Val	Ile	Arg	Tyr	Asn	Arg	Leu	Leu	Gln	Val	Ile	Thr	Gln	Thr	Leu
			355				360					365			
Gln	Asp	Leu	Leu	Lys	Ala	Leu	Lys	Gly	Leu	Val	Val	Met	Ser	Ser	Gln
370						375					380				
Leu	Glu	Leu	Met	Ala	Ala	Ser	Leu	Tyr	Asn	Asn	Thr	Val	Pro	Glu	Leu
385					390					395					400
Trp	Ser	Ala	Lys	Ala	Tyr	Pro	Ser	Leu	Lys	Pro	Leu	Ser	Ser	Trp	Val
				405					410					415	
Met	Asp	Leu	Leu	Gln	Arg	Leu	Asp	Phe	Leu	Gln	Ala	Trp	Ile	Gln	Asp
			420					425					430		
Gly	Ile	Pro	Ala	Val	Phe	Trp	Ile	Ser	Gly	Phe	Phe	Phe	Pro	Gln	Ala
			435				440						445		
Phe	Leu	Thr	Gly	Thr	Leu	Gln	Asn	Phe	Ala	Arg	Lys	Phe	Val	Ile	Ser
450						455					460				
Ile	Asp	Thr	Ile	Ser	Phe	Asp	Phe	Lys	Val	Met	Phe	Glu	Ala	Pro	Ser
465					470					475					480
Glu	Leu	Thr	Gln	Arg	Pro	Gln	Val	Gly	Cys	Tyr	Ile	His	Gly	Leu	Phe
			485						490					495	
Leu	Glu	Gly	Ala	Arg	Trp	Asp	Pro	Glu	Ala	Phe	Gln	Leu	Ala	Glu	Ser
			500				505						510		
Gln	Pro	Lys	Glu	Leu	Tyr	Thr	Glu	Met	Ala	Val	Ile	Trp	Leu	Leu	Pro
			515				520						525		
Thr	Pro	Asn	Arg	Lys	Ala	Gln	Asp	Gln	Asp	Phe	Tyr	Leu	Cys	Pro	Ile
530					535					540					
Tyr	Lys	Thr	Leu	Thr	Arg	Ala	Gly	Thr	Leu	Ser	Thr	Thr	Gly	His	Ser
545					550				555						560
Thr	Asn	Tyr	Val	Ile	Ala	Val	Glu	Ile	Pro	Thr	His	Gln	Pro	Gln	Arg

				565			570			575				
His	Trp	Ile	Lys	Arg	Gly	Val	Ala	Leu	Ile	Cys	Ala	Leu	Asp	Tyr
				580				585				590		
<210> 5671														
<211> 818														
<212> DNA														
<213> Homo sapiens														
<400> 5671														
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180	gtg	tcetac	t	ttgt	ctct	ctctt	ccgg	ctc	gagat	ga	atgt	gcag	cc	ctgttctag
240	tgt	gggtat	g	gggttt	tatc	tgcc	gaga	ag	atcag	ctgt	a	tagat	cagat	atggcataa
300	gcct	gtttt	c	actgt	gaag	ttg	caag	atg	atg	ctgt	ctg	ttaata	aact	tgtgagtcac
360	cagaaaa	ag	c	gtact	gtca	c	gcccc	ataac	c	ctaaga	aaca	acactt	ttc	cagtgtctat
420	cacact	ccat	t	aaat	ctaaa	tgt	gagg	aca	t	ttccag	ag	g	ccatcag	tgtg
480	gaag	gtgc	ac	taac	agg	ca	gccact	gg	ca	aatg	agag	ag	cctatt	tg
540	gaag	gg	gaat	g	ctt	gg	tccc	agg	ag	ctct	g	ccag	acccc	g
600	gctc	gaa	gt	g	gtg	ta	ggaat	ata	ca	gaag	act	atg	ag	caacc
660	ag	cttt	cc	ag	cat	ca	ac	ctg	ctt	at	caagg	g	ccaa	ccagctg
720	ag	cca	agt	g	g	ag	ata	ag	ag	ag	g	ag	g	g
780	gata	ct	ctg	ct	acg	gag	ca	agg	g	ctg	gg	g	g	g
818														

```

Glu Ala Ile Ser Gly Ile His Asp Gln Glu Asp Gly Glu Gln Cys Lys
      85                      90                      95
Ser Val Phe His Trp Asp Met Lys Ser Lys Asp Lys Glu Gly Ala Pro
      100                      105                      110
Asn Arg Gln Pro Leu Ala Asn Glu Arg Ala Tyr Trp Thr Gly Tyr Gly
      115                      120                      125
Glu Gly Asn Ala Trp Cys Pro Gly Ala Leu Pro Asp Pro Glu Ile Val
      130                      135                      140
Arg Met Val Glu Ala Arg Lys Ser Leu Gly Glu Tyr Thr Glu Asp
      145                      150                      155
Tyr Glu Gln Pro Arg Gly Lys Gly Ser Phe Pro Ala Met Ile Thr Pro
      165                      170                      175
Ala Tyr Gln Arg Ala Lys Lys Ala Asn Gln Leu Ala Ser Gln Val Glu
      180                      185                      190
Tyr Lys Arg Gly His Asp Glu Arg Ile Ser Arg Phe Ser Thr Val Ala
      195                      200                      205
Asp Thr Pro Glu Leu Leu Arg Ser Lys Ala Trp Gly
      210                      215                      220

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<210> 5673

<211> 1279

<212> DNA

<213> Homo sapiens

<400> 5673

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120
ccgagacgat aaaagaacag ttgggtgttt ataggatgcc ctcaaagtga gctggctaag
180
tgagctgggc tctaacttca ctcaaaatt tatagtacag ctaagaagggc cagtctgtcc
240
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300
gggggtcccc catggtccac acttctgcag catccgcaga acatgtggcc gggctcctgc
360
cagcagcagg gacagccaag tgggaggcag gcatggtgca cacctgggga ggccctgggt
420
gcagaagcag cccacacagta gcagcccat ccagaggaag accactccgg agggccacag
480
gcctctgcag ccctggcact gccgcccagc cctccatctc agcgggatgt gcagggtgag
540
acagggaatgc agggacgttc tgcccctagg tcagcctctt catccgctgt ttgtgtctcg
600
atgggtcaagg ttgccctgtc cacagctgct gcaacgccat ccagggtctc gtctgtcttc
660
tccagctcac tctcggcctc cgggcccagc ccttcacctt cctcaggatc tgggttagtt
720
cctgggtatc tgcctcagaa agggctggca ggcttgtctg cagggtcagt gctgtgccct
780
cctgggtctcc tgcgggtggc tcacgggtgca ggggtacggc catcagccca gatgctgcat
840

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gccagactga gcagctcttc tctgcggggg aagaggttct tgcgcttctg agcaccaatg
 900
 catcttctaa cagctccatc ttcttgctga actgcacttc taaaatgggg ataacctctg
 960
 gcattctggc agatatcaaa cgataggcca tgtctggcct tccaataaac cgctggcgga
 1020
 tgctaatttc gtaaggtagg tggacctga tgcgtccac gtcttctctt tcaaacctgt
 1080
 gcatgagcaa agaactggag tcatgtattt ccaaccaga cacaaggacg gtgagcctcc
 1140
 ctggtttaac gtgagactct gttctgtggg aaataacagc aggaattttt atcagtatcc
 1200
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 1260
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 1279

<210> 5674

<211> 81

<212> PRT

<213> Homo sapiens

<400> 5674

Leu	His	Ser	Gln	Ile	Tyr	Ser	Thr	Ala	Lys	Lys	Ala	Ser	Leu	Ser	Met
1				5					10				15		
Lys	Gly	Ser	Arg	Asp	Lys	Thr	Arg	Ala	Ala	Ser	Ser	Arg	Pro	Val	Pro
			20					25				30			
Ser	Val	Leu	Gly	Val	Pro	Pro	Trp	Ser	Thr	Leu	Leu	Gln	His	Pro	Gln
		35					40					45			
Asn	Met	Trp	Pro	Gly	Pro	Ala	Gln	Gln	Gln	Gly	Gln	Pro	Ser	Gly	Arg
	50				55					60					
Gln	Ala	Trp	Cys	Thr	Pro	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Ala	Ala	Pro
65				70					75					80	
Gln															

<210> 5675

<211> 1074

<212> DNA

<213> Homo sapiens

<400> 5675

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 120
 gggctggggc aggggctgag gctgaaagca gcagcctgcc tagtgggtga cgccagggggc
 180
 cggtgtaaca tggcacccgag gttggggcca cagcaatgtg tgggacgggt ggggtgggctg
 240
 gggcccttgg ctccaagcat tagttctcca agctctggtc cgttctccta cctccttcaa
 300
 ggggcaccag gggtacaagg tggtagtga gtattggggc ccgactcctg gggcactgga
 360

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 420
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 480
 tacaggctgt aggcaggagg agccgtggag tccaggcca gctcccaaa gggcagggggc
 540
 aaccgcacgc ccagtgggta ctgcacggag ctgtaggagg tcacagtgc gtgtacaggg
 600
 ctgtcactgt ccatagggat gactgccacg tcgcagggct gccgtgctgg tggcagatgt
 660
 ggctggggcct gtgcctgctt ccggaggcag cagaaccgga cacaaccagc tgtgacacca
 720
 cacagcagaa gcaggaggac cgccagcagg atgagcctag gagagcaagg ctctaccact
 780
 ggactgaccc tcggccaccg ggcacctgca cctggggaa tgcctgggca caaccaccga
 840
 agacaggtta acaggataaa aagcagacaa tgtctctcca tgcggagac cgccgtggcc
 900
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 960
 ggccttgggc tcaactccag gactcgtgt cctcagcgag tgcccactg ctgagcggga
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 1074

<210> 5676

<211> 145

<212> PRT

<213> Homo sapiens

<400> 5676

Glu Val Thr Val Leu Cys Thr Gly Leu Ser Leu Ser Ile Gly Met Thr
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 Ala Thr Ser Gln Gly Cys Arg Ala Gly Gly Arg Cys Gly Trp Ala Cys
 20 25 30
 Ala Cys Phe Arg Arg Gln Gln Asn Arg Thr Gln Pro Ala Val Thr Pro
 35 40 45
 His Ser Arg Ser Arg Arg Thr Ala Ser Arg Met Ser Leu Gly Glu Gln
 50 55 60
 Gly Ser Thr Thr Gly Leu Thr Leu Gly His Arg Ala Pro Ala Pro Trp
 65 70 75 80
 Gly Met Ser Trp His Asn His Arg Arg Gln Val Asn Arg Ile Lys Ser
 85 90 95
 Arg Gln Cys Leu Ser Met Ser Glu Thr Ala Val Ala Arg Ala Trp Pro
 100 105 110
 Arg Ala Ala Gly Pro Ala Leu Ala Ile Ser Pro Gly Leu Ala Arg Gly
 115 120 125
 Gly Leu Gly Leu Thr Pro Arg Thr Arg Cys Pro Gln Arg Val Pro His
 130 135 140
 Cys
 145

<210> 5677

<211> 477

<212> DNA

<213> Homo sapiens

<400> 5677

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 120
 agggaaagca agatgcagca gtgaggccct ctctggtatc cattcattca cttcactcaa
 180
 cagctgttta tgaccatgag caatacaagc cttgtgaaga tcctggagca gggcacaagc
 240
 cgctgacgtc tgctccagtg agaagccctg ctgccttccc caattcgctt tctttccgca
 300
 gccgccgctg ccccgacccc ggatctgcat gtggaagtac ctggacgtcc attccatgca
 360
 ccagctggag aagaccacca atgctgagat gaggagggtg ctggctgagc tgctggagct
 420
 aggggtgctc gagcagagcc tgagcgacgc catcaccctg gacctcttct gccgcgg
 477

<210> 5678

<211> 151

<212> PRT

<213> Homo sapiens

<400> 5678

Met Ala Ser Leu Arg Leu Cys Ser Gly His Pro Ser Ser Ser Ser Ser
 1 5 10 15
 Ala Ser Thr Ser Leu Ile Ser Ala Leu Val Val Phe Ser Ser Trp Cys
 20 25 30
 Met Glu Trp Thr Ser Arg Tyr Phe His Met Gln Ile Arg Gly Arg Gly
 35 40 45
 Ser Gly Gly Cys Gly Lys Lys Ala Asn Trp Gly Arg Gln Gln Gly Phe
 50 55 60
 Ser Leu Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His
 65 70 75 80
 Lys Ala Cys Ile Ala His Gly His Lys Gln Leu Leu Ser Glu Val Asn
 85 90 95
 Glu Trp Ile Pro Glu Arg Ala Ser Leu Leu His Leu Ala Phe Pro Thr
 100 105 110
 Ser Asn Pro Leu Gly Gln Arg Gly Gly Val Leu Pro Leu Leu His Gln
 115 120 125
 Cys Pro Phe Leu Pro Trp Ser Gln Ala Ala Ser Phe Gln His Arg Pro
 130 135 140
 Leu Gln Arg Gly Thr Ala Ala
 145 150

<210> 5679

<211> 665

<212> DNA

<213> Homo sapiens

<400> 5679

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120
tccacctccc agcatgctgg ctccaattcc acctctcagc agcctagccc tgaatccaca
180
ccacagcagc ctagtctctga atccacacca cagcagccta gccctgaatc cacaccacag
240
cattccagcc ttgaaaccac ctcccggcag ccagcattcc aagcccttcc agcacccgaa
300
atccgcgcgt cctcttgctg ccttttatct ccagatgcta acgtgaaggc agccctctaa
360
tccaggaaag cagaaaatct tcaagaaaac cctccagtca tcgtaacgcg tgtcctccaa
420
gccctcgaa ctgtggctgt ggctctgggg gctctaggag ctgcctacta catcactgaa
480
tccttgtgaa caagccccta ggcccacagt ctggcagacc tccaccagcc ccaggagtgt
540
atagggtgatg gcgctgggag aagatgttca gaatatctca aaagccaagt ccagaagatc
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665

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<210> 5680

<211> 143

<212> PRT

<213> Homo sapiens

<400> 5680

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Val Gly Arg Ile Tyr His Glu Glu Gly Gln Glu Glu Lys Val Arg Gly
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Gln Thr Pro Pro Asp Ser Thr Ser Gln His Ala Gly Ser Asn Ser Thr
20      25      30
Ser Gln Gln Pro Ser Pro Glu Ser Thr Pro Gln Gln Pro Ser Pro Glu
35      40      45
Ser Thr Pro Gln Gln Pro Ser Pro Glu Ser Thr Pro Gln His Ser Ser
50      55      60
Leu Glu Thr Thr Ser Arg Gln Pro Ala Phe Gln Ala Leu Pro Ala Pro
65      70      75      80
Glu Ile Arg Arg Ser Ser Cys Cys Leu Leu Ser Pro Asp Ala Asn Val
85      90      95
Lys Ala Ala Pro Gln Ser Arg Lys Ala Glu Asn Leu Gln Glu Asn Pro
100     105     110
Pro Val Ile Val Thr Arg Val Leu Gln Ala Leu Gly Thr Val Ala Val
115     120     125
Ala Leu Gly Ala Leu Gly Ala Ala Tyr Tyr Ile Thr Glu Ser Leu
130     135     140

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<210> 5681

<211> 1402

<212> DNA

<213> Homo sapiens

<400> 5681
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120
tagacattga tggaagcaga aacaaaaact cttccctctg agaatgcac ctccttttca
180
gagggctctc tgcaggaagg acaccgatta tggattggca acctggaccc caaaattacc
240
gaataccacc tcctcaagct cctccagaag tttggcaagg taaagcagtt tgacttcctc
300
ttccacaagt caggtgcttt ggagggacag cctcgaggct actgttttgt taactttgaa
360
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420
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540
agtgtcactg caaagataaa agccattgaa gcaaaactga aaatgatggc gaaaaatcct
600
gatgcagagt atccagcagc gcctgtttat tcctacttta agccaccaga taaaaaaagg
660
actactccat attctagaac agcatggaaa tctcgaagat gatggttgtg aattactgtg
720
gcagcaaaag caaattggtc tccacaccta aaatcgtctg cctgtgtact ttgtagatgt
780
gaatgggtact attcaacgga gcacaatcac atgttagcat ttggtaacat aatgtttttg
840
gatgttctta tggatgttcc ttcctaaac tatgtatgga attgagcatc atccagaata
900
aatagcgttg tatcccaaat tgtgatttga accctgggat gctctaattg gctggttggt
960
ttggatttgt aactccagaa acattctata gtgtgccaga gcaaaaggca aatacacaaa
1020
atattattta aatcaggaaa ctaaaaaatat taacatctat taaaaaattg agcatttttc
1080
tacgctcgtg tgtcttttac aacataaaga aaaagtaaaa ggagggaggg gaagtgcag
1140
acagatttta aatcatgttc agaactgttg ttccagaatt tactacggca atccctccaa
1200
ctggactgaa aaagagaaag ttcttggcaa aaaggagctg attctttgaa caaatgttgt
1260
agtaatctgt ttaagaatta tgcttattgt ttcaaaatcc caactaggaa aacatgggtg
1320
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1380
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1402

<210> 5682

<211> 190

<212> PRT

<213> Homo sapiens

<400> 5682

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Met Glu Ala Glu Thr Lys Thr Leu Pro Leu Glu Asn Ala Ser Ile Leu
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Ser Glu Gly Ser Leu Gln Glu Gly His Arg Leu Trp Ile Gly Asn Leu
      20              25              30
Asp Pro Lys Ile Thr Glu Tyr His Leu Leu Lys Leu Gln Lys Phe
 35              40              45
Gly Lys Val Lys Gln Phe Asp Phe Leu Phe His Lys Ser Gly Ala Leu
 50              55              60
Glu Gly Gln Pro Arg Gly Tyr Cys Phe Val Asn Phe Glu Thr Lys Gln
 65              70              75              80
Glu Ala Glu Gln Ala Ile Gln Cys Leu Asn Gly Lys Leu Ala Leu Ser
      85              90              95
Lys Lys Leu Val Val Arg Trp Ala His Ala Gln Val Lys Arg Tyr Asp
 100              105              110
His Asn Lys Asn Asp Lys Ile Leu Pro Ile Ser Leu Glu Pro Ser Ser
 115              120              125
Ser Thr Glu Pro Thr Gln Ser Asn Leu Ser Val Thr Ala Lys Ile Lys
 130              135              140
Ala Ile Glu Ala Lys Leu Lys Met Met Ala Glu Asn Pro Asp Ala Glu
 145              150              155              160
Tyr Pro Ala Ala Pro Val Tyr Ser Tyr Phe Lys Pro Pro Asp Lys Lys
      165              170              175
Arg Thr Thr Pro Tyr Ser Arg Thr Ala Trp Lys Ser Arg Arg
 180              185              190

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<210> 5683

<211> 328

<212> DNA

<213> Homo sapiens

<400> 5683

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 120
atgctttcag aaggcaccac atgtgatgca cagcctctat ttacatgtga ataattacac
 180
tgctgctttc tgggttaaaag tagggaaata cagtgtttca gggcatagga atgggtctct
 240
gggtagaaaa gtttattttg ctggtgaggag gcagggttttg ttaataaaagc tttgaaatac
 300
acaaatttca ttctggatgc tgatgctg
 328

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<210> 5684

<211> 103

<212> PRT

<213> Homo sapiens

<400> 5684

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Met Lys Phe Val Tyr Phe Lys Ala Leu Leu Thr Lys Pro Ala Ser His

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      1             5             10             15
Gln Gln Asn Lys Leu Phe Tyr Pro Glu His His Ser Tyr Ala Leu Glu
      20             25             30
His Cys Ile Ser Leu Leu Leu Thr Arg Lys Gln Gln Cys Asn Tyr Ser
      35             40             45
His Val Asn Arg Gly Cys Ala Ser His Val Val Pro Ser Glu Ser Ile
      50             55             60
Gly Trp Ile Val Cys Val Pro Trp Leu Met Leu Thr His Gln Tyr Arg
      65             70             75             80
Ser Ala Leu Arg Val Cys Arg Asp Gly Gln Cys Leu Thr Ala Glu Ala
      85             90             95
Ser Leu Gly Gln Arg Met Asp
      100

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<210> 5685

<211> 604

<212> DNA

<213> Homo sapiens

<400> 5685

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120
gagcggcagg agtgaagcgg cttcatcgag gagcggctgc tcatgtactc cttcgtcaat
180
gacaagtatg ttccctccca gaggcctcga cagacttggg gtccacaggg gaagccagag
240
gtgcccttgg caagggtgga gctgggggct gggctctgcg gggccctgtg gccatgggag
300
gttgcgggtc ttggctccag gcagctttga gagtgagacg gatagctcac cacataggag
360
aaatcagacc gggaccaggc aggctgtggg gtggagagag tggctaattt gggagataga
420
gccgtagcac ttatgagggg atgtatgtgg ttgatgggtc cagggtggcct ctctacgaac
480
caacatggca tctctcgagc agaggccatg ggccagtggg tgcgggctgc catccccgga
540
cgacttcagg gagggagttc ccctaaaggt gcccatgggc tgtggccctc tagacggggg
600
atcc
604

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<210> 5686

<211> 69

<212> PRT

<213> Homo sapiens

<400> 5686

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Pro Cys Ser Arg Val Gly Gly Lys Arg Val Val Cys Tyr Asp Asp Arg
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Phe Ile Val Lys Leu Ala Tyr Glu Ser Asp Gly Ile Val Val Ser Asn
20             25             30
Asp Thr Tyr Arg Asp Leu Gln Gly Glu Arg Gln Glu Trp Lys Arg Phe

```


tgaacaatca gaatcataga agagtgtgag cactggctct ttgtcttcca ggtgggacag
120
tgtgtgtgtg tcttcagcca ggctcctagt gggagagccc cactcagccc cagtttgaac
180
tctcgcccat cacctatcag tgccactncc tccagctctc gttcctgaaa cccgagagta
240
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300
aacactgaga cccagggtc aaaggcagac tcctcagggt cccgggaagg gagcctttcc
360
ccagccagag gagacggctc tcctatcctc aatgggtgga gtttgtctcc aggaacggca
420
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<210> 5690

<211> 54

<212> PRT

<213> Homo sapiens

<400> 5690

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<210> 5691

<211> 1227

<212> DNA

<213> Homo sapiens

<400> 5691

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 <212> PRT
 <213> Homo sapiens

<400> 5692
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 35 40 45
 Arg Val Ser Tyr His Arg Asn Ile His Tyr Asn Ser Val Val Asn Pro
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 <211> 389
 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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<210> 5695
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<210> 5696

<211> 368

<212> PRT

<213> Homo sapiens

<400> 5696

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Tyr Gly Lys Gly Val Tyr Phe Ala Arg Arg Ala Ser Leu Ser Val Gln				
	260		265	270
Asp Arg Tyr Ser Pro Pro Asn Ala Asp Gly His Lys Ala Val Phe Val				
	275		280	285
Ala Arg Val Leu Thr Gly Asp Tyr Gly Gln Gly Arg Arg Gly Leu Arg				
	290		295	300
Ala Pro Pro Leu Arg Gly Pro Gly His Val Leu Leu Arg Tyr Asp Ser				
305		310		320
Ala Val Asp Cys Ile Cys Gln Pro Ser Ile Phe Val Ile Phe His Asp				
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<211> 3362

<212> DNA

<213> Homo sapiens

<400> 5697

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<210> 5698

<211> 403

<212> PRT

<213> Homo sapiens

<400> 5698

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Thr	Ser	Arg	Gly	Cys	Gly	Leu	Asp	Leu	Leu	Pro	Gln	Tyr	Val	Ser	Leu
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Cys Ala Tyr Glu Pro Met Asp Phe Val Met Ala Leu Ile Tyr Asp Met
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<210> 5699

<211> 1565

<212> DNA

<213> Homo sapiens

<400> 5699

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<210> 5700

<211> 197

<212> PRT

<213> Homo sapiens

<400> 5700

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 Ser Gln Ala Asp Ser Lys Lys Lys Ser Asn Leu Met Met Ser Leu Phe
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 Glu Pro Gly Pro Glu Pro Leu Pro Trp Leu Gly Lys Met Ala Gln Leu

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      35              40              45
Gly Pro Ile Ser Asp Ala Lys Glu Asn Pro Tyr Gly Glu Asp Asp Asn
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Lys Ser Pro Phe Pro Leu Gln Pro Lys Asn Lys Arg Ser Tyr Ala Gln
  65              70              75              80
Asn Val Thr Val Trp Ile Lys Pro Ser Gly Leu Gln Thr Asp Val Gln
      85              90              95
Lys Ile Leu Arg Asn Ala Arg Lys Leu Pro Glu Lys Thr Gln Thr Phe
      100              105              110
Tyr Lys Glu Leu Asn Arg Leu Arg Lys Ala Ala Leu Ala Phe Gly Phe
      115              120              125
Leu Asp Leu Leu Lys Gly Val Ala Asp Met Leu Glu Arg Glu Cys Thr
      130              135              140
Leu Leu Pro Glu Thr Ala His Pro Asp Ala Ala Phe Gln Leu Thr His
      145              150              155              160
Ala Ala Gln Gln Leu Lys Leu Ala Ser Thr Gly Thr Ser Glu Tyr Ala
      165              170              175
Ala Tyr Asp Gln Asn Ile Thr Pro Leu His Thr Asp Phe Ser Gly Ser
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Ser Thr Glu Arg Ile
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<210> 5701

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 5701

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<210> 5702

<211> 348

<212> PRT

<213> Homo sapiens

<400> 5702

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 20 25 30
 Leu Leu Tyr Glu Asp Ile Gly Thr Ser Arg Val Arg Tyr Trp Asp Leu
 35 40 45
 Leu Leu Leu Ile Pro Asn Val Leu Phe Leu Ile Phe Leu Leu Trp Lys
 50 55 60
 Leu Pro Ser Ala Arg Ala Lys Ile Arg Ile Thr Ser Ser Pro Ile Phe


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65          70          75          80
Ile Thr Phe Tyr Ile Leu Val Phe Val Val Ala Leu Val Gly Ile Ala
      85          90          95
Arg Ala Val Val Ser Met Thr Val Ser Thr Ser Asn Ala Ala Thr Val
      100          105          110
Ala Asp Lys Ile Leu Trp Glu Ile Thr Arg Phe Phe Leu Leu Ala Ile
      115          120          125
Glu Leu Ser Val Ile Ile Leu Gly Leu Ala Phe Gly His Leu Glu Ser
      130          135          140
Lys Ser Ser Ile Lys Arg Val Leu Ala Ile Thr Thr Val Leu Ser Leu
      145          150          155          160
Ala Tyr Ser Val Thr Gln Gly Thr Leu Glu Ile Leu Tyr Pro Asp Ala
      165          170          175
His Leu Ser Ala Glu Asp Phe Asn Ile Tyr Gly His Gly Gly Arg Gln
      180          185          190
Phe Trp Leu Val Ser Ser Cys Phe Phe Phe Leu Val Tyr Ser Leu Val
      195          200          205
Val Ile Leu Pro Lys Thr Pro Leu Lys Glu Arg Ile Ser Leu Pro Ser
      210          215          220
Arg Arg Ser Phe Tyr Val Tyr Ala Gly Ile Leu Ala Leu Leu Asn Leu
      225          230          235          240
Leu Gln Gly Leu Gly Ser Val Leu Leu Cys Phe Asp Ile Ile Glu Gly
      245          250          255
Leu Cys Cys Val Asp Ala Thr Thr Phe Leu Tyr Phe Ser Phe Phe Ala
      260          265          270
Pro Leu Ile Tyr Val Ala Phe Leu Arg Gly Phe Phe Gly Ser Glu Pro
      275          280          285
Lys Ile Leu Phe Xaa Leu Gln Met Pro Ser Gly Arg Asp Arg Gly Ala
      290          295          300
Arg Cys Thr Pro Thr Pro Ala Leu Arg Cys Gly Pro Ala Gly Gly Pro
      305          310          315          320
Gly Gly Cys Arg Gly Cys Trp Gly Leu Ser Cys Gln Leu Leu Glu His
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Ala Val Arg Leu Cys Arg Arg Gly Gly Leu Pro Gly
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<210> 5703

<211> 1496

<212> DNA

<213> Homo sapiens

<400> 5703

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180
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240
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300
atggaaatcg taggggtgca gagcgccctg tgcggcctgg tgctatccct gctcatctgc
360

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<210> 5704

<211> 269

<212> PRT

<213> Homo sapiens

<400> 5704

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			20				25					30			
Glu	Gly	Ser	Val	Leu	Arg	Arg	Gly	Phe	Gln	Thr	Cys	Glu	His	Trp	Lys
			35				40				45				
Gln	Ile	Phe	Met	Glu	Ile	Val	Gly	Val	Gln	Ser	Ala	Leu	Cys	Gly	Leu
	50					55					60				
Val	Leu	Ser	Leu	Leu	Ile	Cys	Val	Ala	Ala	Val	Ala	Val	Phe	Thr	Thr

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65              70              75              80
His Ile Leu Leu Leu Leu Pro Val Leu Leu Ser Ile Leu Gly Ile Val
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Cys Leu Val Val Thr Ile Met Tyr Trp Ser Gly Trp Glu Met Gly Ala
              100              105              110
Val Glu Ala Ile Ser Leu Ser Ile Leu Val Gly Ser Ser Val Asp Tyr
              115              120              125
Cys Val His Leu Val Glu Gly Tyr Leu Leu Ala Gly Glu Asn Leu Pro
              130              135              140
Pro His Gln Ala Glu Asp Ala Arg Thr Gln Arg Gln Trp Arg Thr Leu
145              150              155              160
Glu Ala Val Arg His Val Gly Val Ala Ile Val Ser Ser Ala Leu Thr
              165              170              175
Thr Val Ile Ala Thr Val Pro Leu Phe Phe Cys Ile Ile Ala Pro Phe
              180              185              190
Ala Lys Phe Gly Lys Ile Val Ala Leu Asn Thr Gly Val Ser Ile Leu
              195              200              205
Tyr Thr Leu Thr Val Ser Thr Ala Leu Leu Gly Ile Met Ala Pro Ser
              210              215              220
Ser Phe Thr Arg Thr Arg Thr Ser Phe Leu Lys Ala Leu Gly Ala Val
225              230              235              240
Leu Leu Ala Gly Ala Leu Gly Leu Gly Ala Cys Leu Val Leu Leu Gln
              245              250              255
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<210> 5705

<211> 768

<212> DNA

<213> Homo sapiens

<400> 5705

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660

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<210> 5706

<211> 202

<212> PRT

<213> Homo sapiens

<400> 5706

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Arg	Ala	Arg	Leu	Gly	Lys	Met	Pro	Arg	Pro	Glu	Leu	Pro	Leu	Pro	Glu
			20					25					30		
Gly	Trp	Glu	Glu	Ala	Arg	Asp	Phe	Asp	Gly	Lys	Val	Tyr	Tyr	Ile	Asp
		35					40				45				
His	Thr	Asn	Arg	Thr	Thr	Ser	Trp	Ile	Asp	Pro	Arg	Asp	Arg	Tyr	Thr
	50					55				60					
Lys	Pro	Leu	Thr	Phe	Ala	Asp	Cys	Ile	Ser	Asp	Glu	Leu	Pro	Leu	Gly
	65				70				75					80	
Trp	Glu	Glu	Ala	Tyr	Asp	Pro	Gln	Val	Gly	Asp	Tyr	Phe	Ile	Asp	His
			85					90					95		
Asn	Thr	Lys	Thr	Thr	Gln	Ile	Glu	Asp	Pro	Arg	Val	Gln	Trp	Arg	Arg
			100				105						110		
Glu	Gln	Glu	His	Met	Leu	Lys	Asp	Tyr	Leu	Val	Val	Ala	Gln	Glu	Ala
			115				120					125			
Leu	Ser	Ala	Gln	Lys	Glu	Ile	Tyr	Gln	Val	Lys	Gln	Gln	Arg	Leu	Glu
	130					135				140					
Leu	Ala	Gln	Gln	Glu	Tyr	Gln	Gln	Leu	His	Ala	Val	Trp	Glu	His	Lys
	145				150				155					160	
Leu	Gly	Ser	Gln	Val	Ser	Leu	Val	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Lys
			165					170					175		
Tyr	Asp	Pro	Glu	Ile	Leu	Lys	Ala	Glu	Ile	Ala	Thr	Ala	Val	Gln	Arg
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<210> 5707

<211> 6988

<212> DNA

<213> Homo sapiens

<400> 5707

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<212> DNA

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<400> 5709

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<211> 441

<212> PRT

<213> Homo sapiens

<400> 5710

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Lys	Cys	Arg	Thr	Pro	Pro
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<212> DNA

<213> Homo sapiens

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<212> DNA

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<211> 408

<212> PRT

<213> Homo sapiens

<400> 5714

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<211> 1458

<212> DNA

<213> Homo sapiens

<400> 5715

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<210> 5716

<211> 148

<212> PRT

<213> Homo sapiens

<400> 5716

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Thr Ser Lys Tyr Cys Pro Met Cys Asn Ile Lys Ile His Glu Thr Gln
      50      55      60
Pro Leu Leu Asn Leu Lys Leu Asp Arg Val Met Gln Asp Ile Val Tyr
      65      70      75      80
Lys Leu Val Pro Gly Leu Gln Asp Ser Glu Glu Lys Arg Ile Arg Glu
      85      90      95
Phe Tyr Gln Ser Arg Gly Leu Asp Arg Val Thr Gln Pro Thr Gly Glu
      100      105      110
Glu Pro Ala Leu Ser Asn Leu Gly Leu Pro Phe Ser Ser Phe Asp His
      115      120      125
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<210> 5717

<211> 1419

<212> DNA

<213> Homo sapiens

<400> 5717

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<210> 5718

<211> 228

<212> PRT

<213> Homo sapiens

<400> 5718

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			20					25					30		
Thr	Val	His	Gly	Asn	Val	Ile	Thr	Thr	Asn	Thr	Ile	Phe	Glu	Asn	Leu
			35				40					45			
Trp	Phe	Ser	Cys	Ala	Thr	Asp	Ser	Leu	Gly	Val	Tyr	Asn	Cys	Trp	Glu
			50			55				60					
Phe	Pro	Ser	Met	Leu	Ala	Leu	Ser	Gly	Tyr	Ile	Gln	Ala	Cys	Arg	Ala
			65		70				75					80	
Leu	Met	Ile	Thr	Ala	Ile	Leu	Leu	Gly	Phe	Leu	Gly	Leu	Leu	Leu	Gly
			85					90					95		
Ile	Ala	Gly	Leu	Arg	Cys	Thr	Asn	Ile	Gly	Gly	Leu	Glu	Leu	Ser	Arg
			100				105					110			
Lys	Ala	Lys	Leu	Ala	Ala	Thr	Ala	Gly	Ala	Leu	His	Ile	Leu	Ala	Gly
			115			120					125				
Ile	Cys	Gly	Met	Val	Ala	Ile	Ser	Trp	Tyr	Ala	Phe	Asn	Ile	Thr	Arg
			130			135				140					
Asp	Phe	Phe	Asp	Pro	Leu	Tyr	Pro	Gly	Thr	Lys	Tyr	Glu	Leu	Gly	Pro
			145		150				155					160	
Ala	Leu	Tyr	Leu	Gly	Trp	Ser	Ala	Ser	Leu	Ile	Ser	Ile	Leu	Gly	Gly
			165			170							175		
Leu	Cys	Leu	Cys	Ser	Ala	Cys	Cys	Cys	Gly	Ser	Asp	Glu	Asp	Pro	Ala
			180			185						190			
Ala	Ser	Ala	Arg	Arg	Pro	Tyr	Gln	Ala	Pro	Val	Ser	Val	Met	Pro	Val
			195			200					205				
Ala	Thr	Ser	Asp	Gln	Glu	Gly	Asp	Ser	Ser	Phe	Gly	Lys	Tyr	Gly	Arg
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Asn	Ala	Tyr	Val												

225

<210> 5719

<211> 2267

<212> DNA

<213> Homo sapiens

<400> 5719

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360
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<210> 5720

<211> 455

<212> PRT

<213> Homo sapiens

<400> 5720

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			20					25					30		
His	Asp	Val	Pro	Gln	Gly	Leu	His	Pro	Pro	Val	Ala	Pro	Ser	Gly	Gly
		35				40						45			
Val	Asp	Ser	Ala	Val	Ala	Ala	Leu	Leu	Leu	Arg	Arg	Arg	Gly	Tyr	Gln
	50				55					60					
Val	Thr	Gly	Val	Phe	Met	Lys	Asn	Trp	Asp	Ser	Leu	Asp	Glu	His	Gly
65					70				75					80	
Val	Cys	Thr	Ala	Asp	Lys	Asp	Cys	Glu	Asp	Ala	Tyr	Arg	Val	Cys	Gln
			85					90						95	
Ile	Leu	Asp	Ile	Pro	Phe	His	Gln	Val	Ser	Tyr	Val	Lys	Glu	Tyr	Trp
							105						110		
Asn	Asp	Val	Phe	Ser	Asp	Phe	Leu	Asn	Glu	Tyr	Glu	Lys	Gly	Arg	Thr
		115					120						125		
Pro	Asn	Pro	Asp	Ile	Val	Cys	Asn	Lys	His	Ile	Lys	Phe	Ser	Cys	Phe

130 135 140
 Phe His Tyr Ala Val Asp Asn Leu Gly Ala Asp Ala Ile Ala Thr Gly
 145 150 155 160
 His Tyr Ala Arg Thr Ser Leu Glu Asp Glu Val Phe Glu Gln Lys
 165 170 175
 His Val Lys Lys Pro Glu Gly Leu Phe Arg Asn Arg Phe Glu Val Arg
 180 185 190
 Asn Ala Val Lys Leu Leu Gln Ala Ala Asp Ser Phe Lys Asp Gln Thr
 195 200 205
 Phe Phe Leu Ser Gln Val Ser Gln Asp Ala Leu Arg Arg Thr Ile Phe
 210 215 220
 Pro Leu Gly Gly Leu Thr Lys Glu Phe Val Lys Lys Ile Ala Ala Glu
 225 230 235 240
 Asn Arg Leu His His Val Leu Gln Lys Lys Glu Ser Met Gly Met Cys
 245 250 255
 Phe Ile Gly Lys Arg Asn Phe Glu His Phe Leu Leu Gln Tyr Leu Gln
 260 265 270
 Pro Arg Pro Gly His Phe Ile Ser Ile Glu Asp Asn Lys Val Leu Gly
 275 280 285
 Thr His Lys Gly Trp Phe Leu Tyr Thr Leu Gly Gln Arg Ala Asn Ile
 290 295 300
 Gly Gly Leu Arg Glu Pro Trp Tyr Val Val Glu Lys Asp Ser Val Lys
 305 310 315 320
 Gly Asp Val Phe Val Ala Pro Arg Thr Asp His Pro Ala Leu Tyr Arg
 325 330 335
 Asp Leu Leu Arg Thr Ser Arg Val His Trp Ile Ala Glu Glu Pro Pro
 340 345 350
 Ala Ala Leu Val Arg Asp Lys Met Met Glu Cys His Phe Arg Phe Arg
 355 360 365
 His Gln Met Ala Leu Val Pro Cys Val Leu Thr Leu Asn Gln Asp Gly
 370 375 380
 Thr Val Trp Val Thr Ala Val Gln Ala Val Arg Ala Leu Ala Thr Gly
 385 390 395 400
 Gln Phe Ala Val Phe Tyr Lys Gly Asp Glu Cys Leu Gly Ser Gly Lys
 405 410 415
 Ile Leu Arg Leu Gly Pro Ser Ala Tyr Thr Leu Gln Lys Gly Gln Arg
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 Arg Ala Gly Met Ala Thr Glu Ser Pro Ser Asp Ser Pro Glu Asp Gly
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 Pro Gly Leu Ser Pro Leu Leu
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<210> 5721

<211> 400

<212> DNA

<213> Homo sapiens

<400> 5721

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 180

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 300
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<210> 5722

<211> 80

<212> PRT

<213> Homo sapiens

<400> 5722

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Glu	Arg	Lys	Ala	Leu	Met	Leu	Ala	Met	Gly	Tyr	His	Glu	Lys	Gly	Arg
			20					25					30		
Ala	Phe	Leu	Lys	Arg	Lys	Glu	Tyr	Gly	Ile	Ala	Leu	Pro	Cys	Leu	Leu
			35				40					45			
Asp	Ala	Asp	Lys	Tyr	Phe	Trp	Trp	Ala	Leu	Leu	Tyr	Leu	Val	Asn	Thr
	50					55					60				
Ser	Phe	Lys	Glu	Asp	Gly	Pro	Asp	Tyr	Thr	Glu	His	Leu	Pro	Cys	Pro
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<210> 5723

<211> 376

<212> DNA

<213> Homo sapiens

<400> 5723

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 180
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 240
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<210> 5724

<211> 125

<212> PRT

<213> Homo sapiens

<400> 5724

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Met Gly Val Pro Glu Val Trp Gly Leu Ser Lys Glu Trp Trp His			
	35	40	45
Ala Gly Leu Ser Gly Ala Met Trp His Gly Trp Trp Ala Ser Ile Cys			
	50	55	60
Ser Gly Cys Leu Leu Ser Asp Glu Gly Thr Gly Cys Pro Cys Leu Pro			
65	70	75	80
Gln His Ala Pro Cys Pro Ala Cys Pro Leu Pro Cys Met Ser Pro Val			
	85	90	95
Leu His Ile Pro Cys Pro Ala Gly Pro Ile Leu Ser Cys Met Ser Pro			
	100	105	110
Val Leu His Met Pro Cys Pro Ala Leu Leu Leu His Ala			
	115	120	125

<210> 5725

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 5725

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 420
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<210> 5726

<211> 273

<212> PRT

<213> Homo sapiens

<400> 5726

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			20					25					30		
Ser	Arg	Pro	Pro	Gly	Ser	Arg	Pro	Thr	Ala	His	Gly	Arg	Ala	Trp	Gly
			35					40				45			
Ala	Ser	Arg	Ala	Arg	Arg	Pro	Ala	Pro	Gly	Gly	Pro	Phe	Pro	Gly	Val
			50			55					60				
Ser	Thr	Asp	Asp	Ser	Ala	Val	Pro	Pro	Pro	Gly	Gly	Ala	Pro	His	Phe
					70					75				80	
Gly	His	Tyr	Arg	Thr	Gly	Gly	Gly	Ala	Met	Gly	Leu	Arg	Ser	Ala	Ser
					85				90					95	
Val	Ser	Ser	Val	Ala	Gly	Met	Gly	Met	Asp	Pro	Ser	Thr	Ala	Gly	Gly
			100					105						110	
Val	Pro	Phe	Gly	Leu	Tyr	Thr	Pro	Ala	Ser	Arg	Gly	Thr	Gly	Asp	Ser
			115					120				125			
Glu	Arg	Ala	Pro	Gly	Gly	Gly	Gly	Ser	Ala	Ser	Asp	Ser	Thr	Tyr	Ala
			130			135					140				
His	Gly	Asn	Gly	Tyr	Gln	Glu	Thr	Gly	Gly	Gly	His	His	Arg	Asp	Gly
					150					155				160	
Met	Leu	Tyr	Leu	Gly	Ser	Arg	Ala	Ser	Leu	Ala	Asp	Ala	Leu	Pro	Leu
				165					170					175	
His	Ile	Ala	Pro	Arg	Trp	Phe	Ser	Ser	His	Ser	Gly	Phe	Lys	Cys	Pro
			180				185						190		
Ile	Cys	Ser	Lys	Ser	Val	Ala	Ser	Asp	Glu	Met	Glu	Met	His	Phe	Ile
			195				200						205		
Met	Cys	Leu	Ser	Lys	Pro	Arg	Leu	Ser	Tyr	Asn	Asp	Asp	Val	Leu	Thr
			210			215					220				
Lys	Asp	Ala	Gly	Glu	Cys	Val	Ile	Cys	Leu	Glu	Glu	Leu	Leu	Gln	Gly
			225			230				235				240	
Asp	Thr	Ile	Ala	Arg	Leu	Pro	Cys	Leu	Cys	Ile	Tyr	His	Lys	Ser	Cys
			245					250						255	
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Asp

<210> 5727

<211> 1237

<212> DNA

<213> Homo sapiens

<400> 5727

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 780
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 1080
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<210> 5728

<211> 368

<212> PRT

<213> Homo sapiens

<400> 5728

Xaa Arg Arg Glu Val Thr Thr Arg Thr Gly Ser Val Ser Thr Thr Gln

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	20	25	30
Lys Tyr Arg Asp Ile Asp Glu Asp Glu Ile Leu Arg Thr Leu Ser Pro			
	35	40	45
Glu Glu Leu Glu Gln Leu Asp Cys Glu Leu Gln Glu Met Asp Pro Glu			
	50	55	60
Asn Met Leu Leu Pro Ala Gly Leu Arg Gln Arg Asp Gln Thr Lys Lys			
65	70	75	80
Ser Pro Thr Gly Pro Leu Asp Arg Glu Ala Leu Leu Gln Tyr Leu Glu			
	85	90	95
Gln Gln Ala Leu Glu Val Lys Glu Arg Asp Asp Leu Val Pro Phe Thr			
	100	105	110
Gly Glu Lys Lys Gly Lys Pro Tyr Ile Gln Pro Lys Arg Glu Ile Pro			
	115	120	125
Ala Glu Glu Gln Ile Thr Leu Glu Pro Glu Leu Glu Glu Ala Leu Ala			
	130	135	140
His Ala Thr Asp Ala Glu Met Cys Asp Ile Ala Ala Ile Leu Asp Met			
145	150	155	160
Tyr Thr Leu Met Ser Asn Lys Gln Tyr Tyr Asp Ala Leu Cys Ser Gly			
	165	170	175
Glu Ile Cys Asn Thr Glu Gly Ile Ser Ser Val Val Gln Pro Asp Lys			
	180	185	190
Tyr Lys Pro Val Pro Asp Glu Pro Pro Asn Pro Thr Asn Ile Glu Glu			
	195	200	205
Ile Leu Lys Arg Val Arg Ser Asn Asp Lys Glu Leu Glu Glu Val Asn			
	210	215	220
Leu Asn Asn Ile Gln Asp Ile Pro Ile Pro Met Leu Ser Glu Leu Cys			
225	230	235	240
Glu Ala Met Lys Ala Asn Thr Tyr Val Arg Ser Phe Ser Leu Val Ala			
	245	250	255
Thr Arg Ser Gly Asp Pro Ile Ala Asn Ala Val Ala Asp Met Leu Arg			
	260	265	270
Glu Asn Arg Ser Leu Gln Ser Leu Asn Ile Glu Ser Asn Phe Ile Ser			
	275	280	285
Ser Thr Gly Leu Met Ala Val Leu Lys Ala Val Arg Glu Asn Ala Thr			
	290	295	300
Leu Thr Glu Leu Arg Val Asp Asn Gln Arg Gln Trp Pro Gly Asp Ala			
	305	310	315
Val Glu Met Glu Met Ala Thr Val Leu Glu Gln Cys Pro Ser Ile Val			
	325	330	335
Arg Phe Gly Tyr His Phe Thr Gln Gln Gly Pro Arg Ala Arg Ala Ala			
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Gln Ala Met Thr Arg Asn Asn Glu Leu Arg Arg Gln Gln Lys Lys Arg			
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<210> 5729

<211> 381

<212> DNA

<213> Homo sapiens

<400> 5729

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 cagccagatg cgcctcaggt ctttctcgaa cttgatctgc aagacgcaga gagagggacc
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 240
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<210> 5730

<211> 64

<212> PRT

<213> Homo sapiens

<400> 5730

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Ala	Gly	Gly	His	Ser	Pro	Ala	Cys	Val	Ser	Gly	Val	Pro	Pro	Gly	Pro
			20				25					30			
Ser	Ser	Ala	Gly	Thr	Ala	Ser	Ser	Ser	Pro	Ala	Ser	Gly	Thr	Cys	Gly
		35				40					45				
Gly	Ser	Ser	Ser	Ala	Gly	Gly	Ser	Ser	Ala	Arg	Phe	Cys	Thr	Lys	Phe
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<210> 5731

<211> 891

<212> DNA

<213> Homo sapiens

<400> 5731

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 120
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 360
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 420
 aagatgaggg ggggcttctg gccggcgctg aggatgaact ggcgggtgtg gacgccacta
 480
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 660
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 891

<210> 5732
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 5732
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 35 40 45
 Leu Ala Gln Met Ile Glu Lys Lys Arg Lys Lys Glu Asn Ser Arg Ser
 50 55 60
 Leu Asp Val Gly Gly Pro Leu Arg Tyr Ala Val Tyr Gly Phe Phe Phe
 65 70 75 80
 Thr Gly Pro Leu Ser His Phe Phe Tyr Phe Phe Met Glu His Trp Ile
 85 90 95
 Pro Pro Glu Val Pro Leu Ala Gly Leu Arg Arg Leu Leu Leu Asp Arg
 100 105 110
 Leu Val Phe Ala Pro Ala Phe Leu Met Leu Phe Phe Leu Ile Met Asn
 115 120 125
 Phe Leu Glu Gly Lys Asp Ala Ser Ala Phe Ala Ala Lys Met Arg Gly
 130 135 140
 Gly Phe Trp Pro Ala Leu Arg Met Asn Trp Arg Val Trp Thr Pro Leu
 145 150 155 160
 Gln Phe Ile Asn Ile Asn Tyr Val Pro Leu Lys Phe Arg Val Leu Phe
 165 170 175
 Ala Asn Leu Ala Ala Leu Phe Trp Tyr Ala Tyr Leu Ala Ser Leu Gly
 180 185 190
 Lys

<210> 5733
 <211> 950
 <212> DNA
 <213> Homo sapiens

<400> 5733
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 120

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360
ccacacaaca tcaagaaggc cgacaaccag gttggaacc aagacggagc tcagaccac
420
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480
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780
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840
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<210> 5734

<211> 82

<212> PRT

<213> Homo sapiens

<400> 5734

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Xaa His Val Val Ile Leu Pro Gly Asp Gly Gly Ser Gly Thr Ala Ala
 1           5           10          15
Ile Ser Phe Thr Gly Ala Leu Lys Ile Pro Gly Val Ile Glu Phe Ser
          20          25          30
Leu Cys Leu Leu Phe Ala Lys Leu Val Ser Tyr Thr Phe Leu Phe Trp
          35          40          45
Leu Pro Leu Tyr Ile Thr Asn Val Asp His Leu Asp Ala Lys Lys Ala
          50          55          60
Gly Cys Thr Gly Ser Pro Asp Pro Leu Arg His Ser Ser His Arg Thr
65          70          75          80
Ser Lys

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<210> 5735

<211> 4241

<212> DNA

<213> Homo sapiens

<400> 5735

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120
cccttctctg ggagtgcgcc aatgcctggg ccgacccaaa ccctgtcccc aaatggcgag
180
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240
gtgcgcgggg agcgttccta cagttgggga atggcggtca atgtgtatcc tacctcgata
300
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360
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420
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480
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<210> 5736

<211> 327

<212> PRT

<213> Homo sapiens

<400> 5736

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 Thr Val Arg Gly Glu Arg Ser Tyr Ser Trp Gly Met Ala Val Asn Val
 35 40 45
 Tyr Ser Thr Ser Ile Thr Gln Glu Thr Met Ser Arg His Asp Ile Ile
 50 55 60
 Ala Trp Val Asn Asp Ile Val Ser Leu Asn Tyr Thr Lys Val Glu Gln
 65 70 75 80
 Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met Asp Met Leu Phe Pro
 85 90 95
 Gly Cys Ile Ser Leu Lys Lys Val Lys Phe Gln Ala Lys Leu Glu His

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      100              105              110
Glu Tyr Ile His Asn Phe Lys Leu Leu Gln Ala Ser Phe Lys Arg Met
      115              120              125
Asn Val Asp Lys Val Ile Pro Val Glu Lys Leu Val Lys Gly Arg Phe
      130              135              140
Gln Asp Asn Leu Asp Phe Ile Gln Trp Phe Lys Lys Phe Tyr Asp Ala
      145              150              155              160
Asn Tyr Asp Gly Lys Glu Tyr Asp Pro Val Glu Ala Arg Gln Gly Gln
      165              170              175
Asp Ala Ile Pro Pro Pro Asp Pro Gly Glu Gln Ile Phe Asn Leu Pro
      180              185              190
Lys Lys Ser His His Ala Asn Ser Pro Thr Ala Gly Ala Ala Lys Ser
      195              200              205
Ser Pro Ala Ala Lys Pro Gly Ser Thr Pro Ser Arg Pro Ser Ser Ala
      210              215              220
Lys Arg Ala Ser Ser Ser Gly Ser Ala Ser Lys Ser Asp Lys Asp Leu
      225              230              235              240
Glu Thr Gln Val Ile Gln Leu Asn Glu Gln Val His Ser Leu Lys Leu
      245              250              255
Ala Leu Glu Gly Val Glu Lys Glu Arg Asp Phe Tyr Phe Gly Lys Leu
      260              265              270
Arg Glu Ile Glu Leu Leu Cys Gln Glu His Gly Gln Glu Asn Asp Asp
      275              280              285
Leu Val Gln Arg Leu Met Asp Ile Leu Tyr Ala Ser Glu Glu His Glu
      290              295              300
Gly His Thr Glu Glu Pro Glu Ala Glu Glu Gln Ala His Glu Gln Gln
      305              310              315              320
Pro Pro Gln Gln Glu Glu Tyr
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<210> 5737

<211> 340

<212> DNA

<213> Homo sapiens

<400> 5737

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240
aagatgttgc agtgccatcc tcacctgggt gcttgaaatc ggccaagggt ggagcattta
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<210> 5738

<211> 99

<212> PRT

<213> Homo sapiens

<400> 5738

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Gln His Leu Pro Leu Arg Leu Gln Leu Pro Ser Gln Val His Gln Glu
      20           25           30
Thr Thr Gly His His Trp Gln Trp Arg Gly Asp Met Glu His Gly Leu
      35           40           45
Gly Ser Arg Leu Leu Ala Pro Asp Val Gln Pro Gln Thr Pro Pro Val
      50           55           60
Met Gly Glu Val Trp Arg Pro Val Gln Leu Ser Gln Gly His Ala His
65           70           75           80
Leu Ser Leu Gly Ser Val Gly Lys Ala Tyr Pro Lys Ser His Ile Gln
      85           90           95
Gly Gly Xaa

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<210> 5739

<211> 780

<212> DNA

<213> Homo sapiens

<400> 5739

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ttactcgta attggaaca cctctagcct gtactaaatt tccatattha ttggccccgt
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gagccagcac catggcccgt ccctgagcat gtccagcaaa cctgcccagg ctctgcagct
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660
aaggccatgc cagagtccat cgttgcctcc accctacctg tgcaggaaac ctggacatca
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<210> 5740

<211> 120

<212> PRT

<213> Homo sapiens

<400> 5740

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Leu Pro Val Cys Gly Gly Gln Lys Arg Lys Thr Thr Gln Gly Glu Cys
35 40 45
Leu Leu Pro Pro Ala Gly Lys Gln Leu Gly His His Leu Ser Glu Ser
50 55 60
Arg Cys Cys Ser Ser Trp Gln Gln Ser His Ser Glu Arg Ser Cys Val
65 70 75 80
His Cys Leu Ser Gly Arg Pro Cys Gln Ser Pro Ser Leu Pro Pro Pro
85 90 95
Tyr Leu Cys Arg Lys Pro Gly His His His Phe Lys Ala Leu Pro Ser
100 105 110
Phe Leu Gly Arg Ala Gln Pro Gln
115 120

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<210> 5741

<211> 2444

<212> DNA

<213> Homo sapiens

<400> 5741

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120
gagtatgagg cggctgcagc acgcatcgag gctatggacc ctgccactgt cgagcagcag
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900

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<210> 5742

<211> 427

<212> PRT

<213> Homo sapiens

<400> 5742

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              20              25              30
Gly Ala Gly Tyr Asn Ser Glu Asp Glu Tyr Glu Ala Ala Ala Arg
 35              40              45
Ile Glu Ala Met Asp Pro Ala Thr Val Glu Gln Gln Glu His Trp Phe
 50              55              60
Glu Lys Ala Leu Arg Asp Lys Lys Gly Phe Ile Lys Gln Met Lys
 65              70              75
Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val Tyr Gly
 85              90              95
Asp Gln Asp Met His Glu Val Val Arg Lys His Cys Met Asp Tyr Leu
 100              105              110
Met Lys Asn Ala Asp Tyr Phe Ser Asn Tyr Val Thr Glu Asp Phe Thr
 115              120              125
Thr Tyr Ile Asn Arg Lys Arg Lys Asn Asn Cys His Gly Asn His Ile
 130              135              140
Glu Met Gln Ala Met Ala Glu Met Tyr Asn Arg Pro Val Glu Val Tyr
 145              150              155
Gln Tyr Ser Thr Glu Pro Ile Asn Thr Phe His Gly Ile His Gln Asn
 165              170              175
Glu Asp Glu Pro Ile Arg Val Ser Tyr His Arg Asn Ile His Tyr Asn
 180              185              190
Ser Val Val Asn Pro Asn Lys Ala Thr Ile Gly Val Gly Leu Gly Leu
 195              200              205
Pro Ser Phe Lys Pro Gly Phe Ala Glu Gln Ser Leu Met Lys Asn Ala
 210              215              220
Ile Lys Thr Ser Glu Glu Ser Trp Ile Glu Gln Gln Met Leu Glu Asp
 225              230              235
Lys Lys Arg Ala Thr Asp Trp Glu Ala Thr Asn Glu Ala Ile Glu Glu
 245              250              255
Gln Val Ala Arg Glu Ser Tyr Leu Gln Trp Leu Arg Asp Gln Glu Lys
 260              265              270
Gln Ala Arg Gln Val Arg Gly Pro Ser Gln Pro Arg Lys Ala Ser Ala
 275              280              285
Thr Cys Ser Ser Ala Thr Ala Ala Ala Ser Ser Gly Leu Glu Glu Trp
 290              295              300
Thr Ser Arg Ser Pro Arg Gln Arg Ser Ser Ala Ser Ser Pro Glu His
 305              310              315
Pro Glu Leu His Ala Glu Leu Gly Met Lys Pro Pro Ser Pro Gly Thr
 325              330              335
Val Leu Ala Leu Ala Lys Pro Pro Ser Pro Cys Ala Pro Gly Thr Ser
 340              345              350
Ser Gln Phe Ser Ala Gly Ala Asp Arg Ala Thr Ser Pro Leu Val Ser
 355              360              365
Leu Tyr Pro Ala Leu Glu Cys Arg Ala Leu Ile Gln Gln Met Ser Pro
 370              375              380
Ser Ala Phe Gly Leu Asn Asp Trp Asp Asp Asp Glu Ile Leu Ala Ser

```

```

385                      390                      395                      400
Val Leu Ala Val Ser Gln Gln Glu Tyr Leu Asp Ser Met Lys Lys Asn
                      405                      410                      415
Lys Val His Arg Asp Pro Pro Pro Asp Lys Ser
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<210> 5743
 <211> 550
 <212> DNA
 <213> Homo sapiens

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<400> 5743
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120
gcgtctcagg cgtccctcct ggaccttccc ctatctggct gggcggacac tggtaggatt
180
gcggtggagc cacatgtcct gcggtcccggt tatccagtct gggcaggaag cagcggggccg
240
tgagccagct ctccaggggg ctgacggaca tcttctggg gaccagcatc tcctccagct
300
ccagctggggc ccccttgcca gggagagagg ccgcccctacc tgggccggcc ggcgatgtgc
360
tgtaaaagggg cccgcagacc cggctgccca actccagaga cgggccaagg cggggcgccgc
420
ccgaaaggtc ccagaacggg gaggccggcc cctcccccg gttcaccccc gcgcgaatcg
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540
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550

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<210> 5744
 <211> 95
 <212> PRT
 <213> Homo sapiens

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<400> 5744
Arg Thr Ser Ser Trp Gly Pro Ala Ser Pro Pro Ala Pro Ala Gly Pro
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Pro Cys Glu Gly Glu Arg Pro Pro Tyr Leu Gly Arg Pro Ala Met Cys
20      25      30
Cys Lys Gly Ala Arg Arg Pro Gly Cys Pro Thr Pro Glu Thr Gly Gln
35      40      45
Gly Gly Arg Pro Pro Lys Gly Pro Arg Thr Gly Arg Pro Ala Pro Ser
50      55      60
Pro Gly Ser Pro Pro Arg Glu Ser Arg Cys Leu Ala Pro Xaa Asp Pro
65      70      75      80
Leu Gly Trp Thr Pro Gly Pro Pro Ala Ala Pro Gly Ala Leu
85      90      95

```

<210> 5745
 <211> 849

<212> DNA

<213> Homo sapiens

<400> 5745

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cgataaaaaa caccagggga cgggactacc aggggaaatg cttattgagt aaagtatccg
120
aggaagtgat gcagggcagg taaacagctg gtgctcagca gcgagaggac gcgtcactct
180
gccgttctgc aggggtgacgc cctccccgta cctcgctgag agccacctgc agacacagca
240
ggccacagca gaatgcacag gtcactgttg taggggaaca aatcgtaatg cccagagaaa
300
acctgatagt gaaatgtaaa cagacaggac aggggtgggtc cagggtggcca ccaccgccag
360
gcccttcccg tgattgatct gagagcttca cagccggcgg cactgggacc catttccaga
420
aacactggaa caccaggctc ctcagatgcc gcggggaggg gcccaggga ggcctttctc
480
agcatcagct tttgggtgac aaacccata cagcaaaatc gtacaaatac acacaacgga
540
ccccagctg acagtgcagc caggacccta ggaaggtcag gtggtgggtga agtcatcccc
600
tctccaaccg agcagagcct ggggttgggc tctgatgacc tccggggcaa agtgtccagg
660
tggaggaagc aaactcccaa atggggcaca aaghtaataa aaagcagctg agagattgag
720
ggatggggtc ggggccactt ggccgacacc ttctgcctcg cctggccggg cggggccagg
780
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840
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849

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<210> 5746

<211> 140

<212> PRT

<213> Homo sapiens

<400> 5746

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Met Thr Ser Pro Pro Asp Leu Pro Arg Val Leu Val Ser Leu Ser
1          5          10          15
Ala Gly Gly Pro Leu Cys Val Phe Val Gln Phe Cys Cys Met Gly Phe
20          25          30
Val Thr Gln Lys Leu Met Leu Arg Lys Ala Ser Leu Gly Pro Leu Pro
35          40          45
Arg Ala Ser Glu Arg Pro Gly Val Pro Val Phe Leu Glu Met Gly Pro
50          55          60
Ser Ala Ala Gly Cys Glu Ala Leu Arg Ser Ile Thr Gly Arg Ala Trp
65          70          75          80
Arg Trp Trp Pro Pro Gly Thr Thr Leu Ser Cys Leu Phe Thr Phe His
85          90          95
Tyr Gln Val Phe Ser Gly His Tyr Asp Leu Phe Pro Tyr Asn Ser Asp

```


	100		105		110
Leu Cys Ile	Leu Leu Trp Pro	Ala Val Ser Ala	Gly Gly Ser	Gln Arg	
	115		120		125
Gly Thr Gly	Arg Ala Ser Pro	Cys Arg Thr Ala	Glu		
	130		135		140

<210> 5747

<211> 1999

<212> DNA

<213> Homo sapiens

<400> 5747

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120
actcggggcg cgggggaccc ggccccgtac ctccagcccc gctggggcag cgcgagcgag
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240
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300
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420
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480
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540
aacctcccca gcaagatgct cctgggtctat gatctctact tgtctcctaa gctgtgggct
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660
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960
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1080
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1200
gaggaaggta gactgaactg cagcaccagc cctgagatct tccgcaagtg tatggattat
1260

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tcctctgaca gcagcgtaac tccctctggc agccctggg tccggaggcg tcgccaagcc
 1320
 gagatgggga cccaggagaa aagccccggt acgagtcgcc tgctctcccg gaagatgcag
 1380
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 1440
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 1560
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 1620
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 1860
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 1920
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 1980
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 1999

<210> 5748

<211> 492

<212> PRT

<213> Homo sapiens

<400> 5748

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 Glu Asp Glu Glu Glu Gly Ala Glu Thr Arg Gly Ala Gly Asp Pro Ala
 35 40 45
 Arg Tyr Leu Ser Pro Gly Trp Gly Ser Ala Ser Glu Glu Glu Pro Ser
 50 55 60
 Arg Gly His Ser Gly Thr Thr Ala Ser Gly Gly Glu Asn Glu Arg Glu
 65 70 75 80
 Asp Leu Glu Gln Glu Trp Lys Pro Pro Asp Glu Glu Leu Ile Lys Lys
 85 90 95
 Leu Val Asp Gln Ile Glu Phe Tyr Phe Ser Asp Glu Asn Leu Glu Lys
 100 105 110
 Asp Ala Phe Leu Leu Lys His Val Arg Arg Asn Lys Leu Gly Tyr Val
 115 120 125
 Ser Val Lys Leu Leu Thr Ser Phe Lys Lys Val Lys His Leu Thr Arg
 130 135 140
 Asp Trp Arg Thr Thr Ala His Ala Leu Lys Tyr Ser Val Val Leu Glu
 145 150 155 160
 Leu Asn Glu Asp His Arg Lys Val Arg Arg Thr Thr Pro Val Pro Leu

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165              170              175
Phe Pro Asn Glu Asn Leu Pro Ser Lys Met Leu Leu Val Tyr Asp Leu
180              185              190
Tyr Leu Ser Pro Lys Leu Trp Ala Leu Ala Thr Pro Gln Lys Asn Gly
195              200              205
Arg Val Gln Glu Lys Val Met Glu His Leu Leu Lys Leu Phe Gly Thr
210              215              220
Phe Gly Val Ile Ser Ser Val Arg Ile Leu Lys Pro Gly Arg Glu Leu
225              230              235
Pro Pro Asp Ile Arg Arg Ile Ser Ser Arg Tyr Ser Gln Val Gly Thr
245              250              255
Gln Glu Cys Ala Ile Val Glu Phe Glu Glu Val Glu Ala Ala Ile Lys
260              265              270
Ala His Glu Phe Met Ile Thr Glu Ser Gln Gly Lys Glu Asn Met Lys
275              280              285
Ala Val Leu Ile Gly Met Lys Pro Pro Lys Lys Lys Pro Ala Lys Asp
290              295              300
Lys Asn His Asp Glu Glu Pro Thr Ala Ser Ile His Leu Asn Lys Ser
305              310              315
Leu Asn Lys Arg Val Glu Glu Leu Gln Tyr Met Gly Asp Glu Ser Ser
325              330              335
Ala Asn Ser Ser Ser Asp Pro Glu Ser Asn Pro Thr Ser Pro Met Ala
340              345              350
Gly Arg Arg His Ala Ala Thr Asn Lys Leu Ser Pro Ser Gly His Gln
355              360              365
Asn Leu Phe Leu Ser Pro Asn Ala Ser Pro Cys Thr Ser Pro Trp Ser
370              375              380
Ser Pro Leu Ala Gln Arg Lys Gly Val Ser Arg Lys Ser Pro Leu Ala
385              390              395
Glu Glu Gly Arg Leu Asn Cys Ser Thr Ser Pro Glu Ile Phe Arg Lys
405              410              415
Cys Met Asp Tyr Ser Ser Asp Ser Ser Val Thr Pro Ser Gly Ser Pro
420              425              430
Trp Val Arg Arg Arg Arg Gln Ala Glu Met Gly Thr Gln Glu Lys Ser
435              440              445
Pro Gly Thr Ser Pro Leu Leu Ser Arg Lys Met Gln Thr Ala Asp Gly
450              455              460
Leu Pro Val Gly Val Leu Arg Leu Pro Arg Gly Pro Asp Asn Thr Arg
465              470              475
Gly Phe His Gly His Glu Arg Ser Arg Ala Cys Val
485              490

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<210> 5749

<211> 2849

<212> DNA

<213> Homo sapiens

<400> 5749

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120
gaaataaaac ccatttcaaa agttattgga aagaaagtaa ggtatggctc ttatgggtta
180

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actagtggta gtcagtttct gctttttact ccctctgaat tattaattgt ttgccaggtt
240
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600
cgtcataaca acatcaccag catttccacg ggcagttttt ccacaactcc aaatttgaag
660
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720
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1800

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<210> 5750

<211> 522

<212> PRT

<213> Homo sapiens

<400> 5750

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20      25      30
Val Gly Pro Gly Ala Ser Gly Val Cys Pro Thr Ala Cys Ile Cys Ala
35      40      45
Thr Asp Ile Val Ser Cys Thr Asn Lys Asn Leu Ser Lys Val Pro Gly
50      55      60
Asn Leu Phe Arg Leu Ile Lys Arg Leu Asp Leu Ser Tyr Asn Arg Ile
65      70      75      80
Gly Leu Leu Asp Ser Glu Trp Ile Pro Val Ser Phe Ala Lys Leu Asn

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				85				90				95			
Thr	Leu	Ile	Leu	Arg	His	Asn	Asn	Ile	Thr	Ser	Ile	Ser	Thr	Gly	Ser
				100				105					110		
Phe	Ser	Thr	Thr	Pro	Asn	Leu	Lys	Cys	Leu	Asp	Leu	Ser	Ser	Asn	Lys
				115				120					125		
Leu	Lys	Thr	Val	Lys	Asn	Ala	Val	Phe	Gln	Glu	Leu	Lys	Val	Leu	Glu
				130				135					140		
Val	Leu	Leu	Leu	Tyr	Asn	Asn	His	Ile	Ser	Tyr	Leu	Asp	Pro	Ser	Ala
				145				150					155		
Phe	Gly	Gly	Leu	Ser	Gln	Leu	Gln	Lys	Leu	Tyr	Leu	Ser	Gly	Asn	Phe
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Leu	Thr	Gln	Phe	Pro	Met	Asp	Leu	Tyr	Val	Gly	Arg	Phe	Lys	Leu	Ala
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<211> 926

<212> DNA

<213> Homo sapiens

<400> 5751

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<211> 129

<212> PRT

<213> Homo sapiens

<400> 5752

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Pro Met Phe Leu Ala Leu Asp Arg Arg Gly Gly Pro Arg Pro Gly Gly				
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<211> 5668

<212> DNA

<213> Homo sapiens

<400> 5753

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1080

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<211> 221

<212> PRT

<213> Homo sapiens

<400> 5754

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      65             70             75             80
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Glu Lys Glu Val Pro Val Ile Phe Ile His Pro Leu Asn Thr Gly Leu
      115            120            125
Phe Arg Ile Lys Ile Gln Gly Ala Thr Gly Lys Phe Asn Met Val Ile
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Pro Leu Val Asp Gly Met Ile Val Ser Arg Arg Ala Leu Gly Phe Leu
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Val Arg Gln Thr Val Ile Asn Ile Cys Arg Arg Lys Arg Leu Glu Ser
      165            170            175
Asp Ser Tyr Ser Pro Pro His Val Arg Arg Lys Gln Lys Ile Thr Asp
      180            185            190
Ile Val Asn Lys Tyr Arg Asn Lys Gln Leu Glu Pro Glu Phe Tyr Thr
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<211> 1513

<212> DNA

<213> Homo sapiens

<400> 5755

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<211> 415

<212> PRT

<213> Homo sapiens

<400> 5756

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195              200              205
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Gln Val His Gln Glu Leu Arg Glu Glu Leu Ala Lys Val Lys Thr Leu
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355              360              365
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<210> 5757

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 5757

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<210> 5758

<211> 440

<212> PRT

<213> Homo sapiens

<400> 5758

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 Ile Tyr Gly Val Gln Glu Val His Val Asn Gly Ala Val Val Leu Ala
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 Phe Glu Leu Tyr Tyr His Thr Thr Gln Asp Leu Gln Leu Phe Arg Glu
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 Met Ser Pro Asp Glu Tyr His Ser Gly Val Asn Asn Ser Val Tyr Thr
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 Asp Leu Gly Leu Pro Ile Pro Ser Gln Trp Leu Ala Val Ala Asp Lys
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 Ile Lys Val Pro Phe Asp Val Glu Gln Asn Phe His Pro Glu Phe Asp
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 Gly Tyr Glu Pro Gly Glu Val Val Lys Gln Ala Asp Val Val Leu Leu
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 Gly Tyr Pro Val Pro Phe Ser Leu Ser Pro Asp Val Arg Arg Lys Asn
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 Trp Ser Met Phe Ala Val Gly Trp Met Glu Leu Lys Asp Ala Val Arg


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Arg Ala Gly Pro Trp Ala Pro His Leu Glu Ala Glu Leu Trp Pro Ser
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<210> 5759

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 5759

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<211> 273

<212> PRT

<213> Homo sapiens

<400> 5760

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 Gly Leu Val Phe Gly Ala Leu Thr Glu Asp Gly His Ile Asp Lys Glu
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 His Arg Ala Phe Asp Met Val His Asp Pro Met Ala Ala Leu Glu Thr
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<211> 333

<212> PRT

<213> Homo sapiens

<400> 5762

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<212> DNA

<213> Homo sapiens

<400> 5763

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<212> PRT

<213> Homo sapiens

<400> 5764

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<212> DNA

<213> Homo sapiens

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<210> 5766

<211> 873

<212> PRT

<213> Homo sapiens

<400> 5766

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 Cys Met Val Thr Gly Tyr Asp Trp Trp Asp Ile Leu Leu His Val Gln
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 Cys Cys Thr Cys Trp Pro Ala Tyr Pro Thr Ser Pro Ala Pro Pro Arg
 625 630 635 640
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 Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg
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 690 695 700
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 705 710 715 720
 Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly
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 Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe

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Cys Gly Cys Val Thr Met	Leu Lys Ser Pro Asn	Arg Thr Thr Ala Val		
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Lys Gln Trp Glu Gln Arg	Trp Ile Lys Asn Cys	Leu Cys Gly Gly Leu		
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<210> 5767

<211> 1910

<212> DNA

<213> Homo sapiens

<400> 5767

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<211> 360

<212> PRT

<213> Homo sapiens

<400> 5768

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			20					25					30		
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		35				40						45			
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	50				55					60					
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	65				70				75					80	
Ile	Val	Trp	Ala	Thr	Leu	Tyr	Arg	Cys	Ala	Leu	Asp	Ile	Met	Ile	Trp
			85					90					95		
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		100					105						110		
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			260				265						270				
Lys	Ala	Lys	Lys	Leu	Glu	His	Gln	Leu	Ser	Leu	Cys	Thr	Gln	Ile	Ser		
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Glu	Gly	Ala	Glu	Asp	Asp	Asp	Asp	Val	Phe	Glu	Pro	Ala	Ser	Pro	Asn		
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<210> 5769

<211> 427

<212> DNA

<213> Homo sapiens

<400> 5769

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<210> 5770

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<212> PRT

<213> Homo sapiens

<400> 5770

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Ile Lys Ile Phe Trp Gly Pro Glu Leu Lys Lys Glu Arg Ala Leu Arg
 35             40             45
Lys Asp Glu Ala Ser Lys Ile Pro Ile Trp Lys Glu Gln Tyr Arg Val
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<210> 5771

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<212> DNA

<213> Homo sapiens

<400> 5771

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<211> 642

<212> PRT

<213> Homo sapiens

<400> 5772

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Val Arg Cys Ala Thr Pro Pro Gln Leu Ala Asn Gly Val Thr Glu Gly
 35          40          45
Leu Asp Tyr Gly Phe Met Lys Glu Val Thr Phe His Cys His Gly Leu
 50          55          60
His Leu Ala Arg Cys Ser Lys Thr His Leu Ser Val Arg Gly Asn Trp
 65          70          75
Asp Ala Glu Ile Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu
 85          90          95
Asp Leu Ala His Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly
100          105          110
His Ile Gln Tyr Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser
115          120          125
Ser Arg Arg Cys Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser
130          135          140
Cys Leu Pro Cys Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val
145          150          155
Asn Gly Thr Asp Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe
165          170          175
Lys Gly Phe Lys Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp
180          185          190
Gly Gln Trp Ser Ser Gly Phe Pro His Cys Glu His Thr Ser Cys Gly
195          200          205
Ser Leu Pro Met Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp
210          215          220
Lys Glu Asn Val Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln
225          230          235
Gly Ser Ser Asp Leu Ile Cys Thr Glu Lys Gly Val Trp Asn Gln Pro
245          250          255
Tyr Pro Val Cys Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser Val Ala
260          265          270
Asn Ala Val Ala Thr Gly Glu Ala His Thr Tyr Glu Ser Glu Val Lys
275          280          285
Leu Arg Cys Leu Glu Gly Tyr Thr Met Asp Thr Asp Thr Asp Thr Ile
290          295          300
Thr Cys Gln Lys Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser
305          310          315
Pro Lys Lys Cys Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His
325          330          335
Gly Asp Asp Phe Ser Val Asn Arg Gln Val Ser Val Ser Cys Ala Glu
340          345          350
Gly Tyr Thr Phe Glu Gly Val Asn Ile Ser Val Cys Gln Leu Asp Gly

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      355              360              365
Thr Trp Glu Pro Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys
  370              375              380
Gly Lys Pro Glu Ser Pro Glu His Gly Phe Val Val Gly Ser Lys Tyr
  385              390              395              400
Thr Phe Glu Ser Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu
      405              410              415
Glu Gly Asn Arg Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly
      420              425              430
Gly Val Ala Ile Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe
      435              440              445
Leu Asn Gly Lys Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val
      450              455              460
Val Tyr Ser Cys Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala
      465              470              475              480
His Cys Thr Glu Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys
      485              490              495
Pro Asn Pro Cys Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu
      500              505
Ser Glu Lys Glu Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg
      515              520              525
Glu Gly Phe Leu Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro Asp
      530              535              540
Glu Thr Trp Thr Gln Thr Ser Ala Lys Cys Glu Lys Ile Ser Cys Gly
      545              550              555              560
Pro Pro Ala His Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln
      565              570              575
Tyr Gly Asp Met Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu
      580              585              590
Gly Phe Leu Arg Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro
      595              600              605
Pro Ile Cys Arg Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly His
      610              615              620
Leu Pro Thr Pro Lys Cys Leu Phe Leu Ser Arg Gly Leu Asp Gly Ala
      625              630              635              640
Pro Leu

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<210> 5773

<211> 579

<212> DNA

<213> Homo sapiens

<400> 5773

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nnacgcgtga ggggcctgag gcgagcgtt agagcgtctc ccggaaggat gggccggtct
60
cggagccgga gctcgtccc ctccaagcac accaagagca gcaagcaca caagaagcgc
120
agcccggtccc ggtcgcgatc ccgggacaag gagcgcgtgc ggaagcgttc caaatctcgg
180
gaaagtaaac ggaaccggcg gcgggagtcg cggtcccgtt cgcgctccc caacacggcc
240
gtgtcccggc gcgagcggga ccgggagcgc cctcgtcccc gcccgaccgc atcgacatct
300

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tcgggcgcac ggtgagcaag cgcagcagcc tggacgagaa gcagaagcga gagggaggagg
 360
 agaagaaagc ggagttcgcag cggcagcgaa aaattcgaca gcaagaaata gaagaaaaac
 420
 tcacgcagga agaaacagca cgaagagtag aagaattggt agcaanaaag ggtggaggaa
 480
 gaactggaga aaaggaagga tgaattgaa cgagaagttc tccgaagggt ggaggaagcc
 540
 aaacgcacga tggaaaagca gttgctcgaa gaactcgag
 579

<210> 5774

<211> 104

<212> PRT

<213> Homo sapiens

<400> 5774

Xaa	Arg	Val	Arg	Gly	Leu	Arg	Arg	Ala	Val	Arg	Ala	Ser	Pro	Gly	Arg
1				5					10					15	
Met	Gly	Arg	Ser	Arg	Ser	Arg	Ser	Ser	Ser	Arg	Ser	Lys	His	Thr	Lys
			20					25					30		
Ser	Ser	Lys	His	Asn	Lys	Lys	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg
		35					40					45			
Asp	Lys	Glu	Arg	Val	Arg	Lys	Arg	Ser	Lys	Ser	Arg	Glu	Ser	Lys	Arg
	50					55				60					
Asn	Arg	Arg	Arg	Glu	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Thr	Asn	Thr	Ala
65					70					75				80	
Val	Ser	Arg	Arg	Glu	Arg	Asp	Arg	Glu	Arg	Pro	Arg	Pro	Arg	Pro	Thr
			85					90					95		
Ala	Ser	Thr	Ser	Ser	Gly	Ala	Arg								
			100												

<210> 5775

<211> 1441

<212> DNA

<213> Homo sapiens

<400> 5775

cgctctctc cgcctcgaa ggtcccaagg tgagacacct tcagcaggtc tcaggggaaga
 60
 tggcagccct aggggacatt caggagtccc cttctgtccc gtccctctgtc agtctctcat
 120
 caccggggac acctggaacc cagcaccacg agcctcagct tcacctccat gggcatcaac
 180
 atgcctaagg tgctctccca gccgtccgac ctggatctcc aagacgtaga ggaagtggag
 240
 atcggcagag acacctctctg gcccgactcc gagcccaagc cggagcaggc tccacgctct
 300
 cctggctctc agggccctga cgagggggcg ggcgggggcg tgcgcacctc cgtgaggagc
 360
 cttcccgcga gggcccggtg cagcgccggc ttcgggacct aatccagcgc ggagcgggcg
 420
 gcggggccagc cgcctggggc cgtcccttgc gcccgccgc ggggcccctg gcgcgtgacg
 480

ctctgtgcagc aagcagcggc cggggcccag ggtgcgcccg agcgggctgc cgagctggga
 540
 gtcaacttcg gtcggagccg gcagggcagc gcgcggggga ccaagccgca caggtgcgag
 600
 gcctgcggca agagtgttaa gtataactcg ctgctcctga agcaccagcg catccacacg
 660
 ggcgagaagc cctacgcctg ccacgagtgc ggcaagtgtt tcgcccagc ttgcgccttc
 720
 atccagcacc agcgcattca cagcggcgag aagccctacg cctgccccga gtgcagcaag
 780
 accttcacgc gcagctccaa cctcatcaag caccagggtca tccacagcgg cgagcggccc
 840
 ttccgctgcg gcgactgcgg caaactgttc gcgccgagct tcgcgctcct ggagcacgcg
 900
 cgctgcgaca gcggcgagaa gccctacgag tgctccgact gcggcaagtgc ctccgcggc
 960
 cgctcgcact tcttcgggca caaccgcaca cacacgggag agaagcccta ccactgcctc
 1020
 gactgcggca agagcttcag ccacagctcg cacctcatca agcaccagcg caccacccgt
 1080
 ggcggtgcgc cctacgcctg cccgttgtgt ggcaagagct tcagccggcg ctccaacctg
 1140
 caccggcacg agaagatcca caccaccggg cccaaggccc tggccatgct gatgctgggg
 1200
 gcggcgcgcg cgggggctct ggccacaccc ccaccgcct ccacctagga ggccaggaaa
 1260
 gggggagcgg ggcccagc gccactggaa cagccccact ggagtcaagg ctccgagggg
 1320
 ggagagaggg gctcgggaag ggagctgggg cggtgagggc atggggtgag gcattggcgt
 1380
 gggggagggc gagggcgaga aagggcagcg actctgcgaa ttaaggcct tggacttgaa
 1440
 a
 1441

<210> 5776

<211> 359

<212> PRT

<213> Homo sapiens

<400> 5776

Met Gly Ile Asn Met Pro Lys Val Leu Ser Gln Pro Ser Asp Leu Asp
 1 5 10 15
 Leu Gln Asp Val Glu Glu Val Glu Ile Gly Arg Asp Thr Phe Trp Pro
 20 25 30
 Asp Ser Glu Pro Lys Pro Glu Gln Ala Pro Arg Ser Pro Gly Ser Gln
 35 40 45
 Ala Pro Asp Glu Gly Ala Gly Gly Ala Leu Arg Thr Ser Val Arg Ser
 50 55 60
 Leu Pro Arg Arg Ala Arg Cys Ser Ala Gly Phe Gly Pro Glu Ser Ser
 65 70 75 80
 Ala Glu Arg Pro Ala Gly Gln Pro Pro Gly Ala Val Pro Cys Ala Gln
 85 90 95
 Pro Arg Gly Ala Trp Arg Val Thr Leu Val Gln Gln Ala Ala Ala Gly

```

      100      105      110
Pro Glu Gly Ala Pro Glu Arg Ala Ala Glu Leu Gly Val Asn Phe Gly
      115      120      125
Arg Ser Arg Gln Gly Ser Ala Arg Gly Thr Lys Pro His Arg Cys Glu
      130      135      140
Ala Cys Gly Lys Ser Phe Lys Tyr Asn Ser Leu Leu Lys His Gln
145      150      155
Arg Ile His Thr Gly Glu Lys Pro Tyr Ala Cys His Glu Cys Gly Lys
      165      170      175
Cys Phe Ala Ala Ala Ser Arg Phe Ile Gln His Gln Arg Ile His Ser
      180      185      190
Gly Glu Lys Pro Tyr Ala Cys Pro Glu Cys Ser Lys Thr Phe Thr Arg
      195      200      205
Ser Ser Asn Leu Ile Lys His Gln Val Ile His Ser Gly Glu Arg Pro
      210      215      220
Phe Ala Cys Gly Asp Cys Gly Lys Leu Phe Arg Arg Ser Phe Ala Leu
225      230      235
Leu Glu His Ala Arg Val His Ser Gly Glu Lys Pro Tyr Glu Cys Ser
      245      250      255
Asp Cys Gly Lys Cys Phe Arg Gly Arg Ser His Phe Phe Arg His Asn
      260      265      270
Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Leu Asp Cys Gly Lys
      275      280      285
Ser Phe Ser His Ser Ser His Leu Ile Lys His Gln Arg Thr His Arg
      290      295      300
Gly Val Arg Pro Tyr Ala Cys Pro Leu Cys Gly Lys Ser Phe Ser Arg
305      310      315
Arg Ser Asn Leu His Arg His Glu Lys Ile His Thr Thr Gly Pro Lys
      325      330      335
Ala Leu Ala Met Leu Met Leu Gly Ala Ala Ala Gly Ala Leu Ala
      340      345      350
Thr Pro Pro Pro Ala Pro Thr
355

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<210> 5777

<211> 1431

<212> DNA

<213> Homo sapiens

<400> 5777

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ggaaggctcg cctgggagct catacctggc tggggcgag gattggtgt tccggggcta
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gggagcgctt tctcccgga accgcggctg tgacccaagt gggccggacc agtttggggc
120
tgctgctggc ctgcctcaag caaccaggta cgtaggctcg cggcccagct cggcgctggc
180
gtgggagccg gagggcgaca gtcagagccg ggggtgccag gggacgcgac cgccagatcc
240
acttaggacc ccgtcgttct gcgaagcggc cacgtctgag tccgggggccc tcctcgtgct
300
gcagatgtcg ccttaggacc tcggccagga taccctctgc catgctcttg tgctgcccgt
360
gatcacgcac tggcccttgt aagcaccttc gcagcaggaa gccacagact ggcctgcgcc
420

```

tttctgaagg ctgtggaaga ggttggagtg ggcgcattct agcttgcccc atccccattt
 480
 gaggtctgtc ggagctgccc ttcagtgtga gcattccaaa tgggtacccc agcctcggtg
 540
 gtcatgtgag caccctcttg gcaggccccc attgaggccc ggggcccga gacggcctcg
 600
 gccaacatct tccaggagcg cgagctgtcg cagatccaag ccctgtttca acgcagcggg
 660
 gaccagctgg ccgaggaacg ggcacagatc atctgggaat gtgcagggga ccaccgtgtg
 720
 gctgaggccc tcaagaggct gcgcaggaag agggccccc aa ggcagaaacc ccctgggcca
 780
 ctgcctacac cactgcagcc gcctcagaat cctggagccc cactctgcac tggccaacct
 840
 acagagtggc acagagacag cctccagtga gcagtatctg cactctagga agaaaagtgc
 900
 caggatccgc cggaaactgga ggaagtcagg cccacaagc tacctccacc agatcagaca
 960
 ctgatccagg gaaagagcca ggaatggcag tgtcttccct cttgccaaaa ggctggggga
 1020
 ggtgaaggaa gagagacttt agggcaagcag cccaaagggg taaatgaaag caagaggctg
 1080
 ctgccactga cctgctccat tcagaacaag actggatgct tctgttgagc tctccattat
 1140
 gtgggaccca ttcctacca aaatgaggag agacagtgc tgttctctgc acagtcttc
 1200
 ccagttctaac actattcctg ggctgcatga tattcccttg ggagcaaagt gacaggcact
 1260
 tagatgcagc atttcaccac tcatgtact aatcatctac ctgtactac tgtaaacatt
 1320
 ggttcacga gcctgttcca cacccccaca ccacaggat agcacaggga aactgtagtt
 1380
 taagtggcaa ataaaaacat ttgcatcaaa aaaaaaaaaa aaaaaaaaaa a
 1431

<210> 5778

<211> 164

<212> PRT

<213> Homo sapiens

<400> 5778

Met Leu Thr Leu Lys Gly Ser Ser Asp Arg Pro Gln Met Gly Met Gly
 1 5 10 15
 Gln Ala Lys Met Arg Pro Leu Gln Pro Leu Pro Gln Pro Ser Glu Arg
 20 25 30
 Ala Gly Ala Ala Leu Gly Phe Leu Leu Arg Arg Cys Leu Gln Gly Pro
 35 40 45
 Val Gly Asp His Gly Gln His Lys Ser Met Ala Glu Gly Ile Leu Ala
 50 55 60
 Glu Val Leu Arg Arg His Leu Gln His Glu Glu Ala Pro Gly Leu Arg
 65 70 75 80
 Arg Gly Arg Phe Ala Glu Arg Arg Gly Pro Lys Trp Ile Trp Arg Ser
 85 90 95
 Arg Pro Ala Gly Thr Pro Ala Leu Thr Val Ala Leu Arg Leu Pro Pro

```

                100                105                110
Gln Arg Arg Ala Gly Pro Pro Thr Tyr Val Pro Gly Cys Leu Arg Gln
                115                120                125
Ala Ala Arg Ser Pro Lys Leu Val Arg Ala Thr Trp Val Thr Ala Ala
                130                135                140
Val Pro Gly Arg Lys Arg Ser Leu Ala Pro Glu Gln Pro Ile Leu Gly
145                150                155                160
Pro Ser Gln Val

```

<210> 5779

<211> 371

<212> DNA

<213> Homo sapiens

<400> 5779

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ctcttgagac gtgtggaggg aaggaaggga agaaccatg atctacccca gaggcattgga
60
cgggagagag ggggtgatttc agccttgctt ggcattccctt gtgtctgcnt gaggggtgtgt
120
gcacacggga atgtgtgctg gtgtgtgtgc gtgcattcag ctgtgtgtgg atgtgcantc
180
gtgtgtgggt gtgtaggtgt gtgtgggtgt gtgcaccagt gcagggtgtgc atgggtgtgt
240
acagggtgggt gtgtgtatgt gtgtgggggt gtgcccattc gtgcagggtgt gtgggtgtgc
300
agggtcncat gcctgtgtgt ggggtgtgnc ccgtgtgtac ccctgtggag gtgtgtgggt
360
gtgtgcagtg t
371

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<210> 5780

<211> 123

<212> PRT

<213> Homo sapiens

<400> 5780

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Leu Leu Arg Arg Val Glu Gly Arg Lys Gly Arg Thr His Asp Leu Pro
1          5          10          15
Gln Arg His Gly Arg Glu Arg Gly Val Ile Ser Ala Leu Ser Gly Ile
20          25          30
Pro Cys Val Cys Xaa Arg Val Cys Ala His Gly Asn Val Cys Gly Cys
35          40          45
Val Cys Val His Ala Ala Val Cys Gly Cys Ala Xaa Val Cys Gly Cys
50          55          60
Val Gly Val Cys Gly Cys Val His Gln Cys Arg Cys Ala Trp Val Cys
65          70          75          80
Thr Gly Gly Cys Val Tyr Val Cys Gly Gly Val Pro Ile Cys Ala Gly
85          90          95
Val Trp Val Cys Arg Val Xaa Cys Leu Cys Val Gly Val Xaa Pro Cys
100         105         110
Val Pro Leu Trp Arg Cys Val Gly Val Cys Ser
115         120

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<210> 5781
 <211> 845
 <212> DNA
 <213> Homo sapiens

<400> 5781
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 60
 ggcgctggcg tgcggtgtca tttctgoggt gtaaatgtc ccacctggc cgatttcaag
 120
 ccaccagggt aggatggcac tgcaacatct tccactgagg ctccagctgc cctctcaggt
 180
 acatcagggc ctggancgtc ctctctcca ggagggccag gactcggccc cctgccagcc
 240
 ccgaagcat tgcagccagg agtgcagcgt gggggccctg caggccatgg ccaggcccca
 300
 gcgccaccag caccagggtc ggctggaagc cataggccag gggcagcacc aagcccaaga
 360
 tgcagctcag gaaaccaccg gtcatcactg gcagtggcgt ggagacatgg aacatggata
 420
 gggcagccgc ctctctggcc ctgatgttca gccacagact cctcccgta tgggcgaggt
 480
 ctggaggccg gtccagctgt cccagggccca cgcacagcag cctggaagaa gagctggcct
 540
 caggacaggt gttcatgttg tccagagtcc attcccagaa ctctctgtgc ttggccagcc
 600
 aggatagggg tgcccacagc tcttgccgtc agaggctcag gatggccaag tgaggcttac
 660
 ctctggggctc cgtgggacag gcctctccga acagccacat ccagggtggc tgctgcagca
 720
 gaggtggag tggctgctat accactgttc acctgtggga tgaataaaca gtggagaatg
 780
 aggcaccaac caactcccaa gccaggtaaa cagatccaca gttcccttca ttcggtgtgt
 840
 ctctg
 845

<210> 5782
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 5782
 Gly Val Pro Cys Pro Lys Ile Glu Gly Ala Val Gly Leu Gly Ser Gly
 1 5 10 15
 Ser Arg Pro Arg Gly Ala Gly Val Arg Cys His Phe Cys Gly Val Asn
 20 25 30
 Ala Pro Thr Leu Ala Asp Phe Lys Pro Pro Gly Glu Asp Gly Thr Ala
 35 40 45
 Thr Ser Ser Thr Glu Ala Pro Ala Ala Leu Ser Gly Thr Ser Gly Pro
 50 55 60
 Gly Xaa Ser Ser Pro Pro Gly Gly Pro Gly Leu Gly Pro Leu Pro Ala
 65 70 75 80
 Pro Glu Ala Leu Gln Pro Gly Val Gln Arg Gly Gly Pro Ala Gly His

	85		90		95									
Gly	Gln	Ala	Pro	Pro	Pro	Ala	Pro	Gly	Gln	Ala	Gly	Ser	His	Arg
	100					105					110			
Pro	Gly	Ala	Ala	Pro	Ser	Pro	Arg	Cys	Ser	Ser	Gly	Asn	His	Arg
	115					120					125			
Ser	Leu	Ala	Val	Ala	Trp	Arg	His	Gly	Thr	Trp	Ile	Gly	Gln	Pro
	130					135					140			
Pro	Cys	Pro												
145														

<210> 5783

<211> 1839

<212> DNA

<213> Homo sapiens

<400> 5783

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 120
 gctgggactc tccttcttag tacacaccga ctgatttgga gagatcagaa aaatcatgag
 180
 tgttgcatgg ccattctcct ttcccaaatt gtgttcattg aagaacaggc ggctggaatt
 240
 gggaagagtg ccaaaatagt gggtcatctt caccagctc ctccatacaa agaactgggc
 300
 ccattccaga gtagtaagaa ctctacatc aaactctct tcaagaaca tggccagatt
 360
 gagttttaca ggcgtttatc agaggaaatg acacaaagaa gatggggaaa tatgccagtt
 420
 tcccagtcac tacaacaaa tagaggacc cagccaggaa gaataagggc ttaggaatt
 480
 gtaggatttg aaaggaaact ggaagaaaaa agaaaagaaa ctgacaaaaa catttctgag
 540
 gcctttgaag acctcagcaa actaatgatc aaggctaagg aaatggtgga attatcaaaa
 600
 tcaattgcta ataaaattaa agacaaacaa ggtgacatca cagaagatga gaccatcagg
 660
 tttaaatcct acttgctgag catgggaata gctaaccagg ttaccagaga aacctcaggc
 720
 tcaggcacac agtaccacat gcagctggcc aaacaactgg ctggaatatt gcaggtgcct
 780
 tttaggaac gagggggaat aatgtcactc acggaggtgt actgcttagt aaaccgagct
 840
 cgaggaatgg aattgctctc accagaagat ttagtgaatg cgtgcaagat gctggaagca
 900
 ctgaaattac ctctcaggct ccgtgtgttt gacagtggcg tcatggtaat tgagcttcag
 960
 tctcacaagg aagaggaaat ggtggcctcg gccctggaga cagtttcaga aaagggatcc
 1020
 ctaacatcag aagagtttgc taagcttggt ggaatgtctg tcctcctagc caaagaaagg
 1080
 ttgctgcttg cagagaagat gggccatctt tgccgtgatg actcagtgga aggcctgcgt
 1140

ttttacccaa atttatttat gacacagagc taagggtttt gtatttaaaa tcctttttgt
 1200
 ccatatgctt gcgtcatgta gaggttgat gacattgagc taagagataa accccgatca
 1260
 attgagaatt tattggaact tcacagtgc atgtaaactc cttttaattt ctcocccaaat
 1320
 atgggtccagg aaattttatt agtatacgca taggaaaaat cagaaaagt aatgccaaata
 1380
 tgaatttaaa atcatgctat agtgcagaac cctcagagtt taacttggaa tatagtggat
 1440
 ttttaactga tcctcaaatc taatcatttt ataaagaagg gaatttagtt ttgcagagaa
 1500
 taaaaagaga agttgcatgt tcagacaggt tagattatta ttttggtgta actgaaattc
 1560
 actgattgca catgacaatg ttgggacaaa atatactgca gcatgctata tgaggctcct
 1620
 cccagggct tttagaagca gtcatagaca tgtcttcaac ataccaaata aaataccttt
 1680
 aaaaatgaaa taatttttatt tgacacatta tttatatata ttctatctag gtttctcttt
 1740
 gtttttttta aagtgatgat ttcattgact gggcatttaa aagaaatggc aactgtggtc
 1800
 catttttggc ttttccaaat gctgtggaat ttttggaat
 1839

<210> 5784

<211> 386

<212> PRT

<213> Homo sapiens

<400> 5784

Met Asp Arg Phe Val Trp Thr Ser Gly Leu Leu Glu Ile Asn Glu Thr
 1 5 10 15
 Leu Val Ile Gln Gln Arg Gly Val Arg Ile Tyr Asp Gly Glu Glu Lys
 20 25 30
 Ile Lys Phe Asp Ala Gly Thr Leu Leu Leu Ser Thr His Arg Leu Ile
 35 40 45
 Trp Arg Asp Gln Lys Asn His Glu Cys Cys Met Ala Ile Leu Leu Ser
 50 55 60
 Gln Ile Val Phe Ile Glu Gln Ala Ala Gly Ile Gly Lys Ser Ala
 65 70 75 80
 Lys Ile Val Val His Leu His Pro Ala Pro Pro Asn Lys Glu Pro Gly
 85 90 95
 Pro Phe Gln Ser Ser Lys Asn Ser Tyr Ile Lys Leu Ser Phe Lys Glu
 100 105 110
 His Gly Gln Ile Glu Phe Tyr Arg Arg Leu Ser Glu Glu Met Thr Gln
 115 120 125
 Arg Arg Trp Glu Asn Met Pro Val Ser Gln Ser Leu Gln Thr Asn Arg
 130 135 140
 Gly Pro Gln Pro Gly Arg Ile Arg Ala Val Gly Ile Val Gly Ile Glu
 145 150 155 160
 Arg Lys Leu Glu Glu Lys Arg Lys Glu Thr Asp Lys Asn Ile Ser Glu
 165 170 175
 Ala Phe Glu Asp Leu Ser Lys Leu Met Ile Lys Ala Lys Glu Met Val

```

      180              185              190
Glu Leu Ser Lys Ser Ile Ala Asn Lys Ile Lys Asp Lys Gln Gly Asp
      195              200              205
Ile Thr Glu Asp Glu Thr Ile Arg Phe Lys Ser Tyr Leu Ser Met
      210              215              220
Gly Ile Ala Asn Pro Val Thr Arg Glu Thr Tyr Gly Ser Gly Thr Gln
      225              230              235
Tyr His Met Gln Leu Ala Lys Gln Leu Ala Gly Ile Leu Gln Val Pro
      245              250              255
Leu Glu Glu Arg Gly Gly Ile Met Ser Leu Thr Glu Val Tyr Cys Leu
      260              265              270
Val Asn Arg Ala Arg Gly Met Glu Leu Leu Ser Pro Glu Asp Leu Val
      275              280              285
Asn Ala Cys Lys Met Leu Glu Ala Leu Lys Leu Pro Leu Arg Leu Arg
      290              295              300
Val Phe Asp Ser Gly Val Met Val Ile Glu Leu Gln Ser His Lys Glu
      305              310              315
Glu Glu Met Val Ala Ser Ala Leu Glu Thr Val Ser Glu Lys Gly Ser
      325              330              335
Leu Thr Ser Glu Glu Phe Ala Lys Leu Val Gly Met Ser Val Leu Leu
      340              345              350
Ala Lys Glu Arg Leu Leu Leu Ala Glu Lys Met Gly His Leu Cys Arg
      355              360              365
Asp Asp Ser Val Glu Gly Leu Arg Phe Tyr Pro Asn Leu Phe Met Thr
      370              375              380
Gln Ser
385

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<210> 5785

<211> 785

<212> DNA

<213> Homo sapiens

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<210> 5794

<211> 209

<212> PRT

<213> Homo sapiens

<400> 5794

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Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln	Asp	Leu	Gln	Ala	Ala
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Arg	Ala	Leu	Val	Ile	Ile	Ser	Ile	Ile	Val	Ala	Ala	Leu	Gly	Val	Leu
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Leu	Ser	Val	Val	Gly	Gly	Lys	Cys	Thr	Asn	Cys	Leu	Glu	Asp	Glu	Ser
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<210> 5795

<211> 993

<212> DNA

<213> Homo sapiens

<400> 5795

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<211> 200

<212> PRT

<213> Homo sapiens

<400> 5796

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Tyr	Leu	Arg	Lys	Glu	Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe
			35				40					45			
Gly	Thr	Thr	Ala	Gly	Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg
			50				55				60				
Arg	Cys	Phe	Lys	Val	Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu
			65			70				75				80	
Ala	Thr	Leu	Pro	Phe	Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val
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Ile	Asp	Ala	Leu	Tyr	Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe


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Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys
145              150              155              160
Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met
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<210> 5797

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<212> DNA

<213> Homo sapiens

<400> 5797

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<210> 5798

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Arg Arg Val Glu Gly Ser Arg Asp Gln Ala Trp Pro Leu Gln Thr Phe
          35          40          45
Ser Gln Arg Asn Tyr Arg Ser Leu Ser Leu Tyr Cys Trp Leu Ala Arg
          50          55          60
Glu Gly Arg Thr Ser Ser Tyr Gln Gly Asn Gln Gly Ser Leu Arg Pro
65          70          75          80
Arg Pro Glu Pro Arg Gly Pro Glu Gly Ser Lys Arg Ser Gly Arg Pro
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<210> 5799

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<400> 5799

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<210> 5800

<211> 535

<212> PRT

<213> Homo sapiens

<400> 5800

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<212> DNA

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<210> 5802

<211> 350

<212> PRT

<213> Homo sapiens

<400> 5802

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Pro Arg Glu Asn Pro Asp Leu Ala Cys Leu Gln Ser Ile Ile Phe Asp			
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Lys Glu Lys Lys Leu Leu Glu Met Arg Ala Lys Ala Asp Lys Leu Lys			
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Arg Ile Glu Gln Arg Asp Val Arg Lys Ala Asn Leu Lys Glu Lys Lys			
	195	200	205
Glu Arg Asn Gln Asn Glu Ala Leu Leu Gln Ala Ile Lys Ala Arg Asn			
	210	215	220
Ile Arg Leu Ser Glu Ala Ala Cys Glu Asp Glu Asp Ser Ala Ser Glu			
225	230	235	240
Gly Leu Gly Glu Leu Phe Leu Asp Gly Leu Ser Thr Glu Asn Pro His			
	245	250	255
Gly Ala Arg Leu Ser Leu Asp Gly Gln Gly Arg Leu Ser Trp Pro Val			
	260	265	270
Leu Phe Leu Tyr Pro Glu Tyr Ala Gln Ser Asp Phe Ile Ser Ala Phe			
	275	280	285
His Glu Asp Ser Arg Phe Ile Asp His Leu Met Val Met Phe Gly Glu			
	290	295	300
Thr Pro Ser Trp Asp Leu Glu Gln Lys Tyr Cys Leu Ile Ile Trp Arg			
305	310	315	320
Ser Thr Leu Arg Met Arg Thr Gly Gln Asn Tyr Thr Gly Cys Leu Pro			
	325	330	335
Arg Ala Pro Cys Tyr Arg Phe Tyr Ser Thr Arg Gly Thr Leu			
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<210> 5803

<211> 692

<212> DNA

<213> Homo sapiens

<400> 5803

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 300
 ctctcgtcga aagaagacag cactctgaaa gcagctggaa tcgccagtga aactgaaatt
 360
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 420
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 480
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 aatctgggta tttctttctc ttcaggtctt tctttctctc tctctttctt tttctttggt
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<210> 5804

<211> 126

<212> PRT

<213> Homo sapiens

<400> 5804

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Glu	His	Arg	Asn	Phe	Lys	Pro	Val	Val	Tyr	His	Gly	Val	Asn	Leu	Asp
			20					25					30		
Gln	Thr	Val	Lys	Glu	Phe	Ile	Val	Phe	Leu	Lys	Gln	Asp	Val	Pro	Leu
		35					40					45			
Arg	Thr	Asn	Leu	Pro	Pro	Pro	Phe	Arg	Asn	Tyr	Lys	Tyr	Asp	Ala	Leu
		50				55					60				
Lys	Ile	Ile	His	Gln	Ala	His	Lys	Ser	Lys	Thr	Asn	Glu	Leu	Val	Leu
		65			70					75				80	
Ser	Leu	Glu	Asp	Asp	Glu	Arg	Leu	Leu	Leu	Lys	Glu	Asp	Ser	Thr	Leu
			85						90				95		
Lys	Ala	Ala	Gly	Ile	Ala	Ser	Glu	Thr	Glu	Ile	Ala	Phe	Phe	Cys	Glu
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Glu	Asp	Tyr	Arg	Asn	Tyr	Lys	Ala	Asn	Pro	Ile	Ser	Ser	Trp		
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<210> 5805

<211> 1112

<212> DNA

<213> Homo sapiens

<400> 5805

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 120

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240
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420
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1020
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<210> 5806

<211> 105

<212> PRT

<213> Homo sapiens

<400> 5806

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35 40 45
Ser Asp Phe Asp Arg Cys Cys Lys Leu Lys Asp Arg Leu Pro Ser Ile
50 55 60
Val Val Glu Pro Thr Glu Gly Glu Val Glu Ser Gly Glu Leu Arg Trp
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Glu Thr Ala Lys Glu Asn Lys Glu Gln

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100

105

<210> 5807
 <211> 1429
 <212> DNA
 <213> Homo sapiens

<400> 5807
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1429

<210> 5808

<211> 261

<212> PRT

<213> Homo sapiens

<400> 5808

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Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp Ala Arg Gln Gly
35 40 45
Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu Ala Pro Leu Ala Trp
50 55 60
Asp Leu Gly Leu Leu Leu Phe Val Gly Gln His Ser Leu Met Ala
65 70 75 80
Ala Glu Arg Val Lys Ala Trp Thr Ser Arg Tyr Phe Gly Val Leu Gln
85 90 95
Arg Ser Leu Tyr Val Ala Cys Thr Ala Leu Ala Leu Gln Leu Val Met
100 105 110
Arg Tyr Trp Glu Pro Ile Pro Lys Gly Pro Val Leu Trp Glu Ala Arg
115 120 125
Ala Glu Pro Trp Ala Thr Trp Val Pro Leu Leu Cys Phe Val Leu His
130 135 140
Val Ile Ser Trp Leu Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr
145 150 155 160
Ala Glu Leu Met Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu
165 170 175
Gly Glu Pro Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser
180 185 190
His Leu Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val
195 200 205
Val Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr
210 215 220
Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg Tyr
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Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg Pro Gln
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Asp Gly Glu Ala Glu
260

<210> 5809

<211> 2009

<212> DNA

<213> Homo sapiens

<400> 5809

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 720
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 1740

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 2009

<210> 5810
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 5810
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 Phe Lys Gln Phe Ser Cys Leu Ser Leu Leu Ser Ser Trp His Tyr Lys
 35 40 45
 His Pro Thr Pro
 50

<210> 5811
 <211> 1607
 <212> DNA
 <213> Homo sapiens

<400> 5811
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<210> 5812

<211> 463

<212> PRT

<213> Homo sapiens

<400> 5812

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			20				25						30		
Thr	Pro	Gln	Ala	Ile	Glu	Pro	Gln	Ala	Ile	Val	Gln	Gln	Val	Pro	Ala
			35				40					45			
Pro	Ser	Arg	Met	Gln	Met	Pro	Gln	Gly	Asn	Pro	Leu	Leu	Leu	Ser	His
			50			55			60						
Thr	Leu	Gln	Glu	Leu	Leu	Ala	Arg	Asp	Thr	Val	Gln	Val	Glu	Leu	Ile
			65			70			75					80	
Pro	Glu	Lys	Lys	Gly	Leu	Phe	Leu	Lys	His	Val	Glu	Tyr	Glu	Val	Ser
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Ser	Gln	Arg	Phe	Lys	Ser	Ser	Val	Tyr	Arg	Arg	Tyr	Asn	Asp	Phe	Val
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Val	Phe	Gln	Glu	Met	Leu	Leu	His	Lys	Phe	Pro	Tyr	Arg	Met	Val	Pro

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165                      170                      175
Gly Ser Asp Val Gln Asn Lys Leu Lys Glu Ser Ala Gln Cys Val Gly
180                      185                      190
Asp Glu Phe Leu Asn Cys Lys Leu Ala Thr Arg Ala Lys Asp Phe Leu
195                      200                      205
Pro Ala Asp Ile Gln Ala Gln Phe Ala Ile Ser Arg Glu Leu Ile Arg
210                      215                      220
Asn Ile Tyr Asn Ser Phe His Lys Leu Arg Asp Arg Ala Glu Arg Ile
225                      230                      235                      240
Ala Ser Arg Ala Ile Asp Asn Ala Ala Asp Leu Leu Ile Phe Gly Lys
245                      250                      255
Glu Leu Ser Ala Ile Gly Ser Asp Thr Thr Pro Leu Pro Ser Trp Ala
260                      265                      270
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275                      280                      285
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290                      295                      300
Lys Gln Glu Glu Asn Asp Val Val Glu Lys Leu Asn Leu Phe Leu Asp
305                      310                      315                      320
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325                      330                      335
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355                      360                      365
Gln Leu Glu Ser Arg Ile Val Glu Gln Glu Asn Ala Ile Gln Thr Met
370                      375                      380
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385                      390                      395                      400
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405                      410                      415
Val Asn Ser Gln Ile Gln Gly His Lys Glu Met Ser Lys Val Trp Asn
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<210> 5813

<211> 2991

<212> DNA

<213> Homo sapiens

<400> 5813

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120

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1680
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1740

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 2040
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 2820
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<210> 5814

<211> 149

<212> PRT

<213> Homo sapiens

<400> 5814

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 Tyr His Pro Asp Lys His Arg Asp Pro Glu Leu Lys Ser Gln Ala Glu
 20 25 30
 Arg Leu Phe Asn Leu Val His Gln Ala Tyr Glu Val Leu Ser Asp Pro

```

          35              40              45
Gln Thr Arg Ala Ile Tyr Asp Ile Tyr Gly Lys Arg Gly Leu Glu Met
      50              55              60
Glu Gly Trp Glu Val Val Glu Arg Arg Arg Thr Pro Ala Glu Ile Arg
      65              70              75              80
Glu Glu Phe Glu Arg Leu Gln Arg Glu Arg Glu Arg Arg Leu Gln
      85              90              95
Gln Arg Thr Asn Pro Lys Leu Cys Asp Asn Lys Leu Cys Ser Ala Val
      100             105             110
Phe Ile Pro Trp Asn Pro Thr Arg Pro Asp His Cys Pro Ser Ser Glu
      115             120             125
Pro Arg Gln Glu His Arg Gly Leu Pro Ala Val Ala Met Gly Tyr Pro
      130             135             140
Val Ser His Glu His
145

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<210> 5815

<211> 590

<212> DNA

<213> Homo sapiens

<400> 5815

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120
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180
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240
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360
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420
gtcaatgaga gaacgggtcag cttggagcac aagattcgag ttcgccttgt actcgattg
480
cagactacgg gcggttacat ccgcatggc cgcggtgtgt cggaggcttc agaccaccac
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<210> 5816

<211> 196

<212> PRT

<213> Homo sapiens

<400> 5816

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Ala Ala Asp Glu Val Leu Ala Val Leu Lys Asn Glu Lys Leu Arg Asp
20           25           30
Lys Glu Arg Arg Lys Glu Ile Asp Leu Leu Gly Gln Thr Asp Asp

```

```

      35              40              45
Thr Arg Tyr His Val Leu Val Asn Leu Gly Leu Pro Ser Leu Phe Ser
      50              55              60
Phe Gly Leu Val Asp Asp Ala His His Leu Ile Asn Ala Leu Arg Gln
      65              70              75              80
Gln Ser Ile Thr Leu His Leu Val Asp Val Met Pro Val Leu Ile Thr
      85              90              95
Leu Ser Ser Leu Gly Ser Ser Phe Leu Leu His Leu Arg Phe Gly Pro
      100              105              110
Leu Ser Leu Val Ser His Thr Gly Ala Leu Gln Leu Pro Asn Lys Gly
      115              120              125
Gln His Leu Ser Cys Gly Phe Ile Pro Ala Gly Pro Val Asn Glu Arg
      130              135              140
Thr Val Ser Leu Glu His Lys Ile Arg Val Arg Leu Val Leu Val Leu
      145              150              155              160
Gln Thr Thr Gly Gly Tyr Ile Arg His Gly Arg Gly Cys Ser Glu Ala
      165              170              175
Ser Asp His His Ala Ser Ile Pro Gln Ala Ala Asn Gly Arg Arg Ser
      180              185              190
Leu Leu Leu Ala
      195

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<210> 5817

<211> 648

<212> DNA

<213> Homo sapiens

<400> 5817

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120
cctagtaggc agtgcctcctg ggacaagtct gagtcacccc agagaagcag catgaacaat
180
ggatccccc cagctctatc aggcagcaaa accaacagcc caaagaacag tggtcacaag
240
ctagatgtgt ctagaagccc cctctctcatg gtcaaaaaga acccagcctt taataagggt
300
agtgggatag ttaccaatgg gtccttcagc agcagtaatg cagaaggctt tgagaaaacc
360
caaaccaccc ccaatggggag cctacaggcc agaaggagct cttcactgaa ggtatctggt
420
accaaaatgg gcacgcacag tgtacagaat ggaacggtgc gcattgggcat tttgaacagc
480
gacacactcg ggaaccccac aaatgttcga aacatgagct ggctgccaaa tggctatgtg
540
accctgaggg ataacaagca gaaagaacaa gctggagagt taggccagca caacagactg
600
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648

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<210> 5818

<211> 191

<212> PRT

<213> Homo sapiens

<400> 5818

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Met Gly Gln Leu Gln Asn Lys Glu Asn Asn Asn Thr Lys Asp Ser Pro
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Ser Arg Gln Cys Ser Trp Asp Lys Ser Glu Ser Pro Gln Arg Ser Ser
              20              25              30
Met Asn Asn Gly Ser Pro Thr Ala Leu Ser Gly Ser Lys Thr Asn Ser
 35              40              45
Pro Lys Asn Ser Val His Lys Leu Asp Val Ser Arg Ser Pro Pro Leu
 50              55              60
Met Val Lys Lys Asn Pro Ala Phe Asn Lys Gly Ser Gly Ile Val Thr
 65              70              75              80
Asn Gly Ser Phe Ser Ser Ser Asn Ala Glu Gly Leu Glu Lys Thr Gln
 85              90              95
Thr Thr Pro Asn Gly Ser Leu Gln Ala Arg Arg Ser Ser Ser Leu Lys
100              105              110
Val Ser Gly Thr Lys Met Gly Thr His Ser Val Gln Asn Gly Thr Val
115              120              125
Arg Met Gly Ile Leu Asn Ser Asp Thr Leu Gly Asn Pro Thr Asn Val
130              135              140
Arg Asn Met Ser Trp Leu Pro Asn Gly Tyr Val Thr Leu Arg Asp Asn
145              150              155              160
Lys Gln Lys Glu Gln Ala Gly Glu Leu Gly Gln His Asn Arg Leu Ser
165              170              175
Pro Met Ile Met Ser Ile Thr Val Leu His Asp Glu Leu Asp Asp
180              185              190

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<210> 5819

<211> 1652

<212> DNA

<213> Homo sapiens

<400> 5819

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120
cgctctgctc tgcagctctt ctggaccgag gagcccaaag ccctaccctc accattcacc
180
aggctcctgtg ggaagagcag cgtggagggt ggctgagggt agaaggtgca gagcgtggaa
240
gaagattgtg agctgagtat tggacatctg ttcttgaata gtcctgggc ctgccatagg
300
aaaggaagtt ctccagggtt acagttctta tcccggtgaa tacacatggc tctgttacga
360
aaaattaatc aggtgctgct gtctcctctg atcgtgaccc tctgtgtgat tctgtataag
420
aaagttcata aggggactgt gcccaagaat gacgcagatg atgaatccga gactcctgaa
480
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540
atggctgcca tcaatagcat ctacagcaac cctgacgcca acatcttgtt ctatgtagtg
600

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ggactccgga atactctgac tcgaatacga aaatggattg aacattccaa actgagagaa
 660
 ataaacttta aaatcgtgga attcaaccgg atggtcctca aaggggaagat cagaccagac
 720
 tcatcgaggc ctgaattgct ccagcctctg aactttgttc gattttatct cctctactt
 780
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 840
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 960
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 1080
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 1140
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 1200
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 1652

<210> 5820

<211> 274

<212> PRT

<213> Homo sapiens

<400> 5820

Met	Ala	Leu	Leu	Arg	Lys	Ile	Asn	Gln	Val	Leu	Leu	Phe	Leu	Leu	Ile
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Val	Thr	Leu	Cys	Val	Ile	Leu	Tyr	Lys	Lys	Val	His	Lys	Gly	Thr	Val
		20					25					30			
Pro	Lys	Asn	Asp	Ala	Asp	Asp	Glu	Ser	Glu	Thr	Pro	Glu	Glu	Leu	Glu
		35				40					45				
Glu	Glu	Ile	Pro	Val	Val	Ile	Cys	Ala	Ala	Ala	Gly	Arg	Met	Gly	Ala
	50				55					60					
Thr	Met	Ala	Ala	Ile	Asn	Ser	Ile	Tyr	Ser	Asn	Pro	Asp	Ala	Asn	Ile
65					70				75					80	
Leu	Phe	Tyr	Val	Val	Gly	Leu	Arg	Asn	Thr	Leu	Thr	Arg	Ile	Arg	Lys

[illegible]

<210> 5821

<211> 3292

<212> DNA

<213> Homo sapiens

<400> 5821

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120	taaaaggaa	aaaatataac	ttagagcccc	ctatgaaaaa	ctaaattagc
180	gatacatctt	ggggagttaa	atttcacagt	acctttattt	aattccaagc
240	ggtaatat	ttctctttat	cagctgtggc	actaaaaata	cagtggaatt
300	gacattcttc	ttttggccga	tgaaaaat	gacttcgata	tttcattgtc
360	gcaaatgaag	atgatgaagt	cttcttcgga	ccctttggac	ataagaaaag
420	gccagcttgg	aattaataaa	tccggttccc	gaacagcctc	cgttggccac
480	ccctttgtcg	ggagccctct	ggcggggagg	aagttcgtgg	agggtgtcaa
540	tacttgctt	tacacattga	gagcagcagc	cgggaaccagg	cagcccaagc
600	gaagaccctc	ggagccaggg	cgtggaagaa	ttcatacagg	agtcaaaatt
660					aaaaataaac

ctcttttgaga aagaaaagga aatgaagaaa agccccacgt ctcttaaaag ggagacatac
720
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780
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 3292

<210> 5822

<211> 712

<212> PRT

<213> Homo sapiens

<400> 5822

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 His Lys Glu Arg Cys Ile Ala Ala Ser Leu Glu Leu Asn Asn Pro Val
 35 40 45
 Pro Glu Gln Pro Pro Leu Pro Thr Ser Glu Ser Pro Phe Ala Trp Ser
 50 55 60
 Pro Leu Ala Gly Glu Lys Phe Val Glu Val Tyr Lys Glu Ala His Leu
 65 70 75 80
 Leu Ala Leu His Ile Glu Ser Ser Ser Arg Asn Gln Ala Ala Gln Ala
 85 90 95
 Ala Lys Pro Glu Asp Pro Arg Ser Gln Gly Val Glu Arg Phe Ile Gln

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100      105      110
Glu Ser Lys Leu Lys Ile Asn Leu Phe Glu Lys Glu Lys Glu Met Lys
115      120      125
Lys Ser Pro Thr Ser Leu Lys Arg Glu Thr Tyr Tyr Leu Ser Asp Ser
130      135      140
Pro Leu Leu Gly Pro Pro Val Gly Glu Pro Arg Leu Leu Ala Ser Ser
145      150      155
Pro Ala Leu Pro Ser Ser Gly Ala Gln Ala Arg Leu Thr Arg Ala Pro
165      170      175
Gly Pro Pro His Ser Ala His Ala Leu Pro Arg Glu Ser Cys Thr Ala
180      185      190
His Ala Ala Ser Gln Ala Ala Thr Gln Arg Lys Pro Gly Thr Lys Leu
195      200      205
Leu Leu Pro Arg Ala Ala Ser Val Arg Gly Arg Ser Ile Pro Gly Ala
210      215      220
Ala Glu Lys Pro Lys Lys Glu Ile Pro Ala Ser Pro Ser Arg Thr Lys
225      230      235
Ile Pro Ala Glu Lys Glu Ser His Arg Asp Val Leu Pro Asp Lys Pro
245      250      255
Ala Pro Gly Ala Val Asn Val Pro Ala Ala Gly Ser His Leu Gly Gln
260      265      270
Gly Lys Arg Ala Ile Pro Val Pro Asn Lys Leu Gly Leu Lys Lys Thr
275      280      285
Leu Leu Lys Ala Pro Gly Ser Thr Ser Asn Leu Ala Arg Lys Ser Ser
290      295      300
Ser Gly Pro Val Trp Ser Gly Ala Ser Ser Ala Cys Thr Ser Pro Ala
305      310      315
Val Gly Lys Ala Lys Ser Ser Glu Phe Ala Ser Ile Pro Ala Asn Ser
325      330      335
Ser Arg Pro Leu Ser Asn Ile Ser Lys Ser Gly Arg Met Gly Pro Ala
340      345      350
Met Leu Arg Pro Ala Leu Pro Ala Gly Pro Val Gly Ala Ser Ser Trp
355      360      365
Gln Ala Lys Arg Val Asp Val Ser Glu Leu Ala Ala Glu Gln Leu Thr
370      375      380
Ala Pro Pro Ser Ala Ser Pro Thr Gln Pro Gln Thr Pro Glu Gly Gly
385      390      395
Gly Gln Trp Leu Asn Ser Ser Cys Ala Trp Ser Glu Ser Ser Gln Leu
405      410      415
Asn Lys Thr Arg Ser Ile Arg Arg Asp Ser Cys Leu Asn Ser Lys
420      425      430
Thr Lys Val Met Pro Thr Pro Thr Asn Gln Phe Lys Ile Pro Lys Phe
435      440      445
Ser Ile Gly Asp Ser Pro Asp Ser Ser Thr Pro Lys Leu Ser Arg Ala
450      455      460
Gln Arg Pro Gln Ser Cys Thr Ser Val Gly Arg Val Thr Val His Ser
465      470      475
Thr Pro Val Arg Arg Ser Ser Gly Pro Ala Pro Gln Ser Leu Leu Ser
485      490      495
Ala Trp Arg Val Ser Ala Leu Pro Thr Pro Ala Ser Arg Arg Cys Ser
500      505      510
Gly Leu Pro Pro Met Thr Pro Lys Thr Met Pro Arg Ala Val Gly Ser
515      520      525
Pro Leu Cys Val Pro Ala Arg Arg Ser Ser Glu Pro Arg Lys Asn

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530		535		540
Ser Ala Met Arg Thr	Glu Pro Thr Arg	Glu Ser Asn Arg	Lys Thr Asp	
545	550	555	560	
Ser Arg Leu Val Asp	Val Ser Pro Asp	Arg Gly Ser Pro	Pro Ser Arg	
	565	570	575	
Val Pro Gln Ala Leu	Asn Phe Ser Pro	Glu Glu Ser Asp	Ser Thr Phe	
	580	585	590	
Ser Lys Ser Thr Ala	Thr Glu Val Ala	Arg Glu Glu Ala	Lys Pro Gly	
	595	600	605	
Gly Asp Ala Ala Pro	Ser Glu Ala Leu	Leu Val Asp Ile	Lys Leu Glu	
	610	615	620	
Pro Leu Ala Val Thr	Pro Asp Ala Ala	Ser Gln Pro Leu	Ile Asp Leu	
625	630	635	640	
Pro Leu Ile Asp Phe	Cys Asp Thr Pro	Glu Ala His Val	Ala Val Gly	
	645	650	655	
Ser Glu Ser Arg Pro	Leu Ile Asp Leu	Met Thr Asn Thr	Pro Asp Met	
	660	665	670	
Asn Lys Asn Val Ala	Lys Pro Ser Pro	Val Val Gly Gln	Leu Ile Asp	
	675	680	685	
Leu Ser Ser Pro Leu	Ile Gln Leu Ser	Pro Glu Ala Asp	Lys Glu Asn	
	690	695	700	
Val Asp Ser Pro Leu	Leu Lys Phe			
705	710			

<210> 5823

<211> 2585

<212> DNA

<213> Homo sapiens

<400> 5823

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Asn Trp Glu Ser Asp Gln Pro Asp Asn Pro Ser Glu Glu Asn Cys Gly
325           330           335
Val Ile Arg Thr Glu Ser Ser Gly Gly Trp Gln Asn Arg Asp Cys Ser
340           345           350
Ile Ala Leu Pro Tyr Val Cys Lys Lys Lys Pro Asn Ala Thr Ala Glu

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      355              360              365
Pro Thr Pro Pro Asp Arg Trp Ala Asn Val Lys Val Glu Cys Glu Pro
  370              375              380
Ser Trp Gln Pro Phe Gln Gly His Cys Tyr Arg Leu Gln Ala Glu Lys
  385              390              395              400
Arg Ser Trp Gln Glu Ser Lys Lys Ala Cys Leu Arg Gly Gly Gly Asp
      405              410              415
Leu Val Ser Ile His Ser Met Ala Glu Leu Glu Phe Ile Thr Lys Gln
  420              425              430
Ile Lys Gln Glu Val Glu Glu Leu Trp Ile Gly Leu Asn Asp Leu Lys
  435              440              445
Leu Gln Met Asn Phe Glu Trp Ser Asp Gly Ser Leu Val Ser Phe Thr
  450              455              460
His Trp His Pro Phe Glu Pro Asn Asn Phe Arg Asp Ser Leu Glu Asp
  465              470              475              480
Cys Val Thr Ile Trp Gly Pro Glu Gly Arg Trp Asn Asp Ser Pro Cys
      485              490              495
Asn Gln Ser Leu Pro Ser Ile Cys Lys Lys Ala Gly Gln Leu Ser Gln
  500              505              510
Gly Ala Ala Glu Glu Asp His Gly Cys Arg Lys Gly Trp Thr Trp His
  515              520              525
Ser Pro Ser Cys Tyr Trp Leu Gly Glu Asp Gln Val Thr Tyr Ser Glu
  530              535              540
Ala Arg Arg Leu Cys Thr Asp His Gly Ser Gln Leu Val Thr Ile Thr
  545              550              555              560
Asn Arg Phe Glu Gln Ala Phe Val Ser Ser Leu Ile Tyr Asn Trp Glu
      565              570              575
Gly Glu Tyr Phe Trp Thr Ala Leu Gln Asp Leu Asn Ser Thr Gly Ser
  580              585              590
Phe Phe Trp Leu Ser Gly Asp Glu Val Met Tyr Thr His Trp Asn Arg
  595              600              605
Asp Gln Pro Gly Tyr Ser Arg Gly Gly Cys Val Ala Leu Ala Thr Gly
  610              615              620
Ser Ala Met Gly Leu Trp Glu Val Lys Asn Cys Thr Ser Phe Arg Ala
  625              630              635              640
Arg Tyr Ile Cys Arg Gln Ser Leu Gly Thr Pro Val Thr Pro Glu Leu
      645              650              655
Pro Gly Pro Asp Pro Thr Pro Ser Leu Thr Gly Ser Cys Pro Gln Gly
  660              665              670
Trp Ala Ser Asp Thr Lys Leu Arg Tyr Cys Tyr Lys Val Phe Ser Ser
  675              680              685
Glu Arg Leu Gln Asp Lys Lys Ser Trp Val Gln Ala Gln Gly Ala Cys
  690              695              700
Gln Glu Leu Gly Ala Gln Leu Leu Ser Leu Ala Ser Tyr Glu Glu Glu
  705              710              715              720
His Phe Val Ala Asn Met Leu Asn Lys Ile Phe Gly Glu Ser Glu Pro
      725              730              735
Glu Ile His Glu Gln His Trp Phe Trp Ile Gly Leu Asn Arg Asp
  740              745              750
Pro Arg Gly Gly Gln Ser Trp Arg Trp Ser Asp Gly Val Gly Phe Ser
  755              760              765
Tyr His Asn Phe Asp Arg Ser Arg His Asp Asp Asp Ile Arg Gly
  770              775              780
Cys Ala Val Leu Asp Leu Ala Ser Leu Gln Trp Val Ala Met Gln Cys

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785					790					795					800
Asp	Thr	Gln	Leu	Asp	Trp	Ile	Cys	Lys	Ile	Pro	Arg	Gly	Thr	Asp	Val
				805					810					815	
Arg	Glu	Pro	Asp	Asp	Ser	Pro	Gln	Gly	Arg	Arg	Glu	Trp	Leu	Arg	Phe
			820					825					830		
Gln	Glu	Ala	Glu	Tyr	Lys	Phe	Phe	Glu	His	His	Ser	Thr	Trp	Ala	Gln
		835					840					845			
Ala	Gln	Arg	Ile	Cys	Thr	Trp	Phe	Gln	Ala	Glu	Leu	Thr	Ser	Val	His
		850				855					860				
Ser	Gln	Ala	Glu	Leu	Asp	Phe	Leu	Ser	His	Asn	Leu	Gln	Lys	Phe	Ser
				870					875					880	
Arg	Ala	Gln	Glu	Gln	His	Trp	Trp	Ile	Gly	Leu	His	Thr	Ser	Glu	Ser
				885					890					895	
Asp	Gly	Arg	Phe	Arg	Trp	Thr	Asp	Gly	Ser	Ile	Ile	Asn	Phe	Ile	Ser
			900					905					910		
Trp	Ala	Pro	Gly	Lys	Pro	Arg	Pro	Val	Gly	Lys	Asp	Lys	Lys	Cys	Val
		915					920					925			
Tyr	Met	Thr	Ala	Ser	Arg	Glu	Asp	Trp	Gly	Asp	Gln	Arg	Cys	Leu	Thr
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Ala	Leu	Pro	Tyr	Ile	Cys	Lys	Arg	Ser	Asn	Val	Thr	Lys	Glu	Thr	Gln
	945				950				955						960
Pro	Pro	Asp	Leu	Pro	Thr	Thr	Ala	Leu	Gly	Gly	Cys	Pro	Ser	Asp	Trp
			965						970					975	
Ile	Gln	Phe	Leu	Asn	Lys	Cys	Phe	Gln	Val	Gln	Gly	Gln	Glu	Pro	Gln
		980					985						990		
Ser	Arg	Val	Lys	Trp	Ser	Glu	Ala	Gln	Phe	Ser	Cys	Glu	Gln	Gln	Glu
		995					1000					1005			
Ala	Gln	Leu	Val	Thr	Ile	Thr	Asn	Pro	Leu	Glu	Gln	Ala	Phe	Ile	Thr
	1010					1015					1020				
Ala	Ser	Leu	Pro	Asn	Val	Thr	Phe	Asp	Leu	Trp	Ile	Gly	Leu	His	Ala
	1025				1030				1035						1040
Ser	Gln	Arg	Asp	Phe	Gln	Trp	Val	Glu	Gln	Glu	Pro	Leu	Met	Tyr	Ala
			1045						1050					1055	
Asn	Trp	Ala	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ser	Pro	Ala	Pro	Ser	Gly
			1060					1065				1070			
Asn	Lys	Pro	Thr	Ser	Cys	Ala	Val	Val	Leu	His	Ser	Pro	Ser	Ala	His
		1075					1080					1085			
Phe	Thr	Gly	Arg	Trp	Asp	Asp	Arg	Ser	Cys	Thr	Glu	Glu	Thr	His	Gly
	1090					1095					1100				
Phe	Ile	Cys	Gln	Lys	Gly	Thr	Asp	Pro	Ser	Leu	Ser	Pro	Ser	Pro	Ala
	1105				1110					1115					1120
Ala	Leu	Pro	Pro	Ala	Pro	Gly	Thr	Glu	Leu	Ser	Tyr	Leu	Asn	Gly	Thr
			1125						1130					1135	
Phe	Arg														

1220 1225 1230
 Ser Cys Asp Thr Lys Leu Gln Gly Ala Val Cys Gly Val Ser Ser Gly
 1235 1240 1245
 Pro Pro Pro Pro Arg Arg Ile Ser Tyr His Gly Ser Cys Pro Gln Gly
 1250 1255 1260
 Leu Ala Asp Ser Ala Trp Ile Pro Phe Arg Glu His Cys Tyr Ser Phe
 1265 1270 1275 1280
 His Met Glu Leu Leu Leu Gly His Lys Glu Ala Arg Gln Arg Cys Gln
 1285 1290 1295
 Arg Ala Gly Gly Ala Val Leu Ser Ile Leu Asp Glu Met Glu Asn Val
 1300 1305 1310
 Phe Val Trp Glu His Leu Gln Ser Tyr Glu Gly Gln Ser Arg Gly Ala
 1315 1320 1325
 Trp Leu Gly Met Asn Phe Asn Pro Lys Gly Gly Thr Leu Val Trp Gln
 1330 1335 1340
 Asp Asn Thr Ala Val Asn Tyr Ser Asn Trp Gly Pro Pro Gly Leu Gly
 1345 1350 1355 1360
 Pro Ser Met Leu Ser His Asn Ser Cys Tyr Trp Ile Gln Ser Asn Ser
 1365 1370 1375
 Gly Leu Trp Arg Pro Gly Ala Cys Thr Asn Ile Thr Met Gly Val Val
 1380 1385 1390
 Cys Lys Leu Pro Arg Ala Glu Gln Ser Ser Phe Ser Pro Ser Ala Leu
 1395 1400 1405
 Pro Glu Asn Pro Ala Ala Leu Val Val Val Leu Met Ala Val Leu Leu
 1410 1415 1420
 Leu Leu Ala Leu Leu Thr Ala Ala Leu Ile Leu Tyr Arg Arg Arg Gln
 1425 1430 1435 1440
 Ser Ile Glu Arg Gly Ala Phe Glu Gly Ala Arg Tyr Ser Arg Ser Ser
 1445 1450 1455
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<210> 5831

<211> 2216

<212> DNA

<213> Homo sapiens

<400> 5831

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aaagaacagg aaaaggtgtc ttctcacaaa taacatgtgc tggagatgac aacttattga

120

actcttaagt tctcagcact atgttatgca cttgacgggc attactttaa tcctccactg

180

tgagatactt gttattgcct cattttgtag acgagaaaac gggcatagag ggtgagacat

240

tggcccagggt tcattccgta aggggtggag cctggaattc agatacagga ggaagttaac

300

atccctaata ggagggttct ggttactgggt gccactgggc ttcttggcag agctgtacac

360

aaagaatttc agcagaataa ttggcatgca gttggctgtg gtttcagaag agcaagacca

420

aaatttgaac aggttaatat gttggattct aatgcagttc atcacatcat tcatgatttt
480
cagcccatcg ttatagtaca ttgtgcagca gagagaagac cagatgttgt agaaaatcag
540
ccagatgctg cctctcaact taatgtggat gcttctggga atttagcaaa ggaagcagct
600
gctgttgag catttctcat ctacattagc tcagattatg tatttgatgg aacaaatcca
660
ccttacagag aggaagacat accagctccc cttaatttgt atggcaaaa aaaattagat
720
ggagaaaagg ctgtccctgga gaacaatcta ggagctgctg ttttgaggat tcctattctg
780
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840
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960
ggaaccttct actggtctgg caatgaacag atgactaagt atgaaatggc atgtgcaatt
1020
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1080
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1140
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1260
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1380
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1680
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1740
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1800
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1860
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1920
agtgatatatt catatgtgtg gttatactca taataatggg ccttgtaagt cttttcacca
1980
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2040

ttcttttttt aaatgtaagg accaaacttc taaactaatt gttcttttgt tgctttaatt
 2100
 tttaaaaaatt acattcttct gatgtaacat gtgatacata caaaagaata tagtttaata
 2160
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<210> 5832

<211> 322

<212> PRT

<213> Homo sapiens

<400> 5832

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Arg	Arg	Val	Leu	Val	Thr	Gly	Ala	Thr	Gly	Leu	Leu	Gly	Arg	Ala	Val	
			20					25					30			
His	Lys	Glu	Phe	Gln	Gln	Asn	Asn	Trp	His	Ala	Val	Gly	Cys	Gly	Phe	
		35				40						45				
Arg	Arg	Ala	Arg	Pro	Lys	Phe	Glu	Gln	Val	Asn	Leu	Leu	Asp	Ser	Asn	
		50				55				60						
Ala	Val	His	His	Ile	Ile	His	Asp	Phe	Gln	Pro	His	Val	Ile	Val	His	
65				70					75					80		
Cys	Ala	Ala	Glu	Arg	Arg	Pro	Asp	Val	Val	Glu	Asn	Gln	Pro	Asp	Ala	
				85				90						95		
Ala	Ser	Gln	Leu	Asn	Val	Asp	Ala	Ser	Gly	Asn	Leu	Ala	Lys	Glu	Ala	
			100				105						110			
Ala	Ala	Val	Gly	Ala	Phe	Leu	Ile	Tyr	Ile	Ser	Ser	Asp	Tyr	Val	Phe	
		115				120						125				
Asp	Gly	Thr	Asn	Pro	Pro	Tyr	Arg	Glu	Glu	Asp	Ile	Pro	Ala	Pro	Leu	
		130				135					140					
Asn	Leu	Tyr	Gly	Lys	Thr	Lys	Leu	Asp	Gly	Glu	Lys	Ala	Val	Leu	Glu	
145				150					155					160		
Asn	Asn	Leu	Gly	Ala	Ala	Val	Leu	Arg	Ile	Pro	Ile	Leu	Tyr	Gly	Glu	
			165					170						175		
Val	Glu	Lys	Leu	Glu	Glu	Ser	Ala	Val	Thr	Val	Met	Phe	Asp	Lys	Val	
			180					185					190			
Gln	Phe	Ser	Asn	Lys	Ser	Ala	Asn	Met	Asp	His	Trp	Gln	Gln	Arg	Phe	
			195				200					205				
Pro	Thr	His	Val	Lys	Asp	Val	Ala	Thr	Val	Cys	Arg	Gln	Leu	Ala	Glu	
		210				215					220					
Lys	Arg	Met	Leu	Asp	Pro	Ser	Ile	Lys	Gly	Thr	Phe	His	Trp	Ser	Gly	
225				230					235					240		
Asn	Glu	Gln	Met	Thr	Lys	Tyr	Glu	Met	Ala	Cys	Ala	Ile	Ala	Asp	Ala	
			245					250						255		
Phe	Asn	Leu	Pro	Ser	Ser	His	Leu	Arg	Pro	Ile	Thr	Asp	Ser	Pro	Val	
		260					265						270			
Leu	Gly	Ala	Gln	Arg	Pro	Arg	Asn	Ala	Gln	Leu	Asp	Cys	Ser	Lys	Leu	
		275					280					285				
Glu	Thr	Leu	Gly	Ile	Gly	Gln	Arg	Thr	Pro	Phe	Arg	Ile	Gly	Ile	Lys	
		290				295					300					
Glu	Ser	Leu	Trp	Pro	Phe	Leu	Ile	Asp	Lys	Arg	Trp	Arg	Gln	Thr	Val	
					310					315					320	
Phe	His															

<210> 5833
 <211> 805
 <212> DNA
 <213> Homo sapiens

<400> 5833
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 120
 cctaaacctg tgctccagga agaaaacaac caagagtctt ttattgcatt tgctcgggtg
 180
 ttcagtggtg tggctcgaag aggaaagaaa atttttgtct tggggcccaa atacagtcct
 240
 cttgagtttt tacgaagggt accattaggg ttctcagctc caccagatgg cctccccc
 300
 gtccccaca tggcatactg tgctctggaa aacctgtatc ttctgatggg aagggaactg
 360
 gaatatctag aggaggtacc tccaggaaat gtgctaggaa taggaggcct tcaagatttt
 420
 gtgctgaaat ctgcaacact gtgtagcctg ccattcctgcc caccatttat accactcaac
 480
 ttcgaagcca ctccatttgt gagagtgtgt gttgaaccaa aacatccaag tgaatgcct
 540
 cagctcgtaa aaggaatgaa actgttaaac caggctgac cctgtgtcca gattttaatt
 600
 caggaaacgg gagagcacgt tttagtacac gcaggagaag tccacctta cggatgcctg
 660
 gatgacttaa aagaaagggt tgcaaagatt catatcagtg tatctgaacc tattattcca
 720
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 780
 cagcaaaaag ttgcagtcac acacc
 805

<210> 5834
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 5834
 Lys Leu Ala Ala Gln Gly Gln Ala Pro Leu Glu Pro Thr Gln Asp
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 Gly Ser Ala Ile Glu Thr Cys Pro Lys Gly Asp Glu Pro Arg Gly Asp
 20 25 30
 Glu Gln Gln Val Glu Ser Met Thr Pro Lys Pro Val Leu Gln Glu Glu
 35 40 45
 Asn Asn Gln Glu Ser Phe Ile Ala Phe Ala Arg Val Phe Ser Gly Val
 50 55 60
 Ala Arg Arg Gly Lys Lys Ile Phe Val Leu Gly Pro Lys Tyr Ser Pro
 65 70 75 80
 Leu Glu Phe Leu Arg Arg Val Pro Leu Gly Phe Ser Ala Pro Pro Asp

	85		90		95
Gly Leu Pro Gln Val Pro His Met Ala Tyr Cys Ala Leu Glu Asn Leu					
	100		105		110
Tyr Leu Leu Met Gly Arg Glu Leu Glu Tyr Leu Glu Glu Val Pro Pro					
	115		120		125
Gly Asn Val Leu Gly Ile Gly Gly Leu Gln Asp Phe Val Leu Lys Ser					
	130		135		140
Ala Thr Leu Cys Ser Leu Pro Ser Cys Pro Pro Phe Ile Pro Leu Asn					
	145		150		155
Phe Glu Ala Thr Pro Ile Val Arg Val Ala Val Glu Pro Lys His Pro					
	165		170		175
Ser Glu Met Pro Gln Leu Val Lys Gly Met Lys Leu Leu Asn Gln Ala					
	180		185		190
Asp Pro Cys Val Gln Ile Leu Ile Gln Glu Thr Gly Glu His Val Leu					
	195		200		205
Val Thr Ala Gly Glu Val His Leu Gln Arg Cys Leu Asp Asp Leu Lys					
	210		215		220
Glu Arg Phe Ala Lys Ile His Ile Ser Val Ser Glu Pro Ile Ile Pro					
	225		230		235
Phe Arg Glu Thr Ile Thr Lys Pro Pro Lys Val Asp Met Val Asn Glu					
	245		250		255
Glu Ile Gly Lys Gln Gln Lys Val Ala Val Ile His					
	260		265		

<210> 5835

<211> 420

<212> DNA

<213> Homo sapiens

<400> 5835

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120
gcactgcata agcaagtctt tatgggccca tataatccag acacttgtcc tgaggttgga
180
ttctttgatg tgttggggaa tgacaggagg agagaatggg cagccctggg aaacatgtct
240
aaagaggatg ccatggtgga gttgtcaag ctcttaaata ggtgttgcca tctcttttca
300
acatatgttg cgtcccacaa aatagagaag gaagagcaag acaaaaaaag gaaggaggaa
360
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420

<210> 5836

<211> 140

<212> PRT

<213> Homo sapiens

<400> 5836

Xaa Leu Glu Gln Arg Trp Gly Phe Gly Leu Glu Glu Leu Tyr Gly Leu
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Ala Leu Arg Phe Phe Lys Glu Lys Asp Gly Lys Ala Phe His Pro Thr

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                20                25                30
Tyr Glu Glu Lys Leu Lys Leu Val Ala Leu His Lys Gln Val Leu Met
      35                40                45
Gly Pro Tyr Asn Pro Asp Thr Cys Pro Glu Val Gly Phe Phe Asp Val
      50                55                60
Leu Gly Asn Asp Arg Arg Glu Trp Ala Ala Leu Gly Asn Met Ser
65      70                75                80
Lys Glu Asp Ala Met Val Glu Phe Val Lys Leu Leu Asn Arg Cys Cys
      85                90                95
His Leu Phe Ser Thr Tyr Val Ala Ser His Lys Ile Glu Lys Glu Glu
      100               105               110
Gln Asp Lys Lys Arg Lys Glu Glu Glu Glu Arg Arg Arg Glu Glu
      115               120               125
Glu Glu Arg Glu Arg Leu Gln Lys Glu Glu Glu Lys
      130               135               140

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<210> 5837

<211> 582

<212> DNA

<213> Homo sapiens

<400> 5837

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120
tggggccaagg gggacatcca gggggcaggg gccgcctccc gcogtgcctt cctgctgggg
180
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240
taccttgccct ccgagacccc gccctagttag cccctacagc cctcactgtg aaccttgagg
300
ccggcagccc agcaaactctg tgggcagaga gtgagaatc ttggtggatg aggctgcggc
360
ggcggcagga gcacttagaa acgggagcga gctggactgg aacccttccc ctctctggcc
420
accgctcttc gggcggcagc aacctgagat taaacaccag acacccttgg cctggggtca
480
cgaggaaggg gctgcagttc tccaaggatt cccgcctgct cccagatccc cgggagtcgt
540
aggaaccctg tcctggacgc tgacgtcggc ttccagggat cc
582

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<210> 5838

<211> 88

<212> PRT

<213> Homo sapiens

<400> 5838

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Xaa Arg Leu Ser Pro Phe Leu Pro His Asp His Leu Gly Leu Ala Val
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Phe Ser Met Leu Cys Cys Phe Trp Pro Val Gly Ile Ala Ala Phe Cys
      20      25      30
Leu Ala Gln Lys Thr Asn Lys Ala Trp Ala Lys Gly Asp Ile Gln Gly

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<210> 5839
<211> 1895
<212> DNA
<213> Homo sapiens
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5005

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 1320
 tcttccagcc caggatccct gcagagaacc agaggttaca aatctgcctt cctttctccc
 1380
 ctaaaagggtg gctgagggga ggagaggtgc atgtagctcc agctatagca aatcagtgcc
 1440
 ctgactcaact ggggagaccc agggggttgg gatgttgctg acacctcatg gggcacctca
 1500
 tcagcccatc tttgtagctt caggttcagc tctgggtgct gcaggcaggg acccctctgc
 1560
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 1620
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 1680
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 1740
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 1860
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<210> 5840

<211> 138

<212> PRT

<213> Homo sapiens

<400> 5840

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 Leu Met Val His Gly Trp Cys Pro Val Ile Phe Ser Trp Ala Val Ala
 35 40 45
 Pro Arg Gly Ser Gly Phe Pro Ala Gln Gly Ile Phe Asp Pro Cys Gln
 50 55 60
 Arg Arg Glu Arg Glu Leu Ser Trp Phe Pro Phe His Leu Phe Ser Gly
 65 70 75 80
 Cys Phe Lys Ala Asn Ile Pro Val Pro Asn Val Leu Cys Gly Leu Asn
 85 90 95
 Pro Gly Arg Gly Gln Gly His Ile Gln Val Gly Leu Ala Ser Ser Thr
 100 105 110
 Thr Phe Trp Pro Gln Gln Arg Met Gly Phe His Gln Ser Leu Ser Thr
 115 120 125
 Ser Arg Phe Pro Lys Glu Ser Pro Arg Ser
 130 135

<210> 5841

<211> 3411

<212> DNA

<213> Homo sapiens

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 Ser Asp Ala Gly Pro Ala Gly His Phe Ala Ser Val Tyr Asn Pro Leu
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 Ala Trp Thr Val Thr Thr Ile Val Thr Leu Thr Val Gly Phe Pro Gly
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 Val Arg Val Thr Asp Glu Ala Gly His Pro Val Pro Ser Gln Ile Gln
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 Asn Ser Thr Glu Thr Pro Ser Ala Tyr Asp Leu Leu Ile Leu Thr Thr
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 405 410 415
 Ala Gln Glu Gly Thr Gln Glu Pro Ala Ala Thr Val Ala Ser Thr Leu
 420 425 430
 Gln Phe Gly Arg Arg Leu Arg Arg Arg Thr Ser His Ala Gly Arg Tyr
 435 440 445
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 Thr Asn Leu Met His Ser Ile Trp Glu Arg Gln Ser Asn Arg Thr Val
 465 470 475 480
 Arg Val Thr Gln Glu Phe Leu Glu Tyr His Val Asn Arg Asp Val Lys
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 Gln Gly Pro Ile Ser Asp Asn Tyr Leu Phe Thr Pro Gly Lys Ala Ala
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 Val Pro Ala Trp Glu Ala Val Glu Met Glu Ile Val Ala Gly Gln Leu
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 Tyr Thr Tyr Ala Ile Arg Ser Arg Leu Thr His Val Pro Gln Gly His
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 Asp Gly Glu Leu Leu Cys His Arg Ile Glu Gln Glu Tyr Gln Ala Gly
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 Pro Leu Glu Leu Asn Arg Glu Ala Val Leu Arg Thr Ser Thr Asn Leu
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 Val Leu Leu Ser Glu Arg Ala His Gly Ile Ser Ser Gln Gly Asn Gly
 645 650 655
 Gln Val Glu Val Met Leu His Arg Arg Leu Trp Asn Asn Phe Asp Trp
 660 665 670
 Asp Leu Gly Tyr Asn Leu Thr Leu Asn Asp Thr Ser Val Val His Pro
 675 680 685
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 690 695 700
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 705 710 715 720
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 Ala Val Thr Leu Pro Pro Asn Leu His Leu Gln Ile Leu Ser Ile Pro
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 Gly Trp Arg Tyr Ser Ser Asn His Thr Glu His Ser Gln Asn Leu Arg
 755 760 765
 Lys Gly His Arg Gly Glu Ala Gln Ala Asp Leu Arg Arg Val Leu Leu
 770 775 780
 Arg Leu Tyr His Leu Tyr Glu Val Gly Glu Asp Pro Val Leu Ser Gln
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<210> 5845

<211> 2762

<212> DNA

<213> Homo sapiens

<400> 5845

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<210> 5846

<211> 257

<212> PRT

<213> Homo sapiens

<400> 5846

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			20					25					30		
Gln	Gln	Glu	Lys	Glu	Trp	Leu	Leu	Ala	Glu	Glu	Thr	Ala	Ala	Thr	Ala
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Ser	Ala	Ile	Glu	Ala	Met	Lys	Lys	Ala	Tyr	Gln	Glu	Glu	Leu	Ser	Arg
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Glu	Leu	Ser	Lys	Thr	Arg	Ser	Leu	Gln	Gln	Gly	Pro	Asp	Gly	Leu	Arg
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Lys	Gln	His	Gln	Ser	Asp	Val	Glu	Ala	Leu	Lys	Arg	Glu	Leu	Gln	Val
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Leu	Leu	Arg	Val	Lys	Glu	Asn	Glu	Leu	Gln	Tyr	Leu	Lys	Lys	Glu	Val
			180				185						190		
Gln	Cys	Leu	Arg	Asp	Glu	Leu	Gln	Met	Met	Gln	Lys	Asp	Lys	Arg	Phe
			195				200				205				
Thr	Ser	Gly	Lys	Tyr	Gln	Asp	Val	Tyr	Val	Glu	Leu	Ser	His	Ile	Lys

210		215		220
Thr Arg Ser Glu Arg	Glu Ile Glu Gln Leu Lys	Glu His Leu Arg Leu		
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<210> 5847

<211> 1021

<212> DNA

<213> Homo sapiens

<400> 5847

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<210> 5848

<211> 120

<212> PRT

<213> Homo sapiens

<400> 5848

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Leu Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Phe Leu Phe
 35                               40                               45
Gly Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala
 50                               55                               60
Val Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala
 65                               70                               75                               80
Leu Gly Phe Lys Asn Lys Thr Val Leu Lys Arg Cys Lys Asp Cys
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Tyr Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His
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Pro Arg His Lys Gln Arg Gln Met
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<210> 5849

<211> 3174

<212> DNA

<213> Homo sapiens

<400> 5849

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 720
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 840

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<210> 5850

<211> 154

<212> PRT

<213> Homo sapiens

<400> 5850

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 35 40 45
 Gly Pro Ile His Ile Ala Glu Gly Gly Arg Gly Arg Pro Pro Gly
 50 55 60
 Ser Ala Ser Asn Pro Gln Pro Pro Gly Ser Pro His Cys Pro Ser Ala
 65 70 75 80
 Gly Leu Ser Pro Val Pro Gly Val Gly Gly Arg Gln Cys Pro Gly Thr
 85 90 95
 Val Pro Arg Val Arg Arg Pro Gly Leu Ala Gly His Pro Val Thr His
 100 105 110
 Arg Ile Asn Arg Lys Thr Ala Ser Pro Pro Asn Leu Cys Pro Arg His
 115 120 125
 Asn Met Ser Arg Ser Glu Ser Cys Thr Pro Arg Ser Arg Ala Pro Leu
 130 135 140
 Gln Arg Thr Leu Thr Pro Pro Arg Gly Ala
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<210> 5851

<211> 488

<212> DNA

<213> Homo sapiens

<400> 5851

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<210> 5852

<211> 82

<212> PRT

<213> Homo sapiens

<400> 5852

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 Leu Thr Lys Gly Thr Ser Ala Ala His Leu Asn Ser Met Glu Val Thr
 35 40 45
 Thr Glu Asp Thr Ser Arg Thr Asp Ala Tyr Glu Ser Tyr Lys Lys Lys
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 Glu Met

<210> 5853

<211> 487

<212> DNA

<213> Homo sapiens

<400> 5853

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<210> 5854

<211> 68

<212> PRT

<213> Homo sapiens

<400> 5854

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 Arg Thr Pro Pro Arg Leu Leu Pro Thr Leu Cys Pro Val Thr Pro Val
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 Ser Trp Pro Leu
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<210> 5855

<211> 362

<212> DNA

<213> Homo sapiens

<400> 5855

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<210> 5856

<211> 113

<212> PRT

<213> Homo sapiens

<400> 5856

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      20           25           30
Ser Pro Pro Asp Pro Pro Ala Gly Thr Cys Trp Gly Leu Trp Gly Pro
 35           40           45
Lys Arg Glu Gly Val Asn Glu Val Val Ala Glu Val Leu Leu Ala Ala
 50           55           60
His Glu Gly Val Gly Asp Gln Gly Glu Ala Gly Ala His Pro Val Leu
 65           70           75           80
Ser Asp Ala Gly Leu Leu Val Leu Gly Leu Arg Ala Ala Leu Gly Glu
      85           90           95
His Gln Ala His Leu Gly Ser Ala Leu Asn Glu His Gln Arg Val Leu
      100           105           110
Ala

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<210> 5857

<211> 1751

<212> DNA

<213> Homo sapiens

<400> 5857

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840

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<210> 5858

<211> 434

<212> PRT

<213> Homo sapiens

<400> 5858

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 Gly Gly Gln Gly Arg Gly Gly Glu Lys Pro Pro His Leu Ala Ala Leu
 35 40 45
 Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys
 50 55 60
 His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu
 65 70 75 80
 Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu
 85 90 95
 Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser
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 Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu

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      115              120              125
Phe Leu Asn Tyr His Asn Glu Val Asp Ile Val Gly Asn Ile Gln Ala
  130              135              140
Thr Ser Pro Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met
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Ile Arg Glu Glu Gly Tyr Asp Ser Val Phe Ser Val Val Arg Arg His
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Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu
      180              185              190
Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp
      195              200              205
Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu
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Ile Glu Met Gly Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met
225              230              235              240
Arg Ala Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile
      245              250              255
Ala Glu Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu
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Lys Glu Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn
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Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp
      290              295              300
Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu
305              310              315              320
Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser
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Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala
      340              345              350
Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val
      355              360              365
Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val
      370              375              380
Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Thr Ala Gln Lys Ala
385              390              395              400
Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu
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Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys
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Gln Lys

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<210> 5859

<211> 2267

<212> DNA

<213> Homo sapiens

<400> 5859

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180

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<210> 5860
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 5860
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 35 40 45
 Gln Met Gly Leu Gly Arg Cys Arg Phe Cys Phe Ser Pro Trp Leu Pro
 50 55 60
 Val Arg Pro Gln Pro Ser Gly Cys Asp Ile Ile Glu Ser Ala Val Ser
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 Pro Leu Val Gly Asp Trp Gly Ser Val Phe Ser His Leu Tyr Leu Leu
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<210> 5861
 <211> 1951
 <212> DNA
 <213> Homo sapiens

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<210> 5862
 <211> 514
 <212> PRT
 <213> Homo sapiens

<400> 5862

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Pro Asp Leu Lys Val Ile Tyr Ile Leu Val Arg Pro Lys Ala Gly Gln
      35           40           45
Thr Leu Gln Gln Arg Val Phe Gln Ile Leu Asp Ser Lys Leu Phe Glu
      50           55           60
Lys Val Lys Glu Val Cys Pro Asn Val His Glu Lys Ile Arg Ala Ile
 65           70           75           80
Tyr Ala Asp Leu Asn Gln Asn Asp Phe Ala Ile Ser Lys Glu Asp Met
      85           90           95
Gln Glu Leu Leu Ser Cys Thr Asn Ile Ile Phe His Cys Ala Ala Thr
      100          105          110
Val Arg Phe Asp Asp Thr Leu Arg His Ala Val Gln Leu Asn Val Thr
      115          120          125
Ala Thr Arg Gln Leu Leu Met Ala Ser Gln Met Pro Lys Leu Glu
      130          135          140
Ala Phe Ile His Ile Ser Thr Ala Tyr Ser Asn Cys Asn Leu Lys His
 145          150          155          160
Ile Asp Glu Val Ile Tyr Pro Cys Pro Val Glu Pro Lys Lys Lys Ile
      165          170          175
Ile Asp Ser Leu Glu Trp Leu Asp Asp Ala Ile Ile Asp Glu Ile Thr
      180          185          190
Pro Lys Leu Ile Arg Asp Trp Pro Asn Ile Tyr Thr Tyr Thr Lys Ala
      195          200          205
Leu Gly Glu Met Val Val Gln Gln Glu Ser Arg Asn Leu Asn Ile Ala
      210          215          220
Ile Ile Arg Pro Ser Ile Val Gly Ala Thr Trp Gln Glu Pro Phe Pro
 225          230          235          240
Gly Trp Val Asp Asn Ile Asn Gly Pro Asn Gly Ile Ile Ile Ala Thr
      245          250          255
Gly Lys Gly Phe Leu Arg Ala Ile Lys Ala Thr Pro Met Ala Val Ala
      260          265          270
Asp Val Ile Pro Val Asp Thr Val Val Asn Leu Met Leu Ala Val Gly
      275          280          285
Trp Tyr Thr Ala Val His Arg Pro Lys Ser Thr Leu Val Tyr His Ile
      290          295          300
Thr Ser Gly Asn Met Asn Pro Cys Asn Trp His Lys Met Gly Val Gln
 305          310          315          320
Val Leu Ala Thr Phe Glu Lys Ile Pro Phe Glu Arg Pro Phe Arg Arg
      325          330          335
Pro Asn Ala Asn Phe Thr Ser Asn Ser Phe Thr Ser Gln Tyr Trp Asn
      340          345          350
Ala Val Ser His Arg Ala Pro Ala Ile Ile Tyr Asp Cys Tyr Leu Arg
      355          360          365
Leu Thr Gly Arg Lys Pro Arg Met Thr Lys Leu Met Asn Arg Leu Leu

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      370              375              380
Arg Thr Val Ser Met Leu Glu Tyr Phe Ile Asn Arg Ser Trp Glu Trp
385              390              395              400
Ser Thr Tyr Asn Thr Glu Met Leu Met Ser Glu Leu Ser Pro Glu Asp
      405              410              415
Gln Arg Val Phe Asn Phe Asp Val Arg Gln Leu Asn Trp Leu Glu Tyr
      420              425              430
Ile Glu Asn Tyr Val Leu Gly Val Lys Lys Tyr Leu Leu Lys Glu Asp
      435              440              445
Met Ala Gly Ile Pro Lys Ala Lys Gln Arg Leu Lys Arg Leu Arg Asn
      450              455              460
Ile His Tyr Leu Phe Asn Thr Ala Leu Phe Leu Ile Ala Trp Arg Leu
      465              470              475              480
Leu Ile Ala Arg Ser Gln Met Ala Arg Asn Val Trp Phe Phe Ile Val
      485              490              495
Ser Phe Cys Tyr Lys Phe Leu Ser Tyr Phe Arg Ala Ser Ser Thr Leu
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Lys Val

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<210> 5863

<211> 438

<212> DNA

<213> Homo sapiens

<400> 5863

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<210> 5864

<211> 104

<212> PRT

<213> Homo sapiens

<400> 5864

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      20              25              30
Cys Gln Tyr Leu Ser Tyr Val Pro Phe Met Ala Glu Tyr Gln Ser Lys

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<210> 5866
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 <212> PRT
 <213> Homo sapiens

<400> 5866
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 35 40 45
 Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile Glu Glu Leu
 50 55 60
 Leu Val Glu Arg Thr Gly Ala Pro Phe Cys Ser Pro Thr Ser Ser Gly
 65 70 75 80
 Trp Arg Arg Ser Arg Ala Ser Ala Ile Ala Ala Gly Val His Pro Gln
 85 90 95
 Asp Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu
 100 105 110
 Lys Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr
 115 120 125
 Phe Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro
 130 135 140
 Leu His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr
 145 150 155 160
 Leu Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg
 165 170 175
 Lys Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln
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 Ala Lys Pro Ser
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<210> 5867
 <211> 1882
 <212> DNA
 <213> Homo sapiens

<400> 5867
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1882

<210> 5868
<211> 131
<212> PRT
<213> Homo sapiens

<400> 5868
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<212> PRT

<213> Homo sapiens

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Pro	Thr	Leu	Val	Gln	Thr	Gly	Leu	His	Gly	Arg	His	Ile	Leu	Gly	Arg
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<212> DNA

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<400> 5872

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 5874

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<213> Homo sapiens

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 Val Ala Ser Ala Val Cys Leu Arg Leu His Arg Pro Arg Asp Ala Ser

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<210> 5878

<211> 227

<212> PRT

<213> Homo sapiens

<400> 5878

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 35 40 45
 Arg Leu Arg Gly Cys Arg Asn Leu Tyr Lys Lys Asp Leu Leu Gly His
 50 55 60
 Phe Gly Cys Val Asn Ala Ile Glu Phe Ser Asn Asn Gly Gly Gln Trp
 65 70 75 80
 Leu Val Ser Gly Gly Asp Asp Arg Arg Val Leu Leu Trp His Met Glu
 85 90 95
 Gln Ala Ile His Ser Arg Val Lys Pro Ile Gln Leu Lys Gly Glu His
 100 105 110
 His Ser Asn Ile Phe Cys Leu Ala Phe Asn Ser Gly Asn Thr Lys Val
 115 120 125
 Phe Ser Gly Gly Asn Asp Glu Gln Val Ile Leu His Asp Val Glu Ser
 130 135 140
 Ser Glu Thr Leu Asp Val Phe Ala His Glu Asp Ala Val Tyr Gly Leu
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 Ser Val Ser Pro Val Asn Asp Asn Ile Phe Ala Ser Ser Ser Asp Asp
 165 170 175
 Gly Arg Val Leu Ile Trp Asp Ile Arg Glu Ser Pro His Gly Glu Pro
 180 185 190
 Phe Cys Trp Ala Asn Tyr Pro Ser Ala Phe His Ser Val Met Phe Asn
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<211> 1555

<212> DNA

<213> Homo sapiens

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<400> 5880
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 Phe Tyr Asp Val Glu Ala Leu Arg Asp Tyr Leu Leu Gln Arg Glu Met
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 Tyr Lys Val His Glu Lys Asn Arg Ser Tyr Thr Trp Leu Glu Lys Gln
 65 70 75 80
 His Gly Pro Tyr Gly Ala Gly Ala Phe Phe Ile Leu Lys Gln Gly Gly
 85 90 95
 Ala Val Lys Phe Arg Asp Lys Glu Trp Ile Arg Pro Asp Lys Tyr Gly
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 His Phe Ser Gln Glu Phe Trp Asn Phe Cys Glu Val Pro Val Glu Ala
 115 120 125
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<210> 5881
 <211> 327
 <212> DNA
 <213> Homo sapiens

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<210> 5882
 <211> 109
 <212> PRT

<213> Homo sapiens

<400> 5882

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Ala Lys Glu Asn Met Val Thr Phe Ser His Thr Leu Pro Arg Ala Ser
          35           40           45
Ala Pro Ser Leu Asp Asp Pro Ala Arg Arg His Met Thr Ile His Val
          50           55           60
Pro Leu Asp Ala Ser Arg Ser Lys Gln Leu Ile Ser Glu Trp Lys Gln
65           70           75           80
Lys Ser Leu Glu Gly Arg Gly Leu Gly Leu Pro Asp Asp Ala Ser Pro
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Gly His Leu Arg Ala Pro Ala Glu Pro Met Pro Glu Xaa
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<210> 5883

<211> 579

<212> DNA

<213> Homo sapiens

<400> 5883

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<213> Homo sapiens

<400> 5884

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<210> 5886

<211> 265

<212> PRT

<213> Homo sapiens

<400> 5886

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 Tyr Arg His Asp Met Val Ala Val Leu Gly Glu Thr Thr Gly His Arg
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 Thr Leu Lys Val Leu Arg Asp Gln Met Arg Arg Asp Pro Glu Gly Ala
 85 90 95
 Gln Ile Leu Gln Glu Arg Pro Arg Ile Ser Thr Ser Thr Leu Asp Leu
 100 105 110
 Gly Lys Leu Gln Ser Leu Pro Glu Gly Ser Leu Gly Arg Glu Tyr Leu
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 Arg Phe Leu Asp Val Asn Arg Val Ser Pro Asp Thr Arg Ala Pro Thr
 130 135 140
 Arg Phe Val Asp Asp Glu Glu Leu Ala Tyr Val Ile Gln Arg Tyr Arg
 145 150 155 160
 Glu Val His Asp Met Leu His Thr Leu Leu Gly Met Pro Thr Asn Ile
 165 170 175
 Leu Gly Glu Ile Val Val Lys Trp Phe Glu Ala Val Gln Thr Gly Leu

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Pro Met Cys Ile Leu Gly Ala Phe Phe Gly Pro Ile Arg Leu Gly Ala					
	195		200		205
Gln Ser Leu Gln Val Leu Val Ser Glu Leu Ile Pro Trp Ala Val Gln					
	210		215		220
Asn Gly Arg Arg Ala Pro Cys Val Leu Asn Leu Tyr Tyr Glu Arg Arg					
225		230		235	240
Trp Glu Gln Ser Leu Arg Ala Leu Arg Glu Glu Leu Gly Ile Thr Ala					
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<210> 5887

<211> 3779

<212> DNA

<213> Homo sapiens

<400> 5887

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<211> 166

<212> PRT

<213> Homo sapiens

<400> 5888

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 Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu
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 Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr
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Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu Tyr					
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Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro Leu Glu					
	115		120		125
Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu His Lys Leu					
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<210> 5889

<211> 2198

<212> DNA

<213> Homo sapiens

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 1980
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 2040
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 2100
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<210> 5890

<211> 118

<212> PRT

<213> Homo sapiens

<400> 5890

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		20					25					30			
Glu	Cys	Ser	Gly	Thr	Ile	Thr	Ala	His	Cys	Ser	Leu	Asp	Phe	Pro	Gly
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Ser	Ser	His	Ser	Pro	Thr	Ser	Ala	Ser	Gln	Ala	Val	Gly	Thr	Thr	Gly
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Glu	Glu	Arg	Gln	Gln	His	Gly	Glu	Cys	Pro	Val	Pro	Thr	Pro	Trp	Lys

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65              70              75              80
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Ala Leu Gly Cys Pro Thr Leu Gly Ala Thr Ala Arg Arg Gly Arg Ser
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<210> 5891
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<212> DNA
<213> Homo sapiens

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 1459

<210> 5892

<211> 212

<212> PRT

<213> Homo sapiens

<400> 5892

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 35 40 45
 Leu Val Met Thr Phe Leu Phe Arg Asn Gly Ser Leu Gln Glu Lys Leu
 50 55 60
 Trp Ala Ile Leu Gln Ala Thr Tyr Ile His Ser Trp Asn Leu Ala Arg
 65 70 75 80
 Phe Val Phe Thr Tyr Lys Gly Leu Arg Ala Leu Gln Ser Tyr Ile Gln
 85 90 95
 Gly Lys Thr Tyr Pro Ala His Ala Phe Leu Ala Ala Phe Leu Gly Gly
 100 105 110
 Ile Leu Val Phe Gly Glu Asn Asn Asn Ile Asn Ser Gln Ile Asn Met
 115 120 125
 Tyr Leu Leu Ser Arg Val Leu Phe Ala Leu Ser Arg Leu Ala Val Glu
 130 135 140
 Lys Gly Tyr Ile Pro Glu Pro Arg Trp Asp Pro Phe Pro Leu Leu Thr
 145 150 155 160
 Ala Val Val Trp Gly Leu Val Leu Trp Leu Phe Glu Tyr His Arg Ser
 165 170 175
 Thr Leu Gln Pro Ser Leu Gln Ser Ser Met Thr Tyr Leu Tyr Glu Asp
 180 185 190
 Ser Asn Val Trp His Asp Ile Ser Asp Phe Leu Val Tyr Asn Lys Ser
 195 200 205
 Arg Pro Ser Asn
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<210> 5893

<211> 1389

<212> DNA

<213> Homo sapiens

<400> 5893

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 180
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<210> 5894

<211> 260

<212> PRT

<213> Homo sapiens

<400> 5894

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      35           40           45
Thr Asp Arg Pro Gly Phe His Asp Glu Ser Ala Ile Tyr Pro Val Gly
      50           55           60
Tyr Cys Ser Thr Arg Ile Tyr Ala Ser Met Lys Cys Pro Asp Gln Lys
      65           70           75           80
Cys Leu Tyr Thr Cys Gln Ile Lys Asp Gly Gly Val Gln Pro Gln Phe
      85           90           95
Glu Ile Val Pro Glu Asp Asp Pro Gln Asn Ala Ile Val Ser Ser Ser
      100          105          110
Ala Asp Ala Cys His Ala Glu Leu Leu Arg Thr Ile Ser Thr Thr Met
      115          120          125
Gly Lys Leu Met Pro Asn Leu Leu Pro Ala Gly Ala Asp Phe Phe Gly
      130          135          140
Phe Ser His Pro Ala Ile His Asn Leu Ile Gln Ser Cys Pro Gly Ala
      145          150          155          160
Arg Lys Cys Ile Asn Tyr Gln Trp Val Lys Phe Asp Val Cys Lys Pro
      165          170          175
Gly Asp Gly Gln Leu Pro Glu Gly Leu Pro Glu Asn Asp Ala Ala Met
      180          185          190
Ser Phe Glu Ala Phe Gln Arg Gln Ile Phe Asp Glu Asp Gln Asn Asp
      195          200          205
Pro Leu Leu Pro Gly Ser Leu Asp Leu Pro Glu Leu Gln Pro Ala Ala
      210          215          220
Phe Val Ser Ser Tyr Gln Pro Met Tyr Leu Thr His Glu Pro Leu Val
      225          230          235          240
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Gln Ser Ser Asp
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<210> 5895

<211> 2748

<212> DNA

<213> Homo sapiens

<400> 5895

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360
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420

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<210> 5896

<211> 261

<212> PRT

<213> Homo sapiens

<400> 5896

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			20					25					30		
Arg	Asp	Leu	Gly	Gly	Ser	Ser	Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu
		35					40					45			
Thr	Ala	Thr	Tyr	Pro	Val	Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu
		50				55					60				
Ile	Arg	Ala	Val	Tyr	Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys
					70					75				80	
Leu	Val	Ser	Thr	Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe
				85					90					95	
Thr	Phe	Val	Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe
			100					105					110		
Trp	Thr	Pro	Asn	Val	Ser	Glu	Lys	Ile	Leu	Ile	Asp	Ile	Ile	Gly	Val
		115					120					125			
Asp	Phe	Ala	Phe	Ala	Glu	Leu	Cys	Val	Val	Pro	Leu	Arg	Ile	Phe	Ser
		130				135					140				
Phe	Phe	Pro	Val	Pro	Val	Thr	Val	Arg	Ala	His	Leu	Thr	Gly	Trp	Leu
				150						155				160	
Met	Thr	Leu	Lys	Lys	Thr	Phe	Val	Leu	Ala	Pro	Ser	Ser	Val	Leu	Arg
				165					170					175	
Ile	Ile	Val	Leu	Ile	Ala	Ser	Leu	Val	Val	Leu	Pro	Tyr	Leu	Gly	Val

	180		185		190
His	Gly Ala Thr Leu Gly Val	Gly Ser Leu Leu Ala Gly Phe Val Gly			
	195	200	205		
Glu	Ser Thr Met Val Ala Ile	Ala Ala Cys Tyr Val Tyr Arg Lys Gln			
	210	215	220		
Lys	Lys Lys Met Glu Asn Glu Ser Ala Thr Glu Gly Glu Asp Ser Ala				
	225	230	235		240
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<210> 5897

<211> 1930

<212> DNA

<213> Homo sapiens

<400> 5897

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<210> 5898

<211> 242

<212> PRT

<213> Homo sapiens

<400> 5898

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			20					25					30		
Glu	Ile	Cys	Ala	Asp	Glu	Phe	Pro	Gly	Ser	Ser	Ala	Thr	Tyr	Arg	Ile
		35						40				45			
Leu	Glu	Val	Gly	Cys	Gly	Val	Gly	Asn	Thr	Val	Phe	Pro	Ile	Leu	Gln
		50				55					60				
Thr	Asn	Asn	Asp	Pro	Gly	Leu	Phe	Val	Tyr	Cys	Cys	Asp	Phe	Ser	Ser
65					70				75					80	
Thr	Ala	Ile	Glu	Leu	Val	Gln	Thr	Asn	Ser	Glu	Tyr	Asp	Pro	Ser	Arg
				85					90				95		
Cys	Phe	Ala	Phe	Val	His	Asp	Leu	Cys	Asp	Glu	Glu	Lys	Ser	Tyr	Pro
			100					105					110		
Val	Pro	Lys	Gly	Ser	Leu	Asp	Ile	Ile	Ile	Leu	Ile	Phe	Val	Leu	Ser
			115				120					125			
Ala	Ile	Val	Pro	Asp	Lys	Met	Gln	Lys	Ala	Ile	Asn	Arg	Leu	Ser	Arg

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Asp Met Ala Gln Leu Arg Phe Lys Lys Gly Gln Cys Leu Ser Gly Asn		160
	165	170
Phe Tyr Val Arg Gly Asp Gly Thr Arg Val Tyr Phe Phe Thr Gln Glu		175
	180	185
Glu Leu Asp Thr Leu Phe Thr Thr Ala Gly Leu Glu Lys Val Gln Asn		190
	195	200
Leu Val Asp Arg Arg Leu Gln Val Asn Arg Gly Lys Gln Leu Thr Met		205
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<210> 5899

<211> 1589

<212> DNA

<213> Homo sapiens

<400> 5899

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<211> 345

<212> PRT

<213> Homo sapiens

<400> 5900

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 Thr Thr Met Pro Gly Met Lys Arg Asp Cys Gly Gly Ala Ala Val
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 Tyr Ala Cys Lys Asp Leu Gly Ala Asp Ile Ile Leu Asp Met Ala Thr
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245	250	255
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260	265	270
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<211> 984

<212> DNA

<213> Homo sapiens

<400> 5901

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<212> PRT

<213> Homo sapiens

<400> 5902

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Val	Leu	Gln	Ile	Asn	Val	Leu	Gln	Ala	Lys	Lys	Lys	Phe	Glu	Ile	Leu
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<211> 3734

<212> DNA

<213> Homo sapiens

<400> 5903

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<211> 308

<212> PRT

<213> Homo sapiens

<400> 5904

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<212> PRT

<213> Homo sapiens

<400> 5906

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 165 170 175
 Leu Lys Gly His Arg Ser Val Gly Gly Ile Arg Ala Ser Leu Tyr Asn
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<210> 5908

<211> 454

<212> PRT

<213> Homo sapiens

<400> 5908

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          20          25          30
Gln Ile Ala Ala Ser Ala Glu Leu Glu Ser Gly Ala Met Pro Trp Ser
 35          40          45
Leu Leu Gln His Ile Asp Glu Arg Asp Arg Ala Gly Leu Leu Pro Ala
 50          55          60
Leu Phe Lys Val Leu Ser Val Gly Arg Gly Gly Ser Pro Arg Leu Gln
 65          70          75          80
Pro Asp Ser Arg Ala Leu His Tyr Met Lys Lys Leu Tyr Lys Thr Tyr
          85          90          95
Ala Thr Lys Glu Gly Ile Pro Lys Ser Asn Arg Ser His Leu Tyr Asn
          100          105          110
Thr Val Arg Leu Phe Thr Pro Cys Thr Arg His Lys Gln Ala Pro Gly
          115          120          125
Asp Gln Val Thr Gly Ile Leu Pro Ser Val Glu Leu Leu Phe Asn Leu
          130          135          140
Asp Arg Ile Thr Thr Val Glu His Leu Leu Lys Ser Val Leu Leu Tyr
          145          150          155          160
Asn Ile Asn Asn Ser Val Ser Phe Ser Ser Ala Val Lys Cys Val Cys
          165          170          175
Asn Leu Met Ile Lys Glu Pro Lys Ser Ser Arg Thr Leu Gly Arg
          180          185          190
Ala Pro Tyr Ser Phe Thr Phe Asn Ser Gln Phe Glu Phe Gly Lys Lys
          195          200          205
His Lys Trp Ile Gln Ile Asp Val Thr Ser Leu Leu Gln Pro Leu Val
          210          215          220
Ala Ser Asn Lys Arg Ser Ile His Met Ser Ile Asn Phe Thr Cys Met
          225          230          235          240
Lys Asp Gln Leu Glu His Pro Ser Ala Gln Asn Gly Leu Phe Asn Met
          245          250          255
Thr Leu Val Ser Pro Ser Leu Ile Leu Tyr Leu Asn Asp Thr Ser Ala
          260          265          270
Gln Ala Tyr His Ser Trp Tyr Ser Leu His Tyr Lys Arg Arg Pro Ser
          275          280          285
Gln Gly Pro Asp Gln Glu Arg Ser Leu Ser Ala Tyr Pro Val Gly Glu
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Glu Ala Ala Glu Asp Gly Arg Ser Ser His His Arg His Arg Gly
          305          310          315          320
Gln Glu Thr Val Ser Ser Glu Leu Lys Lys Pro Leu Gly Pro Ala Ser
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Phe Asn Leu Ser Glu Tyr Phe Arg Gln Phe Leu Leu Pro Gln Asn Glu
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Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp
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Asn Trp Ile Val Ala Pro His Arg Tyr Asn Pro Arg Tyr Cys Lys Gly
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Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Ser Pro Val His Thr
          385          390          395          400
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<210> 5909
<211> 4343
<212> DNA
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<211> 899

<212> PRT

<213> Homo sapiens

<400> 5910

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Gly Ser Phe Gly Ala Val Tyr Phe Ala Thr Asn Ala His Thr Ser Glu
 35              40              45
Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys Gln Thr His Glu
 50              55              60
Lys Trp Gln Asp Ile Leu Lys Glu Val Lys Phe Leu Arg Gln Leu Lys
 65              70              75              80
His Pro Asn Thr Ile Glu Tyr Lys Gly Cys Tyr Leu Lys Glu His Thr
 85              90              95
Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala Ser Asp Leu Leu
 100             105             110
Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile Ala Ala Ile Thr
 115             120             125
His Gly Ala Leu His Gly Leu Ala Tyr Leu His Ser His Ala Leu Ile
 130             135             140
His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr Glu Pro Gly Gln
 145             150             155             160
Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala Ser Pro Ala Asn
 165             170             175
Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Ile Leu Ala
 180             185             190
Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Ile Trp Ser Leu Gly
 195             200             205
Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro Leu Phe Asn Met
 210             215             220
Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn Asp Ser Pro Thr
 225             230             235             240
Leu Gln Ser Asn Glu Trp Thr Asp Ser Phe Arg Arg Phe Val Asp Tyr
 245             250             255
Cys Leu Gln Lys Ile Pro Gln Glu Arg Pro Thr Ser Ala Glu Leu Leu
 260             265             270
Arg His Asp Phe Val Arg Arg Asp Arg Pro Leu Arg Val Leu Ile Asp
 275             280             285
Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu Asp Asn Leu Gln
 290             295             300
Tyr Arg Lys Met Lys Lys Ile Leu Phe Gln Glu Thr Arg Asn Gly Pro
 305             310             315             320
Leu Asn Glu Ser Gln Glu Asp Glu Glu Asp Ser Glu His Gly Thr Ser
 325             330             335
Leu Asn Arg Glu Met Asp Ser Leu Gly Ser Asn His Ser Ile Pro Ser
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Met Ser Val Ser Thr Gly Ser Gln Ser Ser Ser Val Asn Ser Met Gln
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Glu Val Met Asp Glu Ser Ser Ser Glu Leu Val Met Met His Asp Asp
 370             375             380
Glu Ser Thr Ile Asn Ser Ser Ser Ser Val Val His Lys Lys Asp His

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Val Phe Ile Arg Asp Glu Ala Gly His Gly Asp Pro Arg Pro Glu Pro
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Arg Pro Thr Gln Ser Val Gln Ser Gln Ala Leu His Tyr Arg Asn Arg
              420              425              430
Glu Arg Phe Ala Thr Ile Lys Ser Ala Ser Leu Val Thr Arg Gln Ile
              435              440              445
His Glu His Glu Gln Glu Asn Glu Leu Arg Glu Gln Met Ser Gly Tyr
              450              455              460
Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Ile Ala Leu Glu Asn
465              470              475              480
Lys Leu Lys Ala Glu Met Asp Glu His Arg Leu Lys Leu Gln Lys Glu
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Val Glu Thr His Ala Asn Asn Ser Ser Ile Glu Leu Glu Lys Leu Ala
              500              505              510
Lys Lys Gln Val Ala Ile Ile Glu Lys Glu Ala Lys Val Ala Ala Ala
              515              520              525
Asp Glu Lys Lys Phe Gln Gln Gln Ile Leu Ala Gln Gln Lys Lys Asp
530              535              540
Leu Thr Thr Phe Leu Glu Ser Gln Lys Lys Gln Tyr Lys Ile Cys Lys
545              550              555              560
Glu Lys Ile Lys Glu Glu Met Asn Glu Asp His Ser Thr Pro Lys Lys
              565              570              575
Glu Lys Gln Glu Arg Ile Phe Lys His Lys Glu Asn Leu Gln His Thr
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Gln Ala Glu Glu Glu Ala His Leu Leu Thr Ser Thr Gly Asp Trp Thr
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Thr Thr Lys Asn Cys Arg Phe Phe Lys Arg Lys Ile Met Ile Lys Arg
610              615              620
His Glu Val Glu Gln Gln Asn Ile Arg Glu Glu Leu Asn Lys Lys Arg
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Thr Met Lys Glu Met Glu His Ala Met Leu Ile Arg His Asp Glu Ser
              645              650              655
Thr Arg Glu Leu Glu Tyr Arg Gln Leu His Thr Leu Gln Lys Leu Arg
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Met Asp Leu Ile Arg Leu Gln His Gln Thr Glu Leu Glu Asn Gln Leu
675              680              685
Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu His Arg Lys His Val Met
690              695              700
Glu Leu Arg Gln Gln Pro Lys Asn Leu Lys Ala Met Glu Met Gln Ile
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Lys Lys Gln Phe Gln Asp Thr Cys Lys Val Gln Thr Lys Gln Tyr Lys
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Ala Leu Lys Asn His Gln Leu Glu Val Thr Pro Lys Asn Glu His Lys
740              745              750
Thr Ile Leu Lys Thr Leu Lys Asp Glu Gln Thr Arg Lys Leu Ala Ile
755              760              765
Leu Ala Glu Gln Tyr Glu Gln Ser Ile Asn Glu Met Met Ala Ser Gln
770              775              780
Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Ala Leu Arg
785              790              795              800
Leu Gln Leu Gln Gln Glu Met Glu Leu Leu Asn Ala Tyr Gln Ser Lys
              805              810              815
Ile Lys Met Gln Thr Glu Ala Gln His Glu Arg Glu Leu Gln Lys Leu

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Glu Glu Leu Ala Ala Leu Gln Lys Glu Arg Ser Glu Arg Ile Lys Asn
      850              855              860
Leu Leu Glu Arg Gln Glu Arg Glu Ile Glu Thr Phe Asp Met Glu Ser
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Leu Arg Met Gly Phe Gly Asn Leu Val Thr Leu Asp Phe Pro Lys Glu
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Asp Tyr Arg

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<210> 5911

<211> 645

<212> DNA

<213> Homo sapiens

<400> 5911

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<210> 5912

<211> 211

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<213> Homo sapiens

<400> 5912

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          20          25          30
Asp Leu Ile Leu Pro Asp Gly Gly Thr Pro Ala Gly Thr Ser Ser Pro
          35          40          45
Ala Ser Ser Ser Ser Leu Leu Asn Arg Leu Gln Leu Asp Asp Ile

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      50              55              60
Asp Gly Glu Thr Arg Asp Leu Phe Val Ile Val Asp Asp Pro Lys Lys
65              70              75              80
His Val Cys Thr Met Glu Thr Tyr Ile Thr Tyr Arg Ile Thr Thr Lys
      85              90              95
Ser Thr Arg Val Glu Phe Asp Leu Pro Glu Tyr Ser Val Arg Arg Arg
      100              105              110
Tyr Gln Asp Phe Asp Trp Leu Arg Ser Lys Leu Glu Glu Ser Gln Pro
      115              120              125
Thr His Leu Ile Pro Pro Leu Pro Glu Lys Phe Val Val Lys Gly Val
      130              135              140
Val Asp Arg Phe Ser Glu Glu Phe Val Glu Thr Arg Arg Lys Ala Leu
      145              150              155              160
Asp Lys Phe Leu Lys Arg Ile Thr Asp His Pro Val Leu Ser Phe Asn
      165              170              175
Glu His Phe Asn Ile Phe Leu Thr Ala Lys Asp Leu Asn Ala Tyr Lys
      180              185              190
Lys Gln Gly Ile Ala Leu Leu Thr Arg Met Gly Glu Ser Val Lys His
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<210> 5913

<211> 2495

<212> DNA

<213> Homo sapiens

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<210> 5916
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 Trp Gly Arg Thr Tyr Ser Phe Thr Ser Ala Met Ser Arg Gly Cys Val
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<211> 981

<212> PRT

<213> Homo sapiens

<400> 5918

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 Arg Glu Ser Ser Gly Gly Gly Gly Phe His Phe Val Cys Tyr Val Phe
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815

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      885              890              895
Pro Leu Ser Asp Asn Gln Arg Met Asp Lys Leu Glu Lys Thr Asn Ser
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<210> 5919

<211> 1320

<212> DNA

<213> Homo sapiens

<400> 5919

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<211> 93

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<213> Homo sapiens

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<212> DNA

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<400> 5922

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<212> DNA

<213> Homo sapiens

<400> 5923

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<210> 5926

<211> 526

<212> PRT

<213> Homo sapiens

<400> 5926

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Gln	Pro	Phe	Leu	Pro	Val	Phe	Thr	Met	Pro	Leu	Leu	Ser	Pro	Ser	Pro	35	40	45	
Ala	Pro	Pro	Pro	Ile	Ser	Pro	Val	Leu	Pro	Leu	Val	Pro	Pro	Pro	Ala	50	55	60	
Thr	Ala	Leu	Asn	Pro	Pro	Ala	Pro	Pro	Thr	Phe	His	Gln	Pro	Gln	Lys	65	70	75	80
Phe	Ala	Gly	Val	Asn	Lys	Ala	Pro	Ser	Val	Ile	Thr	His	Thr	Ala	Ser	85	90	95	
Ala	Thr	Leu	Thr	His	Asp	Ala	Pro	Ala	Thr	Thr	Phe	Ser	Gln	Ser	Gln	100	105	110	
Gly	Leu	Val	Ile	Thr	Thr	His	His	Pro	Ala	Pro	Ser	Ala	Ala	Pro	Cys	115	120	125	
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Phe	Val	His	Pro	Lys	Pro	Val	Ser	Leu	Thr	Gly	Gly	Arg	Pro	Lys	Gln	145	150	155	160
Pro	His	Lys	Ile	Val	Pro	Ala	Pro	Lys	Pro	Glu	Pro	Val	Ser	Leu	Val	165	170	175	
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Arg	Arg	Gln	Phe	Asp	His	Met	Lys	Asp	Met	Phe	Asp	Glu	Tyr	Val	Lys		
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Thr	Arg	Thr	Leu	Gln	Asn	Trp	Lys	Phe	Trp	Ile	Phe	Ser	Ile	Ile	Ile		
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Lys	Pro	Leu	Phe	Glu	Ser	Phe	Lys	Gly	Met	Val	Ser	Thr	Ser	Ser	Leu		
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Glu	Glu	Leu	His	Arg	Thr	Ala	Leu	Ser	Trp	Leu	Asp	Gln	His	Cys	Ser		
465					470					475					480		
Leu	Pro	Ile	Leu	Arg	Pro	Met	Val	Leu	Ser	Thr	Leu	Arg	Gln	Leu	Ser		
				485						490				495			
Thr	Ser	Thr	Ser	Ile	Leu	Thr	Asp	Pro	Ala	Gln	Leu	Pro	Glu	Gln	Ala		
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<210> 5927
<211> 1786
<212> DNA
<213> Homo sapiens
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120
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180
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240
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300
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420

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540
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<210> 5928

<211> 202

<212> PRT

<213> Homo sapiens

<400> 5928

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Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu Ser Glu Lys Ala Lys Glu
35           40           45
Phe Leu Met Glu Asn Arg Val Gln Ser Phe Tyr Gln Gln Glu Leu Glu
50           55           60
Met Val Glu Ser Leu Leu Ser Leu Ala Asn Gln Pro Val Ile His Ser
65           70           75           80
Ala Cys Ser Asp Gln Val Asn Phe Lys Lys Asp Thr Thr Ser Lys Ala
85           90           95
Ile His Ser Ile Phe Lys Asn Ala Ile Gln Leu Leu Gln Glu Lys Gly
100          105          110
Leu Val Phe Gln Lys Asp Asp Gly Phe Asp Asn Leu Tyr Tyr Val Thr
115          120          125
Arg Glu Asp Lys Asp Leu His Arg Lys Ile His Arg Ile Ile Gln Gln
130          135          140
Asp Cys Gln Lys Pro Asn His Met Glu Lys Gly Cys His Phe Leu His
145          150          155          160
Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg Pro Gly Leu Ser Glu Ala
165          170          175
Val Leu Gln Gln Val Leu Glu Leu Leu Glu Asp Gln Ser Asp Ile Val
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<210> 5929

<211> 606

<212> DNA

<213> Homo sapiens

<400> 5929

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<210> 5930
 <211> 144
 <212> PRT
 <213> Homo sapiens

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 Lys Glu Pro Leu Gly Arg Ala Glu Arg Pro Gly Arg Pro Cys Thr Arg
 35 40 45
 Leu Gln Pro Ala Gly Ser Val Ser Ser Thr Pro Leu Ser Thr Pro Cys
 50 55 60
 Ser Ser Val Pro Ser Ser Pro Ser Phe Ser Pro Thr Glu Gln Lys Thr
 65 70 75 80
 His Leu Glu Asp Leu Tyr Trp Met Ala Ser Asn Tyr Gln Gln Met Asn
 85 90 95
 Pro Glu Ala Leu Asn Leu Thr Pro Glu Asp Ala Val Glu Ala Leu Ile
 100 105 110
 Gly Ser His Pro Val Pro Gln Pro Leu Gln Ser Phe Asp Ser Phe Arg
 115 120 125
 Gly Ala His His His His His His His Pro His Pro His His Ala
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<210> 5931
 <211> 478
 <212> DNA
 <213> Homo sapiens

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<210> 5932
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 5932

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 20 25 30
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 35 40 45
 Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln
 50 55 60
 Glu Val Met Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys
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 Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu
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<210> 5933

<211> 1953

<212> DNA

<213> Homo sapiens

<400> 5933

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<210> 5934

<211> 314

<212> PRT

<213> Homo sapiens

<400> 5934

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			20					25					30		
Ser	Lys	Val	Arg	Glu	Gln	Leu	Glu	Gln	Glu	Leu	Glu	Glu	Leu	Thr	Ala
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Ser	Leu	Phe	Glu	Glu	Ala	His	Lys	Met	Val	Arg	Glu	Ala	Asn	Met	Lys
		50				55				60					
Gln	Ala	Ala	Ser	Glu	Lys	Gln	Leu	Lys	Glu	Ala	Arg	Gly	Lys	Ile	Asp
65				70					75					80	
Met	Leu	Gln	Ala	Glu	Val	Thr	Ala	Leu	Lys	Thr	Leu	Val	Ile	Thr	Ser
				85				90						95	
Thr	Pro	Ala	Ser	Pro	Asn	Arg	Glu	Leu	His	Pro	Gln	Leu	Leu	Ser	Pro

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Thr	Lys	Ala	Gly	Pro	Arg	Lys	Gly	His	Ser	Arg	His	Lys	Ser	Thr	Ser
	115		120		125										
Ser	Thr	Leu	Cys	Pro	Ala	Val	Cys	Pro	Ala	Ala	Gly	His	Thr	Leu	Thr
	130		135		140										
Pro	Asp	Arg	Glu	Gly	Lys	Glu	Val	Asp	Thr	Ile	Leu	Phe	Ala	Glu	Phe
	145		150		155									160	
Gln	Ala	Trp	Arg	Glu	Ser	Pro	Thr	Leu	Asp	Lys	Thr	Cys	Pro	Phe	Leu
	165		170		175										
Glu	Arg	Val	Tyr	Arg	Glu	Asp	Val	Gly	Pro	Cys	Leu	Asp	Phe	Thr	Met
	180		185		190										
Gln	Glu	Leu	Ser	Val	Leu	Val	Arg	Ala	Ala	Val	Glu	Asp	Asn	Thr	Leu
	195		200		205										
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Glu	Val	Asp	Cys	Ser	Ser	Thr	Asn	Thr	Cys	Ala	Leu	Ser	Gly	Leu	Thr
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Tyr	Ile	Ser	Pro	Ser	Ser	Arg	Ala	Arg	Ile	Thr	Ala	Val	Cys	Asn	Phe
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Phe	Thr	Tyr	Ile	Arg	Tyr	Ile	Gln	Gln	Gly	Leu	Val	Arg	Gln	Asp	Ala
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Glu	Pro	Met	Phe	Trp	Glu	Ile	Met	Arg	Leu	Arg	Lys	Glu	Met	Ser	Leu
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<210> 5935

<211> 2727

<212> DNA

<213> Homo sapiens

<400> 5935

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600

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<210> 5936

<211> 154

<212> PRT

<213> Homo sapiens

<400> 5936

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			20					25					30		
Asp	Gln	Glu	Pro	Pro	Pro	Pro	Tyr	Gln	Glu	Gln	Val	Pro	Val	Pro	Val
			35				40				45				
Tyr	His	Pro	Thr	Pro	Ser	Gln	Thr	Arg	Leu	Ala	Thr	Gln	Leu	Thr	Glu
	50					55					60				
Glu	Glu	Gln	Ile	Arg	Ile	Ala	Gln	Arg	Ile	Gly	Leu	Ile	Gln	His	Leu
				70					75					80	
Pro	Lys	Gly	Val	Tyr	Asp	Pro	Gly	Arg	Asp	Gly	Ser	Glu	Lys	Lys	Ile
				85					90				95		
Arg	Glu	Cys	Val	Ile	Cys	Met	Met	Asp	Phe	Val	Tyr	Gly	Asp	Pro	Ile
			100					105					110		
Arg	Phe	Leu	Pro	Cys	Met	His	Ile	Tyr	His	Leu	Asp	Cys	Ile	Asp	Asp
			115				120					125			
Trp	Leu	Met	Arg	Ser	Phe	Thr	Cys	Pro	Ser	Cys	Met	Glu	Pro	Val	Asp
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<210> 5937

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 5937

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<210> 5938

<211> 406

<212> PRT

<213> Homo sapiens

<400> 5938

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 20          25          30
Gly Lys Ser Leu Ile Val Pro Phe Lys Gly Ser Arg Val Ile Asp Ser
 35          40          45
Thr Val Leu Pro Gly Ile Leu Ile Glu Met Ser Glu Val Gln Leu Met
 50          55          60
Arg Leu Leu Pro Ile Lys Lys Ser Thr Ala Leu Lys Val Ala Leu Phe
 65          70          75          80
Cys Thr Thr Leu Ser Gly Asp Thr Ser Asp Thr Gly Glu Gly Thr Val
 85          90          95
Val Val Ser Tyr Gly Val Ser Leu Glu Asn Ala Val Leu Asp Gln Leu
100          105          110
Leu Asn Leu Gly Arg Gln Leu Ile Ser Asp His Val Asp Leu Val Leu
115          120          125
Cys Gln Lys Val Ile His Pro Ser Leu Lys Gln Phe Leu Asn Met His
130          135          140
Arg Ile Ile Ala Ile Asp Arg Ile Gly Val Thr Leu Met Glu Pro Leu
145          150          155          160
Thr Lys Met Thr Gly Thr Gln Pro Ile Gly Ser Leu Gly Ser Ile Cys
165          170          175
Pro Asn Ser Tyr Gly Ser Val Lys Asp Val Cys Thr Ala Lys Phe Gly
180          185          190
Ser Lys His Phe Phe His Leu Ile Pro Asn Glu Ala Thr Ile Cys Ser
195          200          205
Leu Leu Leu Cys Asn Arg Asn Asp Thr Ala Trp Asp Glu Leu Lys Leu
210          215          220
Thr Cys Gln Thr Ala Leu His Val Leu Gln Leu Thr Leu Lys Glu Pro
225          230          235          240
Trp Ala Leu Leu Gly Gly Cys Thr Glu Thr His Leu Ala Ala Tyr
245          250          255
Ile Arg His Lys Thr His Asn Asp Pro Glu Ser Ile Leu Lys Asp Asp
260          265          270
Glu Cys Thr Gln Thr Glu Leu Gln Leu Ile Ala Glu Ala Phe Cys Ser
275          280          285
Ala Leu Glu Ser Val Val Gly Ser Leu Glu His Asp Gly Gly Glu Ile
290          295          300
Leu Thr Asp Met Lys Tyr Gly His Leu Trp Ser Val Gln Ala Asp Ser
305          310          315          320
Pro Cys Val Ala Asn Trp Pro Asp Leu Leu Ser Gln Cys Gly Cys Gly
325          330          335
Leu Tyr Asn Ser Gln Glu Glu Leu Asn Trp Ser Phe Leu Arg Ser Thr
340          345          350
Arg Arg Pro Phe Val Pro Gln Ser Cys Leu Pro His Glu Ala Val Gly
355          360          365
Ser Ala Ser Asn Leu Thr Leu Asp Cys Leu Thr Ala Lys Leu Ser Gly
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Val Ile Glu Asp Lys Asn

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405

<210> 5939

<211> 795

<212> DNA

<213> Homo sapiens

<400> 5939

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240
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<210> 5940

<211> 96

<212> PRT

<213> Homo sapiens

<400> 5940

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Lys Lys Gln Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu Ile
20          25          30
Ala Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Val Thr
35          40          45
Ile Ser Gln Gln Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe
50          55          60
Met Asn Ala Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser
65          70          75          80
Thr Ala Pro Gly Gly Pro Ala Gly Ala Thr Ala Thr Phe Ser Lys Ala

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85

90

95

<210> 5941

<211> 2590

<212> DNA

<213> Homo sapiens

<400> 5941

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 120
 gcttaagcata gcacatcaga gcataacaca gtgtgagggg aataaagtgt acaatgacat
 180
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 240
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 360
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 420
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<210> 5942

<211> 89

<212> PRT

<213> Homo sapiens

<400> 5942

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 20 25 30
 Pro Gly Ser Leu Gln Pro Pro Pro Gly Phe Lys Gln Phe Ser Cys

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          35              40              45
Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Leu Ser Ser Arg Leu
   50              55              60
Ala Thr Phe Cys Ile Phe Ser Arg Asp Arg Val Ser Pro Cys Trp Pro
65              70              75              80
Gly Trp Ser Gln Thr Pro Asp Leu Lys
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<210> 5943
<211> 781
<212> DNA
<213> Homo sapiens

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<400> 5943
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<210> 5944
<211> 174
<212> PRT
<213> Homo sapiens

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<400> 5944
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20              25              30
Gly Val Ser Ser Ile Thr Lys Leu Gln Arg Gln Pro Phe Gly Val Glu

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<210> 5946

<211> 121

<212> PRT

<213> Homo sapiens

<400> 5946

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Glu Val Ile Ser Ala Gly Pro Cys Glu Lys Ile His Asp Glu Asn Leu
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Arg Lys Gln Tyr Glu Lys Ser Ser Arg Phe Met Lys Val Gly Tyr Glu
                20             25             30
Arg Asp Phe Leu Arg Tyr Leu Gln Ser Leu Leu Ala Glu Val Glu Arg
                35             40             45
Arg Ile Arg Arg Gly His Ala Arg Leu Ala Leu Ser Gln Asn Gln Gln
                50             55             60
Ser Ser Gly Ala Ala Gly Pro Thr Gly Lys Asn Gly Glu Lys Ile Gln
 65             70             75             80
Val Leu Thr Asp Lys Ile Asp Val Leu Gln Gln Ile Glu Glu Leu
                85             90             95
Gly Ser Glu Gly Lys Val Glu Glu Ala Gln Gly Met Met Lys Leu Val
                100            105            110
Glu Gln Leu Lys Glu Glu Arg Glu Leu
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<210> 5947

<211> 2283

<212> DNA

<213> Homo sapiens

<400> 5947

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 720

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<210> 5948

<211> 76

<212> PRT

<213> Homo sapiens

<400> 5948

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          20             25             30
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<210> 5949

<211> 4706

<212> DNA

<213> Homo sapiens

<400> 5949

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<210> 5950

<211> 397

<212> PRT

<213> Homo sapiens

<400> 5950

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Val	Asp	Glu	Ala	Gly	Ile	Asp	Gln	Asp	Gly	Val	Phe	Lys	Glu	Phe	Leu
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Glu	Glu	Ile	Ile	Lys	Arg	Val	Phe	Asp	Pro	Ala	Leu	Asn	Leu	Phe	Lys
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His	Glu	Asn	Tyr	Leu	Gln	Leu	Phe	Glu	Phe	Val	Gly	Lys	Met	Leu	Gly
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Lys	Ala	Val	Tyr	Glu	Gly	Ile	Val	Val	Asp	Val	Pro	Phe	Ala	Ser	Phe
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Phe	Leu	Ser	Gln	Leu	Leu	Gly	His	His	His	Ser	Val	Phe	Tyr	Ser	Ser
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Val	Asp	Glu	Leu	Pro	Ser	Leu	Asp	Ser	Glu	Phe	Tyr	Lys	Asn	Leu	Thr
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Ser	Ile	Lys	Arg	Tyr	Asp	Gly	Asp	Ile	Thr	Asp	Leu	Gly	Leu	Thr	Leu
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Ile Arg Met Phe Ser Thr Pro Glu Leu Gln Arg Leu Ile Ser Gly Asp
      245              250              255
Asn Ala Glu Ile Asp Leu Glu Asp Leu Lys Lys His Thr Val Tyr Tyr
      260              265              270
Gly Gly Phe His Gly Ser His Arg Val Ile Ile Trp Leu Trp Asp Ile
      275              280              285
Leu Ala Ser Asp Phe Thr Pro Asp Glu Arg Ala Met Phe Leu Lys Phe
      290              295              300
Val Thr Ser Cys Ser Arg Pro Pro Leu Leu Gly Phe Ala Tyr Leu Lys
      305              310              315              320
Pro Pro Phe Ser Ile Arg Cys Val Glu Val Ser Asp Asp Gln Asp Thr
      325              330              335
Gly Asp Thr Leu Gly Ser Val Leu Arg Gly Phe Phe Thr Ile Arg Lys
      340              345              350
Arg Glu Pro Gly Gly Arg Leu Pro Thr Ser Ser Thr Cys Phe Asn Leu
      355              360              365
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Arg Tyr Ala Ile Ser Met Asn Thr Gly Phe Glu Leu Ser
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<210> 5951

<211> 1724

<212> DNA

<213> Homo sapiens

<400> 5951

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720

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<210> 5952

<211> 378

<212> PRT

<213> Homo sapiens

<400> 5952

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 Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu Thr Val Asp Glu Tyr Lys
 50 55 60
 Ile Gly Gln Leu Tyr Met Ile Ser Lys His Ser His Glu Gln Ser Asp
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 Arg Gly Glu Gly Val Glu Val Val Gln Asn Glu Pro Phe Glu Asp Pro
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 His His Gly Asn Gly Gln Phe Thr Glu Lys Arg Val Tyr Leu Asn Ser

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    130              135              140
Cys Ser Phe Leu Pro Lys Phe Ser Ile His Ile Glu Thr Lys Tyr Glu
    145              150              155              160
Asp Asn Lys Gly Ser Asn Asp Thr Ile Phe Asp Asn Glu Ala Lys Asp
    165              170              175
Val Glu Arg Glu Val Cys Phe Ile Asp Ile Ala Cys Asp Glu Ile Pro
    180              185              190
Glu Arg Tyr Tyr Lys Glu Ser Glu Asp Pro Lys His Phe Lys Ser Glu
    195              200              205
Lys Thr Gly Arg Gly Gln Leu Arg Glu Gly Trp Arg Asp Ser His Gln
    210              215              220
Pro Ile Met Cys Ser Tyr Lys Leu Val Thr Val Lys Phe Glu Val Trp
    225              230              235              240
Gly Leu Gln Thr Arg Val Glu Gln Phe Val His Lys Val Val Arg Asp
    245              250              255
Ile Leu Leu Ile Gly His Arg Gln Ala Phe Ala Trp Val Asp Glu Trp
    260              265              270
Tyr Asp Met Thr Met Asp Glu Val Arg Glu Phe Glu Arg Ala Thr Gln
    275              280              285
Glu Ala Thr Asn Lys Lys Ile Gly Ile Phe Pro Pro Ala Ile Ser Ile
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    305              310              315              320
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    325              330              335
Pro Lys Asp Arg Pro Arg Lys Lys Ser Ala Pro Glu Thr Leu Thr Leu
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<210> 5953

<211> 777

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 5954

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<210> 5955

<211> 1459

<212> DNA

<213> Homo sapiens

<400> 5955

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<210> 5956

<211> 431

<212> PRT

<213> Homo sapiens

<400> 5956

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His	Ile	Thr	Ile	His	Met	His	Gly	Gly	Thr	Ser	Ser	Asp	Gly	Ser	Ser				
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Ser	Met			85					90					95					
Glu	Val	Leu	Leu	Val	Ser	Glu	Asp	Gly	Lys	Ile	Leu	Ala	Glu	Ala	Asp				
Gly	Leu	Ser	Thr	Asn	His	Trp	Leu	Ile	Gly	Thr	Asp	Lys	Cys	Val	Glu				
Arg	Ile	Asn	Glu	Met	Val	Asn	Arg	Ala	Lys	Arg	Lys	Ala	Gly	Val	Asp				
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145	Glu	Glu	Asp	Ala	Gly	Arg	Ile	Leu	Ile	Glu	Glu	Leu	Arg	Asp	Arg				
Gln	Glu			165					170					175					
Pro	Tyr	Leu	Ser	Glu	Ser	Tyr	Leu	Ile	Thr	Thr	Asp	Ala	Ala	Gly	Ser				
Ile	Ala	Thr	Ala	Thr	Pro	Asp	Gly	Gly	Val	Val	Leu	Ile	Ser	Gly	Thr				
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Gln	Ala	Met	Phe	His	Tyr	Phe	Gln	Val	Pro	Asp	Arg	Leu	Gly	Ile	Leu				
Thr	His	Leu	Tyr	Arg	Asp	Phe	Asp	Lys	Cys	Arg	Phe	Ala	Gly	Phe	Cys				
Arg	Lys	Ile	Ala	Glu	Gly	Ala	Gln	Gln	Gly	Asp	Pro	Leu	Ser	Arg	Tyr				
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Leu	Pro	Glu	Ile	Asp	Pro	Val	Leu	Phe	Gln	Gly	Lys	Ile	Gly	Leu	Pro				
Ile	Leu	Cys	Val	Gly	Ser	Val	Trp	Lys	Ser	Trp	Glu	Leu	Leu	Lys	Glu				
Gly	Phe	Leu	Leu	Ala	Leu	Thr	Gln	Gly	Arg	Glu	Ile	Gln	Ala	Gln	Asn				
Phc	Phc	Ser	Ser	Phc	Thr	Leu	Met	Lys	Leu	Arg	His	Ser	Ser	Ala	Leu				
385																			
Gly	Gly	Ala	Ser	Leu	Gly	Ala	Arg	His	Ile	Gly	His	Leu	Leu	Pro	Met				
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<210> 5957

<211> 855

<212> DNA

<213> Homo sapiens

<400> 5957

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 240
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 300
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 420
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 480
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 720
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<210> 5958

<211> 106

<212> PRT

<213> Homo sapiens

<400> 5958

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			20					25				30			
Met	Arg	Asn	Ser	Arg	Asp	Arg	Leu	Leu	Asn	Arg	Tyr	Arg	Gln	Ala	Gly
			35				40				45				
Ser	Ser	Gly	Pro	Gly	Asn	Ser	Gln	Asn	Ser	Phe	Leu	Val	Gln	Glu	Val
		50				55				60					
Met	Glu	Glu	Glu	Trp	Asn	Ala	Leu	Gln	Ser	Val	Glu	Asn	Cys	Pro	Glu
65					70				75					80	
Asp	Leu	Ala	Gln	Leu	Glu	Glu	Leu	Ile	Asp	Met	Ala	Val	Leu	Glu	Glu
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100

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 <212> DNA
 <213> Homo sapiens

105

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 180
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 240
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 300
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 360
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 420
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 480
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 600
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 660
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<210> 5960
 <211> 251
 <212> PRT
 <213> Homo sapiens

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 Glu Arg Glu Leu His Ser Val His Gly Tyr Pro Gly Thr Phe Ala Asn
 35 40 45
 Cys Met His Ile Leu Ser Glu Glu Thr Cys Phe Gln Arg Trp Val Thr
 50 55 60
 Gly Glu Arg Lys Phe Ala Leu Gln Lys Met Asp Ser Met Leu Ser Ser
 65 70 75 80
 Glu Ala Ala Trp Val Ser Gln Tyr Lys Asp Ile Thr Asp Val Asp Glu

					85						90						95
Met	Lys	Val	Pro	Asp	Cys	Ala	Glu	Thr	Phe	Met	Thr	Leu	Leu	Val			
					100						105						110
Ile	Thr	Asp	Arg	Tyr	Lys	Asn	Leu	Pro	Thr	Ala	Ser	Arg	Lys	Leu	Gln		
					115						120						125
Phe	Leu	Glu	Leu	Gln	Lys	Asp	Leu	Val	Asp	Asp	Phe	Arg	Ile	Arg	Leu		
					130						135						140
Thr	Gln	Val	Met	Lys	Glu	Glu	Thr	Arg	Ala	Ser	Leu	Gly	Phe	Arg	Tyr		
					145						150						155
Cys	Ala	Ile	Leu	Asn	Ala	Val	Asn	Tyr	Ile	Ser	Thr	Val	Leu	Ala	Asp		
					165						170						175
Trp	Ala	Asp	Asn	Val	Phe	Phe	Leu	Gln	Leu	Gln	Gln	Ala	Ala	Leu	Glu		
					180						185						190
Val	Phe	Ala	Glu	Asn	Asn	Thr	Leu	Ser	Lys	Leu	Gln	Leu	Gly	Gln	Leu		
					195						200						205
Ala	Ser	Met	Glu	Ser	Ser	Val	Phe	Asp	Asp	Met	Ile	Asn	Leu	Leu	Glu		
					210						215						220
Arg	Leu	Lys	His	Asp	Met	Leu	Thr	Arg	Gln	Val	Asp	His	Val	Phe	Arg		
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Glu	Val	Lys	Asp	Ala	Ala	Lys	Leu	Tyr	Lys	Lys							
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<210> 5961

<211> 585

<212> DNA

<213> Homo sapiens

<400> 5961

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120					
aattagagac	tgagacaggg	caggggtgccg	aggtgtctcg	atgcgttttc	tgtggatgcc
180					
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240					
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300					
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360					
cacacctatg	tgactccgcg	atgttttgtg	ccttatgtgt	cccatgcatg	ctcccactc
420					
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480					
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585					

<210> 5962

<211> 114

<212> PRT

<213> Homo sapiens

<400> 5962

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      20           25           30
Leu Ser His Ser His Gln Pro Gly Leu Ser Gly Glu Gly Ala Gln Glu
      35           40           45
Gln Ala Arg Ile Asp Thr Gly Ile His Met Lys Arg Met Gln Thr Pro
      50           55           60
Arg His Pro Ala Leu Ser Gln Ser Leu Ile Lys Phe Gly Ile Leu Phe
      65           70           75           80
Asp Pro Ser Ile Phe Phe Leu Glu Thr Gly Ser Arg Phe Ile Ala Gln
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<210> 5963

<211> 1288

<212> DNA

<213> Homo sapiens

<400> 5963

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720
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900

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 1020
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<211> 222

<212> PRT

<213> Homo sapiens

<400> 5964

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			20					25					30		
Gln	Ile	Arg	Asp	Ile	Gln	Arg	Glu	Glu	Glu	Lys	Val	Lys	Arg	Ser	Val
			35				40					45			
Lys	Asp	Ala	Ala	Lys	Lys	Gly	Gln	Lys	Asp	Val	Cys	Ile	Val	Leu	Ala
	50				55						60				
Lys	Glu	Met	Ile	Arg	Ser	Arg	Lys	Ala	Val	Ser	Lys	Leu	Tyr	Ala	Ser
	65				70				75					80	
Lys	Ala	His	Met	Asn	Ser	Val	Leu	Met	Gly	Met	Lys	Asn	Gln	Leu	Ala
			85						90				95		
Val	Leu	Arg	Val	Ala	Gly	Ser	Leu	Gln	Lys	Ser	Thr	Glu	Val	Met	Lys
			100					105					110		
Ala	Met	Gln	Ser	Leu	Val	Lys	Ile	Pro	Glu	Ile	Gln	Ala	Thr	Met	Arg
			115				120					125			
Glu	Leu	Ser	Lys	Glu	Met	Met	Lys	Ala	Gly	Ile	Ile	Glu	Glu	Met	Leu
	130				135							140			
Glu	Asp	Thr	Phe	Glu	Ser	Met	Asp	Asp	Gln	Glu	Glu	Met	Glu	Glu	Glu
	145				150				155					160	
Ala	Glu	Met	Glu	Ile	Asp	Arg	Ile	Leu	Phe	Glu	Ile	Thr	Ala	Gly	Ala
			165					170					175		
Leu	Gly	Lys	Ala	Pro	Ser	Lys	Val	Thr	Asp	Ala	Leu	Pro	Glu	Pro	Glu
			180				185						190		
Pro	Pro	Gly	Ala	Met	Ala	Ala	Ser	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu
			195				200					205			
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	210						215					220			

<210> 5965

<211> 1011

<212> DNA

<213> Homo sapiens

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 180
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 240
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 300
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 360
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<210> 5966
 <211> 233
 <212> PRT
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<400> 5966
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 35 40 45
 Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln Ala Gly Ser Ser Gly
 50 55 60
 Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val Met Glu Glu
 65 70 75 80
 Glu Trp Asn Ala Leu Gln Xaa Gln Trp Xaa Asn Cys Pro Glu Asp Leu

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	100							105					110		
Gln	Glu	Leu	Ile	Asn	Gln	Glu	Gln	Ser	Ile	Ile	Ser	Glu	Tyr	Glu	Lys
	115						120						125		
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	130					135					140				
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	145				150						155				160
Ile	Thr	Ser	Gly	Val	Val	Cys	Gln	Cys	Gly	Leu	Ser	Ile	Pro	Ser	
			165					170					175		
His	Ser	Ser	Glu	Leu	Thr	Glu	Gln	Lys	Leu	Arg	Ala	Cys	Leu	Glu	Gly
			180					185					190		
Ser	Ile	Asn	Glu	His	Ser	Ala	His	Cys	Pro	His	Thr	Pro	Glu	Phe	Ser
		195					200					205			
Val	Thr	Gly	Gly	Thr	Glu	Glu	Lys	Ser	Ser	Leu	Leu	Met	Ser	Cys	Leu
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Ala	Cys	Asp	Thr	Trp	Ala	Val	Ile	Leu							
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<210> 5967

<211> 1806

<212> DNA

<213> Homo sapiens

<400> 5967

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180
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720
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780
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<210> 5968

<211> 434

<212> PRT

<213> Homo sapiens

<400> 5968

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 Gly Thr Ser Ser Leu Ile Ser Gly Leu Ile Leu Ile Phe Glu Trp Trp
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 Tyr Phe Arg Lys Tyr Gly Thr Ser Phe Ile Glu Gln Val Ser Val Ser
 50 55 60
 His Leu Arg Pro Leu Leu Gly Gly Val Asp Asn Asn Ser Ser Asn Asn
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 Ser Asn Ser Ser Asn Gly Asp Ser Asp Ser Asn Arg Gln Ser Val Ser
 85 90 95
 Glu Cys Lys Val Trp Arg Asn Pro Leu Asn Leu Phe Arg Gly Ala Glu

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Asp Met Asn Leu Ser Ala Gln Asp His Gln Thr Phe Phe Thr Cys Asp
    130                      135                      140
Ser Asp His Leu Arg Pro Ala Asp Ala Ile Met Gln Lys Ala Trp Arg
    145                      150                      155                      160
Glu Arg Asn Pro Gln Ala Arg Ile Ser Ala Ala His Glu Ala Leu Glu
    165                      170                      175
Ile Asn Glu Thr Arg His Gln Cys Leu Gly Val His Gln Lys Lys Ala
    180                      185                      190
Ser Asn Val Cys Gln Lys Thr Arg Glu Asp Gln Gly Ser Lys Ala Leu
    195                      200                      205
Leu Glu Leu Gln Ala Tyr Ala Asp Val Gln Ala Val Leu Ala Lys Tyr
    210                      215                      220
Asp Asp Ile Ser Leu Pro Lys Ser Ala Thr Ile Cys Tyr Thr Ala Ala
    225                      230                      235                      240
Leu Leu Lys Ala Arg Ala Val Ser Asp Lys Phe Ser Pro Glu Ala Ala
    245                      250                      255
Ser Arg Arg Gly Leu Ser Thr Ala Glu Met Asn Ala Val Glu Ala Ile
    260                      265                      270
His Arg Ala Val Glu Phe Asn Pro His Val Pro Lys Tyr Leu Leu Glu
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Met Lys Ser Leu Ile Leu Pro Pro Glu His Ile Leu Lys Arg Gly Asp
    290                      295                      300
Ser Glu Ala Ile Ala Tyr Ala Phe Phe His Leu Ala His Trp Lys Arg
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Val Glu Gly Ala Leu Asn Leu Leu His Cys Thr Trp Glu Gly Thr Phe
    325                      330                      335
Arg Met Ile Pro Tyr Pro Leu Glu Lys Gly His Leu Phe Tyr Pro Tyr
    340                      345                      350
Pro Ile Cys Thr Glu Thr Ala Asp Arg Glu Leu Leu Pro Ser Phe His
    355                      360                      365
Glu Val Ser Val Tyr Pro Lys Lys Glu Leu Pro Phe Phe Ile Leu Phe
    370                      375                      380
Thr Ala Gly Leu Cys Ser Phe Thr Ala Met Leu Ala Leu Leu Thr His
    385                      390                      395                      400
Gln Phe Pro Glu Leu Met Gly Val Phe Ala Lys Ala Val Ser Val Cys
    405                      410                      415
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<210> 5969

<211> 429

<212> DNA

<213> Homo sapiens

<400> 5969

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120

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<210> 5970

<211> 143

<212> PRT

<213> Homo sapiens

<400> 5970

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Gln	Asn	Gly	Gln	Leu	Gly	Gly	Gly	Glu	Gly	Val	Pro	Asp	Leu	Gln	Pro
		20					25				30				
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		35				40				45					
Pro	Arg	Trp	Gln	Asp	Ala	Asn	Phe	Val	Leu	Gly	Ser	Tyr	Lys	Thr	Glu
		50			55					60					
Gln	Cys	Pro	Lys	Pro	Pro	Arg	Leu	Cys	Arg	Gln	Gly	Tyr	Ala	Cys	Pro
65				70					75					80	
His	Tyr	His	Asn	Ser	Arg	Asp	Arg	Arg	Arg	Asn	Pro	Arg	Arg	Phe	Gln
			85					90						95	
Tyr	Arg	Ser	Thr	Pro	Cys	Pro	Ser	Val	Lys	His	Gly	Asp	Glu	Trp	Gly
			100				105						110		
Glu	Pro	Ser	Arg	Cys	Asp	Gly	Gly	Asp	Gly	Cys	Gln	Tyr	Cys	His	Ser
		115				120					125				
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		130				135					140				

<210> 5971

<211> 565

<212> DNA

<213> Homo sapiens

<400> 5971

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 420
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<210> 5972

<211> 104

<212> PRT

<213> Homo sapiens

<400> 5972

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Cys	Pro	Asn	Arg	Gln	His	Pro	Tyr	Phe	Ile	Asp	Gly	His	Pro	His	Phe
			20					25					30		
Arg	Asp	Ser	Ser	Leu	Leu	Tyr	Pro	His	Phe	Thr	Gly	Glu	Gly	Ile	Glu
		35					40					45			
Ala	Gln	Lys	Val	Arg	Ser	Leu	Leu	Gln	Asp	Asp	Gln	Leu	Asn	Gln	Asn
		50				55					60				
Phe	Arg	Ala	Ser	Asn	Thr	Lys	Cys	Val	Pro	Leu	Ser	Ser	Val	Ser	His
65					70					75				80	
Leu	Leu	Pro	Arg	Gly	Ser	Ala	Ser	Ser	Leu	Trp	Pro	Leu	Ser	Ile	Leu
			85						90					95	
Pro	Pro	Thr	Leu	Leu	Pro	Ala	Ser								
			100												

<210> 5973

<211> 797

<212> DNA

<213> Homo sapiens

<400> 5973

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<210> 5974

<211> 107

<212> PRT

<213> Homo sapiens

<400> 5974

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Ser	Leu	Arg	Ile	Met	Asp	Ala	Arg	Ala	Gln	Leu	Leu	Leu	Arg	Val	Pro
		20					25				30				
His	Pro	Gly	Pro	Ser	Leu	Thr	Ser	Gly	Ala	Leu	Thr	His	Ile	Arg	Asp
		35				40				45					
Pro	His	Pro	Gly	Leu	Ser	Pro	Thr	Ser	Gly	Thr	Leu	Met	Pro	Gly	Arg
		50			55					60					
Arg	Arg	Gly	Gly	Pro	Ser	Phe	Gly	Thr	Pro	Ala	Leu	Arg	Arg	Arg	Lys
65				70				75						80	
Cys	His	Arg	Glu	Ala	Pro	Ala	Ser	Gly	Leu	Ser	Thr	Ala	Ala	Arg	Glu
			85					90						95	
Arg	Leu	Trp	Trp	Pro	Arg	Ala	Arg	Val	Cys	Arg					
		100					105								

<210> 5975

<211> 2175

<212> DNA

<213> Homo sapiens

<400> 5975

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<210> 5976

<211> 564

<212> PRT

<213> Homo sapiens

<400> 5976

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Tyr	Ala	Tyr	Pro	Ser	Asp	Tyr	Asp	Met	His	Thr	Gly	Asp	Pro	Lys	Gln
			20					25					30		
Asp	Leu	Ala	Tyr	Glu	Arg	Gln	Tyr	Glu	Gln	Gln	Thr	Tyr	Gln	Val	Ile
	35						40					45			
Pro	Glu	Val	Ile	Lys	Asn	Phe	Ile	Gln	Tyr	Phe	His	Lys	Thr	Val	Ser
	50					55					60				
Asp	Leu	Ile	Asp	Gln	Lys	Val	Tyr	Glu	Leu	Gln	Ala	Ser	Arg	Val	Ser
65					70				75					80	
Ser	Asp	Val	Ile	Asp	Gln	Lys	Val	Tyr	Glu	Ile	Gln	Asp	Ile	Tyr	Glu
			85						90					95	
Asn	Ser	Trp	Thr	Lys	Leu	Thr	Glu	Arg	Phe	Phe	Lys	Asn	Thr	Pro	Trp
			100					105					110		
Pro	Glu	Ala	Glu	Ala	Ile	Ala	Pro	Gln	Val	Gly	Asn	Asp	Ala	Val	Phe
		115					120					125			
Leu	Ile	Leu	Tyr	Lys	Glu	Leu	Tyr	Tyr	Arg	His	Ile	Tyr	Ala	Lys	Val
	130					135					140				
Ser	Gly	Gly	Pro	Ser	Leu	Glu	Gln	Arg	Phe	Glu	Ser	Tyr	Tyr	Asn	Tyr
145					150					155					160
Cys	Asn	Leu	Phe	Asn	Tyr	Ile	Leu	Asn	Ala	Asp	Gly	Pro	Ala	Pro	Leu
			165					170						175	
Glu	Leu	Pro	Asn	Gln	Trp	Leu	Trp	Asp	Ile	Ile	Asp	Glu	Phe	Ile	Tyr
			180					185					190		
Gln	Phe	Gln	Ser	Phe	Ser	Gln	Tyr	Arg	Cys	Lys	Thr	Ala	Lys	Lys	Ser
		195					200					205			
Glu	Glu	Glu	Ile	Asp	Phe	Leu	Arg	Ser	Asn	Pro	Lys	Ile	Trp	Asn	Val
	210					215					220				
His	Ser	Val	Leu	Asn	Val	Leu	His	Ser	Leu	Val	Asp	Lys	Ser	Asn	Ile
225				230					235					240	
Asn	Arg	Gln	Leu	Glu	Val	Tyr	Thr	Ser	Gly	Gly	Asp	Pro	Glu	Ser	Val
			245						250					255	
Ala	Gly	Glu	Tyr	Gly	Arg	His	Ser	Leu	Tyr	Lys	Met	Leu	Gly	Tyr	Phe
		260					265						270		
Ser	Leu	Val	Gly	Leu	Leu	Arg	Leu	His	Ser	Leu	Leu	Gly	Asp	Tyr	Tyr
		275					280					285			
Gln	Ala	Ile	Lys	Val	Leu	Glu	Asn	Ile	Glu	Leu	Asn	Lys	Lys	Ser	Met
	290					295					300				
Tyr	Ser	Arg	Val	Pro	Glu	Cys	Gln	Val	Thr	Thr	Tyr	Tyr	Tyr	Val	Gly
305					310					315				320	
Phe	Ala	Tyr	Leu	Met	Met	Arg	Arg	Tyr	Gln	Asp	Ala	Ile	Arg	Val	Phe

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Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
          355              360              365
Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
          370              375              380
Ser Ile His Leu Gln Leu Arg Glu Lys Tyr Gly Asp Lys Met Leu Arg
          385              390              395
Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
          405              410              415
Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
          420              425              430
Pro Asn Tyr His Lys Glu Pro Phe Leu Gln Gln Leu Lys Val Phe Ser
          435              440              445
Asp Glu Val Gln Gln Gln Ala Gln Leu Ser Thr Ile Arg Ser Phe Leu
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Lys Leu Tyr Thr Thr Met Pro Val Ala Lys Leu Ala Gly Phe Leu Asp
          465              470              475
Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
          485              490              495
Met Lys Asn Leu Val Trp Thr Ser Gly Ile Ser Ala Leu Asp Gly Glu
          500              505              510
Phe Gln Ser Ala Ser Glu Val Asp Phe Tyr Ile Asp Lys Asp Met Ile
          515              520              525
His Ile Ala Asp Thr Lys Val Ala Arg Arg Tyr Gly Asp Phe Phe Ile
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<210> 5977

<211> 2320

<212> DNA

<213> Homo sapiens

<400> 5977

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 2320

<210> 5978

<211> 77

<212> PRT

<213> Homo sapiens

<400> 5978

Met	Thr	Lys	Leu	Ile	Lys	Lys	Ser	Lys	Asn	Thr	Leu	Asn	Leu	Ser	Arg
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Ile	Arg	Leu	Gly	Ser	Val	Ala	His	Ala	Cys	Asp	Pro	Ser	Thr	Leu	Gly
		20					25					30			
Gly	Arg	Gly	Gly	Gln	Ile	Ile	Xaa	Ala	Arg	Ser	Ser	Arg	Pro	Ala	Trp
	35					40					45				
Thr	Thr	Trp	Arg	Xaa	Val	Phe	Thr	Lys	Asn	Thr	Lys	Ile	Ser	Trp	Ala
	50				55					60					
Trp	Trp	Tyr	Thr	Pro	Val	Ile	Pro	Ala	Thr	Gln	Glu	Ala			
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<210> 5979

<211> 1095

<212> DNA

<213> Homo sapiens

<400> 5979

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 120
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 180
 aattgaggcc taaggcaggg tcaettgcct ggccccttcc ccttcaccgc tcagagtcca
 240
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 300
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 420
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cggcagaaga agcgccggct ctgcctgctg ctctgaccca gggcagacag acctcacgac
 720
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 1095

<210> 5980

<211> 169

<212> PRT

<213> Homo sapiens

<400> 5980

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Ser	Pro	Asp	Arg	Glu	Gly	Thr	Ser	Pro	Asp	Pro	Arg	Cys	Ser	Val	Leu
			20					25					30		
Ser	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Gln	Asn
		35					40					45			
Thr	His	Leu	Val	Leu	Ile	Cys	Tyr	Asp	Val	Met	Asn	Pro	Thr	Ser	Tyr
	50					55					60				
Asp	Asn	Val	Leu	Ile	Lys	Trp	Phe	Pro	Glu	Val	Thr	His	Phe	Cys	Arg
	65				70				75					80	
Gly	Ile	Pro	Met	Val	Leu	Ile	Gly	Cys	Lys	Thr	Asp	Leu	Arg	Lys	Asp
			85					90						95	
Lys	Glu	Gln	Leu	Arg	Lys	Leu	Arg	Ala	Ala	Gln	Leu	Glu	Pro	Ile	Thr
		100					105						110		
Tyr	Met	Gln	Gly	Leu	Ser	Ala	Cys	Glu	Gln	Ile	Arg	Ala	Ala	Leu	Tyr
		115					120					125			
Leu	Glu	Cys	Ser	Ala	Lys	Phe	Arg	Glu	Asn	Val	Glu	Asp	Val	Phe	Arg
	130					135					140				
Glu	Ala	Ala	Lys	Val	Ala	Leu	Ser	Ala	Leu	Lys	Lys	Ala	Gln	Arg	Gln
	145				150					155					160
Lys	Lys	Arg	Arg	Leu	Cys	Leu	Leu	Leu							
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<210> 5981

<211> 677

<212> DNA

<213> Homo sapiens

<400> 5981

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 120
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 240
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 300
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 360
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 420
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 540
 aaaacgcaag gggacactta ccttaggggt ggacgaacag ctagcttttt ggaatttggg
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 660
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 677

<210> 5982

<211> 98

<212> PRT

<213> Homo sapiens

<400> 5982

Met Gln Asn Gly Ser Pro Ala Pro Thr Ser Leu Leu Ser Gly Arg Pro
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 20 25 30
 Pro Arg Ala Pro Leu Pro Arg Ser Ser Ala Arg Arg Pro Ser Lys Ala
 35 40 45
 Asn Leu His Thr Leu Gly Gln Leu Lys Leu Ser Arg Arg Cys Arg Glu
 50 55 60
 Pro Arg Leu Gly Arg Ala Gly Gln Gln Arg Leu His Pro Arg Thr Arg
 65 70 75 80
 Pro Arg Arg Gly Ser Gly Pro Leu Val Arg Ala Gly Arg Arg Gly Trp
 85 90 95
 Gly Lys

<210> 5983

<211> 790

<212> DNA

<213> Homo sapiens

<400> 5983

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 120

cattgttttc cttaaattac tggtaaattt tgaataaac agtcccaaga tgtgattatt
 180
 tgtgtaattt ttttttttaa tttgtaaaca gggatatgac agatcttcaa ccatgttaac
 240
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 300
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 420
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 480
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 790

<210> 5984

<211> 186

<212> PRT

<213> Homo sapiens

<400> 5984

Met Leu Thr Leu Gly Pro Phe Arg Asn Ser Asn Leu Thr Glu Leu Gly
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 Leu Gln Glu Ile Lys Thr Ile Gly Tyr Thr Ser Pro Arg Ser Arg Thr
 20 25 30
 Glu Val Asn Arg Gln Cys Pro Gly Glu Lys Glu Pro Val Ser Asp Leu
 35 40 45
 Gln Leu Gly Leu Asp Ala Val Glu Pro Thr Ala Leu His Lys Thr Leu
 50 55 60
 Glu Thr Pro Ala His Asp Arg Ala Glu Pro Asn Ser Gln Leu Asp Ser
 65 70 75 80
 Thr His Ser Gly Arg Gly Thr Met Tyr Ser Ser Trp Val Lys Ser Pro
 85 90 95
 Asp Arg Thr Gly Val Asn Phe Ser Val Asn Ser Asn Leu Arg Asp Leu
 100 105 110
 Thr Pro Ser His Gln Leu Glu Val Gly Gly Gly Phe Arg Ile Ser Glu
 115 120 125
 Ser Lys Cys Leu Met Gln Asp Asp Thr Arg Gly Met Phe Met Glu Thr
 130 135 140
 Thr Val Phe Cys Thr Ser Glu Asp Gly Leu Val Ser Gly Phe Gly Arg
 145 150 155 160
 Thr Val Asn Asp Asn Leu Ile Asp Gly Asn Cys Thr Pro Gln Asn Pro
 165 170 175
 Pro Gln Lys Lys Lys Val Ser Leu Leu Glu

180

185

<210> 5985

<211> 737

<212> DNA

<213> Homo sapiens

<400> 5985

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 120
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 420
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<210> 5986

<211> 165

<212> PRT

<213> Homo sapiens

<400> 5986

Met Ala Ser Gly Asp Phe Cys Ser Pro Gly Glu Gly Met Glu Ile Leu
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 20 25 30
 Asp Leu Leu Gln Asn Pro Tyr Phe Ser Lys Leu Leu Leu Asn Leu Ser
 35 40 45
 Gln His Val Asp Glu Ser Gly Leu Ser Leu Thr Leu Ala Lys Glu Gln
 50 55 60
 Ala Gln Ala Trp Lys Glu Val Arg Leu His Lys Thr Thr Trp Leu Arg
 65 70 75 80
 Ser Glu Ile Leu His Arg Val Ile Gln Glu Leu Leu Val Asp Tyr Tyr
 85 90 95
 Val Lys Ile Gln Asp Thr Asn Val Thr Ser Glu Asp Lys Lys Phe His


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accacacagag aacgtgggggt ccaggttctt tctgcacctt cccagcacat gcagaatgac
1200
tccagtggtt ccacgtctcc ctctgcccgt gtgtacctgc ttgcctttct cagctgcccc
1260
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<210> 5988

<211> 216

<212> PRT

<213> Homo sapiens

<400> 5988

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          20          25          30
Thr Pro Ser Glu Arg Gly Met Thr Tyr Asp Ala Leu His Val Phe Asp
          35          40          45
Trp Ile Lys Ala Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His
          50          55          60
Ser Leu Gly Thr Gly Val Ala Thr Ile Trp Cys Gly Ala Ser Val Ser
          65          70          75          80
Glu Thr Pro Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile
          85          90          95
Arg Glu Glu Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe
          100         105         110
Pro Gly Phe Asp Trp Phe Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile
          115         120         125
Lys Phe Ala Asn Asp Glu Asn Val Lys His Ile Ser Cys Pro Leu Leu
          130         135         140
Ile Leu His Ala Glu Asp Asp Pro Val Val Pro Phe Gln Leu Gly Arg
          145         150         155         160
Lys Leu Tyr Ser Ile Ala Ala Pro Ala Arg Ser Phe Arg Asp Phe Lys
          165         170         175
Val Gln Phe Val Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr
          180         185         190
Ile Tyr Lys Ser Pro Glu Leu Pro Arg Ile Leu Arg Glu Phe Leu Gly
          195         200         205
Lys Ser Glu Pro Glu His Gln His
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<210> 5989

<211> 1583

<212> DNA

<213> Homo sapiens

<400> 5989

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240
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780
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<210> 5990

<211> 260

<212> PRT

<213> Homo sapiens

<400> 5990

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 20          25          30
Pro Pro Ile Ser Cys Phe Tyr Cys Glu Cys Glu Glu Lys Arg Leu Cys
 35          40          45
Val Asn Thr His Val Trp Thr Lys Ser Lys Phe Met Gly Met Ser Val
 50          55          60
Gly Val Ser Met Ile Gly Glu Gly Val Leu Arg Leu Leu Glu His Gly
 65          70          75          80
Glu Glu Tyr Val Phe Thr Leu Pro Ser Ala Tyr Ala Arg Ser Ile Leu
 85          90          95
Thr Ile Pro Trp Val Glu Leu Gly Gly Lys Val Ser Ile Asn Cys Ala
100          105          110
Lys Thr Gly Tyr Ser Ala Thr Val Ile Phe His Thr Lys Pro Phe Tyr
115          120          125
Gly Gly Lys Val His Arg Val Thr Ala Glu Val Lys His Asn Pro Thr
130          135          140
Asn Thr Ile Val Cys Lys Ala His Gly Glu Trp Asn Gly Thr Leu Glu
145          150          155          160
Phe Thr Tyr Asn Asn Gly Glu Thr Lys Val Ile Asp Thr Thr Thr Leu
165          170          175
Pro Val Tyr Pro Lys Lys Ile Arg Pro Leu Glu Lys Gln Gly Pro Met
180          185          190
Glu Ser Arg Asn Leu Trp Arg Glu Val Thr Arg Tyr Leu Arg Leu Gly
195          200          205
Asp Ile Asp Ala Ala Thr Glu Gln Lys Arg His Leu Glu Glu Lys Gln
210          215          220
Arg Val Glu Glu Arg Lys Arg Glu Asn Leu Arg Thr Pro Trp Lys Pro
225          230          235          240
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<210> 5991

<211> 2440

<212> DNA

<213> Homo sapiens

<400> 5991

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180

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 2400
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa
 2440

<210> 5992

<211> 301

<212> PRT

<213> Homo sapiens

<400> 5992

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 20 25 30
 Val Val Phe Asp Glu Ala Asp Arg Leu Phe Glu Met Gly Phe Ala Glu
 35 40 45
 Gln Leu Gln Glu Ile Ile Ala Arg Leu Pro Gly Gly His Gln Thr Val
 50 55 60
 Leu Phe Ser Ala Thr Leu Pro Lys Leu Leu Val Glu Phe Ala Arg Ala
 65 70 75 80
 Gly Leu Thr Glu Pro Val Leu Ile Arg Leu Asp Val Asp Thr Lys Leu
 85 90 95
 Asn Glu Gln Leu Lys Thr Ser Phe Phe Leu Val Arg Glu Asp Thr Lys
 100 105 110
 Ala Ala Val Leu Leu His Leu Leu His Asn Val Val Arg Pro Gln Asp
 115 120 125
 Gln Thr Val Val Phe Val Ala Thr Lys His His Ala Glu Tyr Leu Thr
 130 135 140
 Glu Leu Leu Thr Thr Gln Xaa Val Ser Cys Ala His Ile Tyr Ser Ala
 145 150 155 160
 Leu Asp Pro Thr Ala Arg Lys Ile Asn Leu Ala Lys Phe Thr Leu Gly
 165 170 175
 Lys Cys Ser Thr Leu Ile Val Thr Asp Leu Ala Ala Arg Gly Leu Asp
 180 185 190
 Ile Pro Leu Leu Asp Asn Val Ile Asn Tyr Ser Phe Pro Ala Lys Gly

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<211> 72

<212> PRT

<213> Homo sapiens

<400> 5998

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<211> 2759

<212> DNA

<213> Homo sapiens

<400> 5999

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<211> 757

<212> PRT

<213> Homo sapiens

<400> 6000

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Lys	Asn	Ile	Phe	Ser	Val	Pro	Glu	Ile	Val	Arg	Glu	Thr	Gln	Asp	Leu
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Cys Tyr Val Gln Tyr Met Ile Ala Ile Ile Asn Asn Cys Gln Thr Phe		
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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 6002

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<213> Homo sapiens

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<210> 6004

<211> 140

<212> PRT

<213> Homo sapiens

<400> 6004

Met Val Thr Thr Pro Ser Trp Trp Ala Val Trp Pro Trp Val Ser Gly
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 20 25 30
 Pro Ala Val Pro Lys Val Ala Pro Gly Thr Met Pro Thr Arg Pro Glu
 35 40 45
 Gly Gly Thr Glu Thr Thr Ser Met Leu Xaa Val Pro Gly Val Thr Gln
 50 55 60
 Ser Pro Arg Gly Glu Arg Gly Ser Gly Pro His Ala Val Gln Gly Val
 65 70 75 80
 Ala Leu Pro Xaa Arg Gly Ser Pro Arg Gly Pro Gly Pro Arg Ala Pro
 85 90 95
 Gly Arg Gly Arg Asp Cys Gly Gly Asn Gly Pro Ala Glu Ala Pro Ala

5183

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<210> 6006

<211> 200

<212> PRT

<213> Homo sapiens

<400> 6006

Glu Leu Gly Leu Pro Gly Ala Pro Gly Ile Asp Gly Glu Lys Gly Pro
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 35 40 45
 Leu Lys Gly Glu Lys Gly Glu Ser Ala Ser Gln Pro Thr Gly Glu Pro
 50 55 60
 Gly Ser Ala His Ser Glu Pro Gly Pro Gly Pro Gly Pro Gly Pro
 65 70 75 80
 Gly Pro Met Gly Leu Gln Gly Ile Gln Gly Pro Lys Gly Leu Asp Gly
 85 90 95
 Ala Lys Gly Glu Lys Gly Ala Ser Gly Glu Arg Gly Ser Ser Gly Leu
 100 105 110
 Pro Gly Pro Val Gly Pro Pro Gly Leu Ile Gly Leu Pro Gly Thr Lys
 115 120 125
 Gly Glu Lys Gly Arg Pro Gly Glu Pro Gly Leu Asp Gly Phe Pro Gly
 130 135 140
 Pro Arg Gly Glu Lys Gly Asp Arg Ser Glu Arg Gly Glu Lys Gly Glu
 145 150 155 160
 Arg Gly Val Pro Gly Arg Lys Gly Val Lys Gly Gln Lys Gly Glu Pro
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 Gly Pro Pro Gly Leu Asp Gln Pro Cys Pro Val Gly Pro Asp Gly Leu
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 Pro Val Pro Gly Cys Trp His Lys
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<210> 6007

<211> 693

<212> DNA

<213> Homo sapiens

<400> 6007

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<210> 6008

<211> 214

<212> PRT

<213> Homo sapiens

<400> 6008

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Thr	Ser	Asp	Gly	Ala	Ile	Ser	Val	Pro	Ser	Leu	Ser	Ala	Pro
			20				25					30	Gly
Gly	Lys	Met	Val	Lys	Lys	Val	Cys	Pro	Cys	Asn	Gln	Leu	Cys
		35				40					45		Arg
Ser	Ser	Thr	Asn	Thr	Val	Gly	Ala	Thr	Val	Asn	Ser	Gln	Ala
		50			55				60				Ala
Ala	Gln	Pro	Pro	Ala	Met	Thr	Ser	Ser	Arg	Lys	Gly	Thr	Phe
				70					75				80
Asp	Leu	His	Lys	Leu	Val	Asp	Asn	Trp	Ala	Arg	Asp	Ala	Met
				85				90					95
Ser	Gly	Arg	Arg	Gly	Ser	Lys	Gly	His	Met	Asn	Tyr	Glu	Gly
			100					105				110	Pro
Met	Ala	Arg	Lys	Phe	Ser	Ala	Pro	Gly	Gln	Leu	Cys	Ile	Ser
			115				120				125		Met
Ser	Asn	Leu	Gly	Gly	Ser	Ala	Pro	Ile	Ser	Ala	Ala	Ser	Ala
		130				135					140		Thr
Leu	Gly	His	Phe	Thr	Lys	Ser	Met	Cys	Pro	Pro	Gln	Gln	Tyr
			145		150				155				160
Pro	Ala	Thr	Pro	Phe	Gly	Ala	Gln	Trp	Ser	Gly	Thr	Gly	Gly
												Pro	Ala

	165		170		175
Pro	Gln	Pro	Leu	Gly	Gln
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Asn	Phe	Asn	Ile	Ser	Asn
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<210> 6009

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 6009

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1200

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<210> 6010

<211> 468

<212> PRT

<213> Homo sapiens

<400> 6010

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 Asp Thr Val Tyr Asp Val Val Val Ser Gly Gly Gly Leu Val Gly Ala
 35 40 45
 Ala Met Ala Cys Ala Leu Gly Tyr Asp Ile His Phe His Asp Lys Lys
 50 55 60
 Ile Leu Leu Leu Glu Ala Gly Pro Lys Lys Val Leu Glu Lys Leu Ser
 65 70 75 80
 Glu Thr Tyr Ser Asn Arg Val Ser Ser Ile Ser Pro Gly Ser Ala Thr
 85 90 95
 Leu Leu Ser Ser Phe Gly Ala Trp Asp His Ile Cys Asn Met Arg Tyr
 100 105 110
 Arg Ala Phe Arg Arg Met Gln Val Trp Asp Ala Cys Ser Glu Ala Leu
 115 120 125
 Ile Met Phe Asp Lys Asp Asn Leu Asp Asp Met Gly Tyr Ile Val Glu
 130 135 140
 Asn Asp Val Ile Met His Ala Leu Thr Lys Gln Leu Glu Ala Val Ser
 145 150 155 160
 Asp Arg Val Thr Val Leu Tyr Arg Ser Lys Ala Ile Arg Tyr Thr Trp
 165 170 175
 Pro Cys Pro Phe Pro Met Ala Asp Ser Ser Pro Trp Val His Ile Thr
 180 185 190
 Leu Gly Asp Gly Ser Thr Phe Gln Thr Lys Leu Leu Ile Gly Ala Asp
 195 200 205
 Gly His Asn Ser Gly Val Arg Gln Ala Val Gly Ile Gln Asn Val Ser
 210 215 220
 Trp Asn Tyr Asp Gln Ser Ala Val Val Ala Thr Leu His Leu Ser Glu
 225 230 235 240
 Ala Thr Glu Asn Asn Val Ala Trp Gln Arg Phe Leu Pro Ser Gly Pro
 245 250 255
 Ile Ala Leu Leu Pro Leu Ser Asp Thr Leu Ser Ser Leu Val Trp Ser

260 265 270
 Thr Ser His Glu His Ala Ala Glu Leu Val Ser Met Asp Glu Glu Lys
 275 280 285
 Phe Val Asp Ala Val Asn Ser Ala Phe Trp Ser Asp Ala Asp His Thr
 290 295 300
 Asp Phe Ile Asp Thr Ala Gly Ala Met Leu Gln Tyr Pro Val Ser Leu
 305 310 315 320
 Leu Lys Pro Thr Lys Val Ser Ala Arg Gln Leu Pro Pro Ser Val Pro
 325 330 335
 Trp Val Asp Ala Lys Ser Arg Val Leu Phe Pro Leu Gly Leu Gly His
 340 345 350
 Ala Ala Glu Tyr Val Arg Pro Arg Val Ala Leu Ile Gly Asp Ala Ala
 355 360 365
 His Arg Val His Pro Leu Ala Gly Gln Gly Val Asn Met Gly Phe Gly
 370 375 380
 Asp Ile Ser Ser Leu Ala His His Leu Ser Thr Ala Ala Phe Asn Gly
 385 390 395 400
 Lys Asp Leu Gly Ser Val Ser His Leu Thr Gly Tyr Glu Thr Glu Arg
 405 410 415
 Gln Arg His Asn Thr Ala Leu Leu Ala Ala Thr Asp Leu Leu Lys Arg
 420 425 430
 Leu Tyr Ser Thr Ser Ala Ser Pro Leu Val Leu Leu Arg Thr Trp Gly
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<210> 6011

<211> 1331

<212> DNA

<213> Homo sapiens

<400> 6011

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<210> 6012

<211> 219

<212> PRT

<213> Homo sapiens

<400> 6012

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 20 25 30
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 35 40 45
 Phe Pro Phe Leu Tyr Leu Leu Glu Lys Val Glu Cys Thr Pro Ser Gln
 50 55 60
 Glu His Leu Lys His Gln Thr Val Tyr Arg Leu Lys Cys Ala Pro
 65 70 75 80
 Arg Gly Lys Asn Gly Phe Thr Pro Leu His Met Ala Val Asp Lys Asp
 85 90 95
 Thr Thr Asn Val Gly Arg Tyr Pro Val Gly Arg Phe Pro Ser Leu His
 100 105 110
 Val Val Lys Val Leu Leu Asp Cys Gly Ala Asp Pro Asp Ser Arg Asp
 115 120 125
 Phe Asp Asn Asn Thr Pro Leu His Ile Ala Ala Gln Asn Asn Cys Pro
 130 135 140
 Ala Ile Met Asn Ala Leu Ile Glu Ala Gly Ala His Met Asp Ala Thr
 145 150 155 160
 Asn Ala Phe Lys Lys Thr Ala Tyr Glu Leu Leu Asp Glu Lys Leu Leu

	165		170		175
Ala Arg Gly Thr Met Gln Pro Phe Asn Tyr Val Thr Leu Gln Cys Leu					
	180		185		190
Ala Ala Arg Ala Leu Asp Lys Asn Lys Ile Pro Tyr Lys Gly Phe Ile					
	195		200		205
Pro Glu Asp Leu Glu Ala Phe Ile Glu Leu His					
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<210> 6013

<211> 2204

<212> DNA

<213> Homo sapiens

<400> 6013

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<210> 6014

<211> 182

<212> PRT

<213> Homo sapiens

<400> 6014

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 35 40 45
 Thr Ser Glu Thr Tyr Leu Met Lys His Met Arg Lys His Asn Pro Pro
 50 55 60
 Asp Leu Gln Gln Gln Val Gln Ala Ala Ala Ala Ala Val Ala
 65 70 75 80
 Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
 85 90 95
 Gln Ala Gln Ala Gln Ala Ser Gln Ala Ser Gln Gln Gln Gln Gln

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          100              105              110
Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro His Phe Gln Ser
          115              120              125
Pro Gly Ala Ala Pro Gln Gly Gly Gly Gly Asp Ser Asn Pro Asn
          130              135              140
Pro Pro Pro Gln Cys Ser Phe Asp Leu Thr Pro Tyr Lys Thr Ala Glu
145              150              155              160
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          165              170              175
Glu His Leu Ala Ser Ser
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<210> 6015

<211> 612

<212> DNA

<213> Homo sapiens

<400> 6015

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<210> 6016

<211> 99

<212> PRT

<213> Homo sapiens

<400> 6016

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Pro Arg Ser Pro Glu Arg Leu Pro Ala Ser Gln Gly Ile Ser Arg Gly
20              25              30
Arg Cys Lys Leu Asn Asn Asn Ser Trp Ser Gly Leu Thr Cys Pro Thr
35              40              45
Leu Ser Met Ser Cys Asn Gln Asn Lys Leu Asp Ser Pro Gly Arg Ala

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50		55		60
Ser His Gly Ser Ser Leu Pro Phe Asn Gln Asp Ser Gln Lys Pro Ala				
65	70	75	80	
Phe Tyr Asn Ile Phe Leu Lys Lys Ser His Ser Phe Gln Ser Leu Leu				
	85	90	95	

Gln Tyr Ile

<210> 6017
 <211> 2091
 <212> DNA
 <213> Homo sapiens

<400> 6017
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<211> 537

<212> PRT

<213> Homo sapiens

<400> 6018

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Ala Cys Thr Phe Val His Leu Leu Pro Lys Phe Asp Pro Leu Val Ile		240
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Ile Gly Pro Ser Glu Val Glu Asn Ala Leu Met Lys His Pro Ala Val		430
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Val Lys Ala Phe Val Val Leu Ala Ser Gln Phe Leu Ser His Asp Pro		460
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Glu Gln Leu Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala		480
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Pro Tyr Lys Tyr Pro Arg Lys Ile Glu Phe Val Leu Asn Leu Pro Lys		495
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<211> 3002

<212> DNA

<213> Homo sapiens

<400> 6019

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<211> 387

<212> PRT

<213> Homo sapiens

<400> 6020

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Ser Ile Cys Cys Ser Gly Glu Thr Leu Leu Ile Cys Gly Asn Pro Asp
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Cys Thr Arg Cys Tyr Cys Phe Glu Cys Val Asp Ser Leu Val Gly Pro
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<212> DNA

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<211> 708

<212> PRT

<213> Homo sapiens

<400> 6022

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 Tyr Lys Leu Ala Val Ala Thr Phe Ala Gly Ile Glu Asn Lys Phe Gly
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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<211> 496

<212> PRT

<213> Homo sapiens

<400> 6026

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<212> PRT

<213> Homo sapiens

<400> 6030

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<212> DNA

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<213> Homo sapiens

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 <213> Homo sapiens

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 <213> Homo sapiens

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 Pro Phe Arg Met Glu Pro Leu Ile His Trp Ala His Ser His Gly Gln
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 <213> Homo sapiens

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<211> 214

<212> PRT

<213> Homo sapiens

<400> 6038

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His	Gly	Gly	Thr	Cys	Ser	Arg	Gln	Glu	Leu	Gly	Val	Ser	Asp	Val	Leu
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Pro	Ala	Leu	Lys	Ile	Thr	Arg	Arg	Tyr	Ala	Phe	Ala	His	Ile	Leu	Thr
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Leu	Ile	Leu	Ala	Gln	Gln	Gln	Gln	His	Lys	Lys	Tyr	His	Gly	Ser	Gln
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Gly	Ala	Ser	Ile	Leu	Ala	Thr	Ala	Ala	Asn	Leu	Leu	Arg	His	Tyr	Pro
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Thr	Glu	Glu	Glu	Glu	Gln	Ala	Leu	Glu	Leu	Leu	Ser	Glu	Met	Glu	Glu
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Asn	Glu	Pro	Tyr	Pro	Ala	Glu	Tyr	Glu	Val	Ile	Asn	Gln	Phe	Gln	Pro
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 <212> DNA
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 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 6040
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Ala Gln Ala Gly Arg Leu Pro Leu Leu Pro Cys Ala Arg Ala Tyr Val
   65              70              75              80
Ser Pro Arg Ala Pro Phe Tyr Arg Pro Leu Ala Pro Glu Leu Arg Ala
      85              90              95
Arg Gln Leu Glu Leu Gly Ala Glu His Ala Leu Leu Leu Asp Ala Ala
   100              105              110
Gly Gln Val Phe Ser Trp Gly Gly Gly Arg His Gly Gln Leu Gly His
   115              120              125
Gly Thr Leu Glu Ala Glu Leu Glu Pro Arg Leu Leu Glu Ala Leu Gln
   130              135              140
Gly Leu Val Met Ala Glu Val Ala Ala Gly Gly Trp His Ser Val Cys
   145              150              155              160
Val Ser Glu Thr Gly Asp Ile Tyr Ile Trp Gly Trp Asn Glu Ser Gly
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Gln Leu Ala Leu Pro Thr Arg Asn Leu Ala Glu Asp Gly Glu Thr Val
   180              185              190
Ala Arg Glu Ala Thr Glu Leu Asn Glu Asp Gly Ser Gln Val Lys Arg
   195              200              205
Thr Gly Gly Ala Glu Asp Gly Ala Pro Ala Pro Phe Ile Ala Val Gln
   210              215              220
Pro Phe Pro Ala Leu Leu Asp Leu Pro Met Gly Ser Asp Ala Val Lys
   225              230              235              240
Ala Ser Cys Gly Ser Arg His Thr Ala Val Val Thr Arg Thr Gly Glu
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Leu Tyr Thr Trp Gly Trp Gly Lys Tyr Gly Gln Leu Gly His Glu Asp
   260              265              270
Thr Thr Ser Leu Asp Arg Pro Arg Arg Val Glu Tyr Phe Val Asp Lys
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<210> 6041

<211> 291

<212> DNA

<213> Homo sapiens

<400> 6041

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 <212> PRT
 <213> Homo sapiens

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 Ile Met Ala Ala Leu Asn Ser Gln Thr Ala Val Gln Phe Gln Gln Tyr
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 Ala Ala Gln Gln Tyr Pro Gly Asn Tyr Glu Gln Gln Gln Ile Leu Ile
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<210> 6043
 <211> 558
 <212> DNA
 <213> Homo sapiens

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<210> 6044
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 <212> PRT
 <213> Homo sapiens

<400> 6044

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Lys Ile Ala Pro Leu Glu Ser His His Arg Pro Lys Arg Pro Asp Asp
 35           40           45
Pro Pro Gly Thr Leu Asn Pro Cys Pro Glu Arg Gly Gly Ala Gly Val
 50           55           60
Trp Ile Pro Ala Gly Ser Phe Gly Thr Gly Lys Asn Arg Gly Cys Ser
 65           70           75           80
Asp Arg Val Phe Thr Lys Thr Cys Ile Arg Gln Asp Pro Gly Arg Met
 85           90           95
Trp Val Ala Pro Pro Leu Cys Trp Ala Arg Arg Met Cys Pro His Arg
 100          105          110
Ser Gln Ile Leu Phe Pro Gln Trp Val Val Gln Asp Thr Leu Asn Phe
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<210> 6045

<211> 1916

<212> DNA

<213> Homo sapiens

<400> 6045

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780

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<210> 6046

<211> 457

<212> PRT

<213> Homo sapiens

<400> 6046

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			20					25					30		
Glu	Val	Ile	Ala	Val	Val	Met	Asp	Val	Phe	Thr	Asp	Ile	Asp	Ile	Phe
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Leu	Leu	Asp	Gln	Ala	Leu	Leu	Ser	Gln	Phe	Leu	Asp	Met	Cys	Met	Asp

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			85						90					95	
Thr	Gly	Asn	Ile	Tyr	Tyr	Ala	Arg	Ser	Gly	Thr	Lys	Ile	Ile	Gly	Lys
			100						105					110	
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Ser	Lys	Glu	Leu	Thr	Leu	Gly	Asn	Leu	Leu	Arg	Met	Arg	Leu	Ala	Arg
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Glu	Gly	Lys	Ala	Glu	Arg	Lys	Pro	His	Asp	Cys	Glu	Ser	Ser	Thr	Val
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Ser	Glu	Glu	Asp	Tyr	Phe	Ser	Ser	His	Arg	Asp	Glu	Leu	Gln	Ser	Arg
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Lys	Ala	Ile	Asp	Ala	Ala	Thr	Gln	Thr	Glu	Pro	Gly	Glu	Glu	Met	Pro
			260						265					270	
Gly	Leu	Ser	Val	Ser	Glu	Val	Gly	Thr	Gln	Thr	Ser	Ile	Thr	Thr	Ala
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Thr	Pro	His	Leu	Glu	Leu	Tyr	Leu	Ser	Asp	Ser	Leu	Arg	Asn	Leu	Asn
			385						390					395	
Lys	Glu	Arg	Gln	Phe	His	Phe	Ala	Gly	Ile	Arg	Ser	Arg	Leu	Asn	His
			405						410					415	
Met	Leu	Ala	Met	Leu	Ser	Arg	Arg	Thr	Leu	Phe	Thr	Glu	Asn	His	Leu
			420						425					430	
Gly	Leu	His	Ser	Gly	Asn	Phe	Ser	Arg	Val	Asn	Leu	Leu	Ala	Val	Arg
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<210> 6047

<211> 773

<212> DNA

<213> Homo sapiens

<400> 6047

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<211> 129

<212> PRT

<213> Homo sapiens

<400> 6048

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 His Leu Pro Ser Ala Cys Leu Gly Ala Arg Arg Ser Ser Ser Leu Leu
 50 55 60
 Gly Tyr Gly Ser Cys Arg Asp Thr Gln Ser Trp Thr Pro Asp Pro Leu
 65 70 75 80
 Pro His Pro Pro Ser Leu Ser Pro Gln Ser Leu Leu Tyr Ser Gln Ala
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 Met Arg Ser Pro Ile Ser His Gln Glu Leu Thr Arg Pro Leu Gly Lys
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<210> 6049
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 <213> Homo sapiens

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 Ser Asn Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Thr
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 Pro Pro Leu Gln Pro Arg Asp Ser Ala Ser Pro Ser Thr Ser Ser Phe
 65 70 75 80
 Cys Leu Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Gln Lys
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 Lys Leu Arg Phe Glu Asp Thr Leu Glu Phe Val Gly Phe Asp Ala Lys
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<210> 6052

<211> 518

<212> PRT

<213> Homo sapiens

<400> 6052

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 Gln Pro Gln Val Met Lys Leu Leu Asp Ser Leu Arg Glu Gln Tyr Thr
 65 70 75 80
 Arg Tyr Gln Glu Val Cys Arg Gln Arg Ser Lys Arg Thr Gln Leu Glu
 85 90 95
 Glu Ile Gln Gln Lys Val Met Gln Val Val Asn Trp Leu Glu Gly Pro
 100 105 110
 Gly Ser Glu Gln Leu Arg Ala Gln Trp Gly Ile Gly Asp Ser Ile Arg
 115 120 125
 Ala Ser Gln Ala Leu Gln Gln Lys His Glu Glu Ile Glu Ser Gln His


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      180              185              190
Phe Arg Gln Asn Leu Leu Gln Ala Ala Leu Glu Phe His Gly Val Ala
      195              200              205
Gln Asp Leu Ser Gln Gln Leu Asp Gly Leu Leu Gly Met Leu Cys Val
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Asp Val Ala Pro Ala Asp Gly Ala Ser Ile Gln Gln Thr Leu Lys Leu
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Glu Lys Gly Gln Gly Leu Leu Asp Gln Ile Ser Asn Gln Ala Ser Xaa
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      275              280              285
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Ala Gln Glu Thr Lys Val Leu Leu Glu Lys His Arg Lys Phe Val Asp
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Val Val Leu Cys Gln Ser Leu Arg Cys Thr Ser Arg Ser Ser Gly Asp
      385              390              395              400
Thr Leu Pro Arg Leu Asn Arg Val Trp Lys Gln Phe Thr Ile Ala Ser
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Glu Glu Arg Val His Arg Leu Glu Met Ala Ile Ala Phe His Ser Asn
      420              425              430
Ala Glu Lys Ile Leu Gln Asp Cys Pro Glu Glu Pro Glu Ala Ile Asn
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Asp Glu Glu Gln Phe Asp Glu Ile Glu Ala Val Gly Lys Ser Leu Leu
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Asp Arg Leu Thr Val Pro Val Val Tyr Pro Asp Gly Thr Glu Gln Tyr
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Phe Gly Ser Pro Ser Asp Met Ala Ser Thr Ala Glu Asn Ile Arg Asp
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<210> 6053

<211> 3257

<212> DNA

<213> Homo sapiens

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<210> 6054
 <211> 382
 <212> PRT
 <213> Homo sapiens

<400> 6054
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 Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu Ala Val
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 Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu Phe Leu Phe
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 Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile Glu Met Glu Ile Glu
 115 120 125
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 145 150 155 160
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 180 185 190
 Cys Val Gly Lys Arg Asn Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser
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 Pro Gly Thr Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser
 245 250 255
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 275 280 285
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<210> 6055

<211> 2089

<212> DNA

<213> Homo sapiens

<400> 6055

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<210> 6056

<211> 285

<212> PRT

<213> Homo sapiens

<400> 6056

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<210> 6057

<211> 3924

<212> DNA

<213> Homo sapiens

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<211> 500

<212> PRT

<213> Homo sapiens

<400> 6058

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<212> DNA

<213> Homo sapiens

<400> 6059

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<210> 6064

<211> 233

<212> PRT

<213> Homo sapiens

<400> 6064

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             180             185             190
Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile
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<210> 6065

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 6065

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<211> 80

<212> PRT

<213> Homo sapiens

<400> 6066

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Arg	Val	Leu	Arg	Gly	Val	Asp	Asp	Leu	Asp	Phe	Phe	Ile	Gly	Asp	Glu
		20						25				30			
Ala	Ile	Asp	Lys	Pro	Thr	Tyr	Ala	Thr	Lys	Trp	Pro	Ile	Arg	His	Gly
		35					40					45			
Ile	Ile	Glu	Asp	Trp	Asp	Leu	Met	Glu	Arg	Phe	Met	Glu	Gln	Val	Val
	50					55				60					
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<210> 6067

<211> 406

<212> DNA

<213> Homo sapiens

<400> 6067

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<210> 6068

<211> 117

<212> PRT

<213> Homo sapiens

<400> 6068

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20          25          30
Ser Leu Phe Leu Ser Gly Asn Val Ser Ser Arg Arg Met Arg Thr Ala
35          40          45
Ser Arg Ser Ser Glu Pro Pro Ala Cys Pro Arg His Trp Pro Cys Pro
50          55          60
Pro Gly Leu Pro Phe Gly Gln Gly Ala Val Ala Arg Ala Ala Pro Cys
65          70          75          80
Pro Ala Tyr Ser His Ser Ala Val Gly Arg Pro Pro Leu Pro Arg Lys
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<210> 6069

<211> 456

<212> DNA

<213> Homo sapiens

<400> 6069

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180

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<210> 6070

<211> 148

<212> PRT

<213> Homo sapiens

<400> 6070

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 His Arg Tyr His Arg Lys Glu Asn Leu Glu Tyr Cys Ile Met Val Ile
 35 40 45
 Gly Val Pro Asn Val Gly Lys Ser Ser Leu Ile Asn Ser Leu Arg Arg
 50 55 60
 Gln His Leu Arg Lys Gly Lys Ala Thr Arg Val Gly Gly Glu Pro Gly
 65 70 75 80
 Ile Thr Arg Ala Val Met Ser Lys Ile Gln Val Glu Ser Ser Gly Ala
 85 90 95
 Arg Pro Ser Thr Leu Ser Arg Ala Leu Gln Ala Ser Gly Thr Cys Arg
 100 105 110
 Pro Leu Cys Gly Phe Arg Leu Leu Thr Thr Leu Pro Ser Pro Pro Leu
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<210> 6071

<211> 2633

<212> DNA

<213> Homo sapiens

<400> 6071

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<211> 76

<212> PRT

<213> Homo sapiens

<400> 6072

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<210> 6073

<211> 387

<212> DNA

<213> Homo sapiens

<400> 6073

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<211> 69

<212> PRT

<213> Homo sapiens

<400> 6074

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			20					25					30		
Ala	Pro	Thr	Gly	Pro	Phe	Ser	Pro	Arg	Met	Lys	Pro	Ala	Gly	Ser	Val
		35					40				45				
Asn	Asp	Met	Ala	Leu	Asp	Ala	Phe	Asp	Leu	Asp	Arg	Met	Lys	Gln	Glu
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<212> DNA

<213> Homo sapiens

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<210> 6076

<211> 601

<212> PRT

<213> Homo sapiens

<400> 6076

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			20					25					30		
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Cys	Lys	Ala	Ile	Glu	Arg	Gly	Thr	Gly	Asn	Asp	Asn	Tyr	Arg	Thr	Thr
				70					75					80	
Gly	Ile	Ala	Thr	Ile	Glu	Val	Phe	Leu	Pro	Pro	Arg	Leu	Lys	Lys	Asp
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			100					105					110		
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Val	Leu	Phe	Leu	Arg	Leu	Tyr	Leu	Leu	Gln	Gly	Ile	Arg	Asn	Tyr	His
Ser	Gly	Asn	Asp	Val	Glu	Ala	Tyr	Glu	Tyr	Leu	Asn	Arg	His	Val	Ser
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Ser	Trp	Gly	Leu	Leu	Pro	Arg	Lys	Xaa	Arg	Leu	Gly	Leu	Arg	Ala	Cys
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<210> 6077

<211> 2093

<212> DNA

<213> Homo sapiens

<400> 6077

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<210> 6078

<211> 213

<212> PRT

<213> Homo sapiens

<400> 6078

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			20						25					30	
Ser	Gly	Arg	Glu	Gly	Ala	Ser	Gly	Pro	Gly	Val	Gly	Pro	His	Ile	Tyr
			35					40				45			
Val	Arg	Glu	Ala	Glu	Asp	Arg	Glu	Leu	Val	Thr	Met	Ala	Gly	Pro	Gln
			50				55				60				
Pro	Leu	Ala	Leu	Gln	Leu	Glu	Gln	Leu	Leu	Asn	Pro	Arg	Pro	Ser	Glu
						70				75				80	
Ala	Asp	Pro	Glu	Ala	Asp	Pro	Glu	Glu	Ala	Thr	Ala	Ala	Arg	Val	Ile
				85						90				95	
Asp	Arg	Phe	Asp	Glu	Gly	Glu	Asp	Gly	Glu	Gly	Asp	Phe	Leu	Val	Val
			100					105					110		
Gly	Ser	Ile	Arg	Lys	Leu	Ala	Ser	Ala	Ser	Leu	Leu	Asp	Thr	Asp	Lys
			115					120					125		
Arg	Tyr	Cys	Gly	Lys	Thr	Thr	Ser	Arg	Lys	Ala	Trp	Asn	Glu	Asp	His
			130					135				140			
Trp	Glu	Gln	Thr	Leu	Pro	Gly	Ser	Ser	Asp	Glu	Glu	Ile	Ser	Asp	Glu
						150				155				160	
Glu	Gly	Ser	Gly	Asp	Glu	Asp	Ser	Glu	Gly	Leu	Gly	Leu	Glu	Glu	Tyr
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Asp	Glu	Asp	Asp	Leu	Gly	Ala	Ala	Glu	Glu	Gln	Glu	Cys	Gly	Asp	Gln

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 <211> 162
 <212> PRT
 <213> Homo sapiens
 <400> 6080
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 20 25 30
 Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
 35 40 45
 Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
 50 55 60
 Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
 65 70 75 80
 Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
 85 90 95
 Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro

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          100                      105                      110
Met  Lys  Ser  Val  Leu  Trp  Trp  Leu  Pro  Val  Glu  Lys  Ala  Phe  Trp  Arg
      115                      120                      125
Gln  Pro  Ala  Gly  Pro  Gly  Ser  Gly  Ile  Arg  Glu  Arg  Leu  Glu  His  Pro
      130                      135                      140
Val  Leu  His  Val  Ser  Trp  Asn  Asp  Ala  Arg  Ala  Tyr  Cys  Ala  Trp  Arg
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Gly  Lys

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<210> 6081

<211> 655

<212> DNA

<213> Homo sapiens

<400> 6081

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<210> 6082

<211> 218

<212> PRT

<213> Homo sapiens

<400> 6082

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Ala  Glu  Thr  Asp  Glu  Gly  Trp  Leu  Asp  Val  Val  Gln  Ser  Leu  Ile  Arg
      20      25      30
Val  Ile  Pro  Leu  Glu  Asp  Pro  Leu  Gly  Pro  Ala  Val  Ile  Thr  Leu  Leu
      35      40      45
Leu  Asp  Glu  Cys  Pro  Leu  Pro  Thr  Lys  Asp  Ala  Leu  Gln  Lys  Leu  Thr
      50      55      60
Glu  Ile  Leu  Asn  Leu  Asn  Gly  Glu  Val  Ala  Cys  Gln  Asp  Ser  Ser  His

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Pro Ala Lys His Arg Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu
      85          90          95
Lys Leu Ala Gly Pro Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu
      100          105          110
Glu Tyr Leu Leu Gln Cys Leu Lys Leu Gln Ser His Pro Thr Val Met
      115          120          125
Leu Phe Ala Leu Ile Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn
      130          135          140
Lys Leu Thr Ile Ser Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu
      145          150          155
Glu Ser Trp Ala Asn Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe
      165          170          175
Cys Ala Gln Trp Ser Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln
      180          185          190
Leu Thr Tyr Glu Lys Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn
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<210> 6083

<211> 358

<212> DNA

<213> Homo sapiens

<400> 6083

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<210> 6084

<211> 101

<212> PRT

<213> Homo sapiens

<400> 6084

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      20      25      30
Leu Ile Val Glu Gly His Leu Thr Lys Ala Val Glu Glu Thr Lys Leu
      35      40      45
Ser Lys Glu Asn Gln Thr Arg Ala Lys Glu Ser Asp Phe Ser Asp Thr
      50      55      60
Leu Ser Pro Ser Lys Glu Lys Ser Ser Asp Asp Thr Thr Asp Ala Gln

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65          70          75          80
Met Asp Glu Gln Asp Leu Asn Glu Pro Leu Ala Lys Val Ser Leu Leu
          85          90          95
Lys Asp Asp Leu Gln
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<210> 6085

<211> 2307

<212> DNA

<213> Homo sapiens

<400> 6085

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1260

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<213> Homo sapiens

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<400> 6088

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<211> 4211

<212> DNA

<213> Homo sapiens

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<400> 6090

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<211> 1336

<212> DNA

<213> Homo sapiens

<400> 6091

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<210> 6092

<211> 118

<212> PRT

<213> Homo sapiens

<400> 6092

Met Ala Gln Ser Trp Ala Arg Thr Gln Glu Phe Leu Cys Pro Met Cys

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Thr Pro Asn Trp Tyr Trp Val Leu Gly His Pro Asn Leu Ile Arg Asp
      35             40             45
Val Thr Arg Gln Val Pro Ser Pro Pro Ser Gly Phe Arg Leu Pro Ser
      50             55             60
Ser Arg His Glu Gly Pro Ser Pro Pro Arg Asp Leu Gly Thr Ser Gly
      65             70             75             80
Pro Ser Arg Ala Ala Ser His Lys Pro Ser Asn Glu Gln Arg Asp Ala
      85             90             95
Gly Gln Gln Leu Gln Leu His Leu Leu Pro Ala Leu Lys Gly Ser Phe
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Pro Ala Ser Val Leu Ser
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<210> 6093

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 6093

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<210> 6094

<211> 136

<212> PRT

<213> Homo sapiens

<400> 6094

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 35 40 45
 Trp Asn Pro Lys Pro Leu Pro Arg Leu Gln Ala Pro Asp Gly Leu Leu
 50 55 60
 Ser Cys Asn Phe Leu Gly Glu Glu Thr Phe Ser Ser Phe Pro Phe Leu
 65 70 75 80
 Val His Pro Cys Thr Leu Val Leu Ser Gln Pro Leu Pro His Ile Val

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      85              90              95
Pro Asp Ser Arg Gly Thr Ser Ser Leu His Arg Ala Ala Ala Ala Gly
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Leu Arg Ala Glu Pro Val Gly Ala Glu Ala Leu Ala Pro Glu Val Gln
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Pro Leu Ser Leu Gly Pro Leu Gly
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<210> 6095

<211> 441

<212> DNA

<213> Homo sapiens

<400> 6095

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<210> 6096

<211> 97

<212> PRT

<213> Homo sapiens

<400> 6096

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20      25      30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35      40      45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
50      55      60
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
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Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
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<210> 6097

<211> 2404

<212> DNA

<213> Homo sapiens

<400> 6097

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<210> 6098

<211> 631

<212> PRT

<213> Homo sapiens

<400> 6098

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Arg	Ser	Gly	Asp	Val	Ile	Glu	Tyr	Leu	Leu	Lys	Asn	Gln	Trp	Phe	Val
		35				40					45				
Arg	Cys	Gln	Glu	Met	Gly	Ala	Arg	Ala	Ala	Lys	Ala	Val	Glu	Ser	Gly
	50					55				60					
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65				70					75				80		
Phe	Ser	His	Ile	Gly	Asp	Trp	Cys	Val	Ser	Arg	Gln	Leu	Trp	Trp	Gly
		85					90						95		
His	Gln	Ile	Pro	Ala	Tyr	Leu	Val	Xaa	Xaa	Gly	Pro	Cys	Ala	Xaa	Gly
		100					105					110			
Glu	Glu	Xaa	Thr	Cys	Trp	Val	Val	Gly	Arg	Ser	Gly	Ala	Glu	Ala	Arg

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Pro Phe Ser Ala Leu Gly Trp Pro Gln Glu Thr Pro Asp Leu Ala Arg
165                      170                      175
Phe Tyr Pro Leu Ser Leu Leu Glu Thr Gly Ser Asp Leu Leu Phe
180                      185                      190
Trp Val Gly Arg Met Val Met Leu Gly Thr Gln Leu Thr Gly Gln Leu
195                      200                      205
Pro Phe Ser Lys Val Leu Leu His Pro Met Val Arg Asp Arg Gln Gly
210                      215                      220
Arg Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Pro Arg Asp Ile
225                      230                      235
Ile Ser Gly Val Glu Met Gln Leu Leu Gln Glu Lys Leu Arg Ser Gly
245                      250                      255
Asn Leu Asp Pro Ala Glu Leu Ala Ile Val Ala Ala Ala Gln Lys Lys
260                      265                      270
Asp Phe Pro His Gly Ile Pro Glu Cys Gly Thr Asp Ala Leu Arg Phe
275                      280                      285
Thr Leu Cys Ser His Gly Val Gln Ala Gly Asp Leu His Leu Ser Val
290                      295                      300
Ser Glu Val Gln Ser Cys Arg His Phe Cys Asn Lys Ile Trp Asn Ala
305                      310                      315
Leu Arg Phe Ile Leu Asn Ala Leu Gly Glu Lys Phe Val Pro Gln Pro
325                      330                      335
Ala Glu Glu Leu Ser Pro Ser Ser Pro Met Asp Ala Trp Ile Leu Ser
340                      345                      350
Arg Leu Ala Leu Ala Ala Gln Glu Cys Glu Arg Gly Phe Leu Thr Arg
355                      360                      365
Glu Leu Ser Leu Val Thr His Ala Leu His His Phe Trp Leu His Asn
370                      375                      380
Leu Cys Asp Val Tyr Leu Glu Ala Val Lys Pro Val Leu Trp His Ser
385                      390                      395
Pro Arg Pro Leu Gly Pro Pro Gln Val Leu Phe Ser Cys Ala Asp Leu
405                      410                      415
Gly Leu Arg Leu Leu Ala Pro Leu Met Pro Phe Leu Ala Glu Glu Leu
420                      425                      430
Trp Gln Arg Leu Pro Pro Arg Pro Gly Cys Pro Pro Ala Pro Ser Ile
435                      440                      445
Ser Val Ala Pro Tyr Pro Ser Ala Cys Ser Leu Glu His Trp Arg Gln
450                      455                      460
Pro Glu Leu Glu Arg Arg Phe Ser Arg Val Gln Glu Val Val Gln Val
465                      470                      475
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485                      490                      495
Val Leu Leu Gln Ser Ser Glu Pro Gly Asp Gln Gly Leu Phe Glu Ala
500                      505                      510
Phe Leu Glu Pro Leu Gly Thr Leu Gly Tyr Cys Gly Ala Val Gly Leu
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Ser Asp Thr Ala Gln Val Tyr Met Glu Leu Gln Gly Leu Val Asp Pro

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Gln Leu Asp Ser	Leu Thr Ala Arg Thr	Pro Ser Glu Gly Glu Ala Gly				
	580		585		590	
Thr Gln Arg Gln Gln	Lys Leu Ser Ser	Leu Gln Leu Glu Leu Ser Lys				
	595		600		605	
Leu Asp Lys Ala Ala	Ser His Leu Arg	Gln Leu Met Asp Glu Pro Pro				
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<210> 6099

<211> 3957

<212> DNA

<213> Homo sapiens

<400> 6099

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 aagaagagccc taaaaagctg ttgacttatc tgcgcttggt ccaactctta tgcccccaac
 3660
 ctgcccctacc accaccagc gctcagcctg atgtgtttac atggtactgt atgtatggga
 3720
 gagcagactg caccgccag caacatcaga tgaagccag tgagcctact aaccgtgcca
 3780
 tcttgcaaac tacactttaa aaaaaactca ttgctttgta ttgtagtaac caatatgtgc
 3840
 agtatacgtt gaatgtatat gaacatactt tcctatttct gttctttgaa aatgtcagaa
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 3957

<210> 6100

<211> 1102

<212> PRT

<213> Homo sapiens

<400> 6100

Gly Ala Ala Gly Ala Gly Thr Gly Gly Ala Gly Pro Ala Gly Arg Leu
 1 5 10 15
 Leu Pro Pro Pro Ala Pro Gly Ser Pro Ala Ala Pro Ala Ala Val Ser
 20 25 30
 Pro Ala Ala Gly Gln Pro Arg Pro Pro Ala Pro Ala Ser Arg Gly Pro

[illegible]

465 470 475 480
 Leu Leu Asn Gly Met Gly Pro Leu Gly Arg Ala Ser Asp Gly Gly
 485 490 495
 Ala Asn Ile Gln Leu His Ala Gln Gln Leu Leu Lys Arg Pro Arg Gly
 500 505 510
 Pro Ser Pro Leu Val Thr Met Thr Pro Ala Val Pro Ala Val Thr Pro
 515 520 525
 Val Asp Glu Glu Ser Ser Asp Gly Glu Pro Asp Gln Glu Ala Val Gln
 530 535 540
 Ser Ser Thr Tyr Lys Asp Ser Asn Thr Leu His Leu Pro Thr Glu Arg
 545 550 555 560
 Phe Ser Pro Val Arg Arg Phe Ser Asp Gly Ala Ala Ser Ile Gln Ala
 565 570 575
 Phe Lys Ala His Leu Glu Lys Met Gly Asn Asn Ser Ser Ile Lys Gln
 580 585 590
 Leu Gln Gln Glu Cys Glu Gln Leu Gln Lys Met Tyr Gly Gly Gln Ile
 595 600 605
 Asp Glu Arg Thr Leu Glu Lys Thr Gln Gln Gln His Met Leu Tyr Gln
 610 615 620
 Gln Glu Gln His His Gln Ile Leu Gln Gln Gln Ile Gln Asp Ser Ile
 630 635 640
 Cys Pro Pro Gln Pro Ser Pro Pro Leu Gln Ala Ala Cys Glu Asn Gln
 645 650 655
 Pro Ala Leu Leu Thr His Gln Leu Gln Arg Leu Arg Ile Gln Pro Ser
 660 665 670
 Ser Pro Pro Asn His Pro Asn Asn His Leu Phe Arg Gln Pro Ser
 675 680 685
 Asn Ser Pro Pro Pro Met Ser Ser Ala Met Ile Gln Pro His Gly Ala
 690 695 700
 Ala Ser Ser Ser Gln Phe Gln Gly Leu Pro Ser Arg Ser Ala Ile Phe
 705 710 715 720
 Gln Gln Gln Pro Glu Asn Cys Ser Ser Pro Pro Asn Val Ala Leu Thr
 725 730 735
 Cys Leu Gly Met Gln Gln Pro Ala Gln Ser Gln Gln Val Thr Ile Gln
 740 745 750
 Val Gln Glu Pro Val Asp Met Leu Ser Asn Met Pro Gly Thr Ala Ala
 755 760 765
 Gly Ser Ser Gly Arg Gly Ile Ser Ile Ser Pro Ser Ala Gly Gln Met
 770 775 780
 Gln Met Gln His Arg Thr Asn Leu Met Ala Thr Leu Ser Tyr Gly His
 785 790 795 800
 Arg Pro Leu Ser Lys Gln Leu Ser Ala Asp Ser Ala Glu Ala His Ser
 805 810 815
 Leu Asn Val Asn Arg Phe Ser Pro Ala Asn Tyr Asp Gln Ala His Leu
 820 825 830
 His Pro His Leu Phe Ser Asp Gln Ser Arg Gly Ser Pro Ser Ser Tyr
 835 840 845
 Ser Pro Ser Thr Gly Val Gly Phe Ser Pro Thr Gln Ala Leu Lys Val
 850 855 860
 Pro Pro Leu Asp Gln Phe Pro Thr Phe Pro Pro Ser Ala His Gln Gln
 865 870 875 880
 Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro
 885 890 895
 Thr Pro Pro Asp Tyr Thr Arg His Gln Gln Val Pro His Ile Leu Gln

900 905 910
 Gly Leu Leu Ser Pro Arg His Ser Leu Thr Gly His Ser Asp Ile Arg
 915 920 925
 Leu Pro Pro Thr Glu Phe Ala Gln Leu Ile Lys Arg Gln Gln Gln Gln
 930 935 940
 Arg Gln Gln Gln Gln Gln Gln Gln Gln Glu Tyr Gln Glu Leu
 945 950 955 960
 Phe Arg His Met Asn Gln Gly Asp Ala Gly Ser Leu Ala Pro Ser Leu
 965 970 975
 Gly Gly Gln Ser Met Thr Glu Arg Gln Ala Leu Ser Tyr Gln Asn Ala
 980 985 990
 Asp Ser Tyr His His Thr Ile Gln Asn Ser Asp Asp Ala Tyr Val Gln
 995 1000 1005
 Leu Asp Asn Leu Pro Gly Met Ser Leu Val Ala Gly Lys Ala Leu Ser
 1010 1015 1020
 Ser Ala Arg Met Ser Asp Ala Val Leu Ser Gln Ser Ser Leu Met Gly
 1025 1030 1035 1040
 Ser Gln Gln Phe Gln Asp Gly Glu Asn Glu Glu Cys Gly Ala Ser Leu
 1045 1050 1055
 Gly Gly His Glu His Pro Asp Leu Ser Asp Gly Ser Gln His Leu Asn
 1060 1065 1070
 Ser Ser Cys Tyr Pro Ser Thr Cys Ile Thr Asp Ile Leu Leu Ser Tyr
 1075 1080 1085
 Lys His Pro Glu Val Ser Phe Ser Met Glu Gln Ala Gly Val
 1090 1095 1100

<210> 6101

<211> 1447

<212> DNA

<213> Homo sapiens

<400> 6101

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 120
 catctagaaa tatactccgt gatctttctt gatggccaga ctgtgtataaa ttcatacagt
 180
 gtttactaca gggatcccca aatattgtta gttgaatgaa caaacacaca tttcaaggag
 240
 ggcactacag tgagtagatg aacagttttc tgataggaga ttgtacaagt aatgttttca
 300
 ccagtgattt ttaggcacgc agattcagat taatgcgctg ggactgaatg caaatagtaa
 360
 aattacaaat ataaagtaaa aatttgaac ctttgccaca gagaggaata ataaattgat
 420
 ttaataattt gaaagaactg taagggttag gttttgttct tatttttagt gcgactgaga
 480
 ttggagtctg tttgtagaca tatctgaaaa aagtgaaggg ggagatggaa gatggtaaat
 540
 gccaggaaa agatggaagg ataatcagt gtaataaaaa ggagcacttc tttttcgcca
 600
 acagaagtaa aggtaaaagt taagtgtctg agttaacgaa tggattgttg acctctgggg
 660

aggggtgctcc catcagctca gctttgtgac gacctaagaa tatcccttcc acacctttcc
 720
 tgatccaatc gttctggctg cataaaacca cctaaatcaa tcaactgtta cacttccctt
 780
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 840
 taaaacaaca agattgtgc tacaccaaga aaggatttta aaaaggcctg ttcacaagct
 900
 aagtgagggc cagaggaaag gtgttcgttt aaactgaaat tcgagctgcg ataacacctc
 960
 ctaatgcaat caaacgctgt tgcagcacac ttcttaggag atcgggttca acggcagggg
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 1080
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 1200
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 1260
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 1320
 acttcggtta cgtccctttg tgaaggcagg cccttcgcgg ctcccagat cagtccagcc
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 1440
 agccgcc
 1447

<210> 6102

<211> 123

<212> PRT

<213> Homo sapiens

<400> 6102

Met Ala Leu Asn Asn Val Ser Leu Ser Ser Gly Asp Gln Arg Ser Arg
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 Val Ala Tyr Arg Ser Ser His Gly Asp Leu Arg Pro Arg Ala Ser Ala
 20 25 30
 Leu Ala Met Val Ser Gly Asp Gly Phe Leu Val Ser Arg Pro Glu Ala
 35 40 45
 Ile His Leu Gly Pro Arg Gln Ala Val Arg Pro Ser Val Arg Ala Glu
 50 55 60
 Ser Arg Arg Val Asp Gly Gly Gly Arg Ser Pro Arg Glu Pro Asp Gly
 65 70 75 80
 Arg Gly Arg Ser Arg Gln Ala Arg Phe Ser Pro Tyr Pro Ile Pro Ala
 85 90 95
 Val Glu Pro Asp Leu Leu Arg Ser Val Leu Gln Gln Arg Leu Ile Ala
 100 105 110
 Leu Gly Gly Val Ile Ala Ala Arg Ile Ser Val
 115 120

<210> 6103

<211> 309

<212> DNA

<213> Homo sapiens

<400> 6103

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ctatgcttcc ggccagggtg ccacagccac tgatgagaga cagctccagc cacaatggac
120
agaacctatg ccttgatgaa gaagattggg cagtccccag tgagagtctc gaaggagatt
180
gacggcttcg tctgaaccg cctgcagtac gccgtcatca gtgaggcctg gagactgggtg
240
gaggaagaaa tagtatctcc tagcgaccta gacctgggtca tgtcagacgg gctgggcatg
300
cgggtacgag
309

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<210> 6104

<211> 71

<212> PRT

<213> Homo sapiens

<400> 6104

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Glu Thr Ala Pro Ala Thr Met Asp Arg Thr Tyr Ala Leu Met Lys Lys
1           5           10           15
Ile Gly Gln Ser Pro Val Arg Val Leu Lys Glu Ile Asp Gly Phe Val
20           25           30
Leu Asn Gln Leu Gln Tyr Ala Val Ile Ser Glu Ala Trp Arg Leu Val
35           40           45
Glu Glu Glu Ile Val Ser Pro Ser Asp Leu Asp Leu Val Met Ser Asp
50           55           60
Gly Leu Gly Met Arg Tyr Ala
65           70

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<210> 6105

<211> 1846

<212> DNA

<213> Homo sapiens

<400> 6105

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ncaccagcag cagcaggcag ccttactcca cggggagggg gcctcacagc agccgcggca
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cagggggccag aaccggggat gcccccaac cctatgaact caacacagcc atcaactgca
120
gggatgaagt ggtgtctccc ctccatctg ctctgcaggg gtccctcagg ctccctatca
180
gccccctcag ctgcctcagt tatctctgca cccccatctt cctcctcccg acatcgcaaa
240
cgctcgagga cttccagcaa gtccggaggca ggggctaggg gtggaggcca gggttccaag
300
gaaaagggcc gagggaggtg gggaggccgc caccaccacc accaccact gcctgcagca
360
ggcttcaaaa agcaacagcg caagttccag tatgggaatt attgcaaata ctatgggtac
420

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cgcaatcctt cctgtgagga tgggcgcctt cgggtgttga agcctgagtg gtttcggggc
 480
 cgggacgtcc tagatctggg ctgcaatgtg ggccatctga cctgagcat tgcctgcaag
 540
 tggggcccgct cccgcatggg gggcctggat atcgattccc ggctcatcca ttctgcccgc
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 660
 gacccggggg cagaggggtg ggaaggagacc accaccgttc gaaagaggag ctgcttccca
 720
 gcctcgctga ctgccagcgg ggggtcccatc gctgcccccc aagtgccttt ggatggagcg
 780
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 840
 gatgacctgg tggaggccca aacacctgag tatgatgtgg tgctctgcct cagcctcacc
 900
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 960
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 1020
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 1080
 gagcagttca gttcctacct gacatcccca gacgtgggct tctccagcta tgagcttgtg
 1140
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 1200
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 1260
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 1320
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 1680
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 1740
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 1800
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 1846

<210> 6106

<211> 405

<212> PRT

<213> Homo sapiens

<400> 6106

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Ala Ala Ala Ala Gln Gly Pro Glu Pro Gly Met Pro Pro Asn Pro Met
          20          25          30
Asn Ser Thr Gln Pro Ser Thr Ala Gly Met Lys Trp Cys Leu Pro Phe
          35          40          45
His Leu Leu Cys Arg Gly Pro Ser Gly Ser Leu Ser Ala Pro Pro Ala
          50          55          60
Ala Ser Val Ile Ser Ala Pro Pro Ser Ser Ser Arg His Arg Lys
          65          70          75          80
Arg Arg Arg Thr Ser Ser Lys Ser Glu Ala Gly Ala Arg Gly Gly Gly
          85          90          95
Gln Gly Ser Lys Glu Lys Gly Arg Gly Ser Trp Gly Gly Arg His His
          100          105          110
His His His Pro Leu Pro Ala Ala Gly Phe Lys Lys Gln Gln Arg Lys
          115          120          125
Phe Gln Tyr Gly Asn Tyr Cys Lys Tyr Tyr Gly Tyr Arg Asn Pro Ser
          130          135          140
Cys Glu Asp Gly Arg Leu Arg Val Leu Lys Pro Glu Trp Phe Arg Gly
          145          150          155          160
Arg Asp Val Leu Asp Leu Gly Cys Asn Val Gly His Leu Thr Leu Ser
          165          170          175
Ile Ala Cys Lys Trp Gly Pro Ser Arg Met Val Gly Leu Asp Ile Asp
          180          185          190
Ser Arg Leu Ile His Ser Ala Arg Gln Asn Ile Arg His Tyr Leu Ser
          195          200          205
Glu Glu Leu Arg Leu Pro Pro Gln Thr Leu Glu Gly Asp Pro Gly Ala
          210          215          220
Glu Gly Glu Glu Gly Thr Thr Thr Val Arg Lys Arg Ser Cys Phe Pro
          225          230          235          240
Ala Ser Leu Thr Ala Ser Arg Gly Pro Ile Ala Ala Pro Gln Val Pro
          245          250          255
Leu Asp Gly Ala Asp Thr Ser Val Phe Pro Asn Asn Val Val Phe Val
          260          265          270
Thr Gly Asn Tyr Val Leu Asp Arg Asp Asp Leu Val Glu Ala Gln Thr
          275          280          285
Pro Glu Tyr Asp Val Val Leu Cys Leu Ser Leu Thr Lys Trp Val His
          290          295          300
Leu Asn Trp Gly Asp Glu Gly Leu Lys Arg Met Phe Arg Arg Ile Tyr
          305          310          315          320
Arg His Leu Arg Pro Gly Gly Ile Leu Val Leu Glu Pro Gln Pro Trp
          325          330          335
Ser Ser Tyr Gly Lys Arg Lys Thr Leu Thr Glu Thr Ile Tyr Lys Asn
          340          345          350
Tyr Tyr Arg Ile Gln Leu Lys Pro Glu Gln Phe Ser Ser Tyr Leu Thr
          355          360          365
Ser Pro Asp Val Gly Phe Ser Ser Tyr Glu Leu Val Ala Thr Pro His
          370          375          380
Asn Thr Ser Lys Gly Phe Gln Arg Pro Val Tyr Leu Phe His Lys Ala
          385          390          395          400
Arg Ser Pro Ser His
          405

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<210> 6107

<211> 896

<212> DNA

<213> Homo sapiens

<400> 6107

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120
tggatgtcaa ggagatgctc aaggctgggc tcaacaccac ccccgactcc agcctcccca
180
gtggaggtctc cccgaccttc acccgctctt tcagccttct catcattacc ctctgatgga
240
tggggggagt cagttggctc ggggttgctt tggcctgcca ccagggtgtc cacatgcccc
300
aggtggagga cggatgtgtc gcctgctgac acaatagcgc ccaggagctg gttgctaccg
360
ctgtctgcta cgtaggtaga gagccaagct aggaccaagg ctagaatcag caccaccaca
420
cctgccacca ccatcacctc attaccacaca ccctcaatga gggtgacatc agtgaccccc
480
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540
ggcagccctt cggttcgggt gggcccagac ccagtcctca ccgcagggga ataggaccat
600
ccaaaagcgg aaccttcgcc tcagaaaaag ggtgcgggac ccctcctcac cgtgcgggtc
660
cggtacggac agggtagatc acaggctgag ggacagagca aagaccctg aggccggaca
720
cctgggggtc tgccgggccc ctccccacga gagtccctg tgtctgtgcc aatcgttttc
780
gtctttcttt gccgcagttt cttttctctg aaatcatggt taatgacatt aaccttctta
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896

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<210> 6108

<211> 124

<212> PRT

<213> Homo sapiens

<400> 6108

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Xaa Asn Leu Thr Arg Thr Val Met Arg Pro Gly Leu Gly Gly Arg Gln
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Gly Leu Ser Ser Asp Leu Arg Gly Ala Ser Gly Leu Leu Leu Pro Ala
20     25     30
Pro Ala Cys Leu Leu Gly Arg Pro Trp Met Ser Arg Arg Cys Ser Arg
35     40     45
Leu Gly Ser Thr Pro Pro Pro Ala Pro Ala Ser Pro Val Glu Ser Pro
50     55     60
Arg Pro Ser Pro Ala Ser Ser Ala Phe Ser Ser Leu Pro Ser Asp Gly
65     70     75     80
Trp Gly Ser Ser Val Gly Ser Gly Leu Pro Trp Pro Ala Thr Arg Trp

```

```

      85              90              95
Ser Thr Cys Pro Arg Trp Arg Thr Asp Val Ser Pro Ala Asp Thr Ile
      100              105              110
Ala Pro Arg Ser Trp Leu Leu Pro Leu Ser Ala Thr
      115              120

<210> 6109
<211> 2087
<212> DNA
<213> Homo sapiens

<400> 6109
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120
ggtagcttca gagcctccag tgcctgtggg gctggagggt aagttggggg ccctgggtgt
180
gctgctgggt tcaccctcct ctgcagcctg gtgcccatct gtgtgctgag ccggccagga
240
gctaaccatg aaggctcagc ttcccgcagc aaagccctga gcctagtaag ctgtttcgcg
300
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360
gatgaggccc tggcagcctt gcacgtgacg ctccagttcc cactgcaaga gttcatcctg
420
gccatgggct tcttctcgtt cctggtgatg gagcagatca cactggctta caaggagcag
480
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540
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600
gccttgctg cctgtgtact ggtgttctcc ctggccctcc actccgtggt cgaggggctg
660
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720
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780
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840
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900
ggcatggcag ctggcacctt tctctatata acctttctgg aaatcctgcc ccaggagctg
960
gccagttctg agcaaaaggat cctcaaggct attctgctcc tagcaggctt tgcctgctc
1020
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1080
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1140
agggaaatac tgaggaccaa aaagtctctc gggagctaaa gatagagcct ttggggctat
1200
ctgactaatg agagggaagt gggcagacaa gaggctggcc ccagtcccaa ggaacaagag
1260

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atgggtcaagt cgctagagac atatcagggg acattaggat tggggaagac acttgactgc
 1320
 tagaatcaga ggttggacac tatacataag gacaggctca catggggaggc tggaggtggg
 1380
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 1620
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 1680
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 1740
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 1800
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 1860
 ctgccc aaac atttttttaa atacaccga ggagcccaag ggggaagggc aatgcctacc
 1920
 cccagcgtta tttttgggga gggagggtg tgcataggga catattcttt agaactatt
 1980
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 2040
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 2087

<210> 6110

<211> 323

<212> PRT

<213> Homo sapiens

<400> 6110

Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Gly
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 Ser Phe Arg Ala Ser Ser Ala Cys Gly Ala Gly Gly Glu Val Gly Gly
 20 25 30
 Pro Gly Ala Ala Ala Gly Leu Thr Leu Leu Cys Ser Leu Val Pro Ile
 35 40 45
 Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg
 50 55 60
 Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu
 65 70 75 80
 Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp
 85 90 95
 Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
 100 105 110
 Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
 115 120 125
 Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
 130 135 140
 Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His Asp

```

145          150          155          160
Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala
165          170          175
Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe
180          185          190
Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu
195          200          205
Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu
210          215          220
Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala Gly
225          230          235          240
Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly
245          250          255
Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln Ser
260          265          270
Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu
275          280          285
Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys
290          295          300
Val Ile Leu Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu Phe
305          310          315          320
Ile Gln Ile

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<210> 6111

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 6111

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120
taacttgcca tttgttcatt cttgtctttg ttgtttttca tataatagaa atcccccaa
180
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240
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300
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420
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720

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 840
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 1140
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 1200
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 1560
 gtggttggag actttattta ccaagatggt tactcttccct ttcccccttc attttgagga
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 1680
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 1706

<210> 6112

<211> 110

<212> PRT

<213> Homo sapiens

<400> 6112

Met	Ser	Leu	Phe	Cys	Phe	Val	Leu	Phe	Leu	Arg	Trp	Ser	Phe	Pro	Leu
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Val	Ala	Gln	Ala	Gly	Val	Xaa	Trp	His	Ser	Leu	Gly	Ser	Leu	Gln	Pro
		20					25						30		
Pro	Leu	Pro	Gly	Phe	Lys	Gln	Phe	Ser	Cys	Arg	Ser	Leu	Pro	Ser	Ser
		35				40						45			
Trp	Asp	Tyr	Arg	His	Ala	Pro	Pro	Arg	Gln	Ala	Asn	Phe	Cys	Ile	Phe
	50				55					60					
Ser	Arg	Asp	Gly	Val	Ser	Pro	Cys	Trp	Pro	Gly	Trp	Ser	Gln	Thr	Pro
	65				70				75				80		
Asp	Leu	Arg	Arg	Ser	Thr	His	Leu	Ser	Val	Pro	Lys	Cys	Trp	Asp	Tyr
			85				90						95		
Arg	Arg	Glu	Pro	Pro	His	Leu	Ala	Tyr	Glu	Trp	Ser	Phe	Asn		

100

105

110

<210> 6113
 <211> 1095
 <212> DNA
 <213> Homo sapiens

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 acgtggcgcc agcggaggca ggttgatgtg tttgtgcttc cttctacagc caatatgaaa
 180
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 240
 agccaccacg acgctcttct acggctacgg ctttgtctct gctggatatgg ggggtgggagc
 300
 atacgctgag gccttgcccc tatttcctgg tagaaccgag agttggaagt ccctacggcg
 360
 atcatgttaa ccgcgcgggc tcattctgcg gaacgaagcc gggcagaggg tggggaagac
 420
 taggctagat ttctgtaagg aagcagcgtc tgagccaggt ttgaggccca atattttctt
 480
 tccgtggcca cgtgcagact ggcccagggt agagctgaga atcgctccc agactcagtg
 540
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 600
 atacgctgtt gtgtatgac ccattcta attgtagggg taatgacagg gaattttgac
 660
 tccattctgg atctactgaa tttaattctc tgggatttga aagtagcacg tatgtttgca
 720
 ttaggcattt cgcattagac ttaacgttag gtttggtagc caataacaca agaaaaggat
 780
 ataactccat agtgcgttaa ccgagaacta atcatttggg ttaacagatt tgtgatgtgt
 840
 ttcttttagt agttaagaa agcaagtaaa cgcattgacct gccataagcg gtataaaaaa
 900
 caaaaaaagg ttcgagaaca tcatcgaaaa ttaagaaagg agggtaaaaa gcggggtcac
 960
 aagaagcccta ggaaagaccc aggagttcca aacagtgtc ctttaagga ggctcttctt
 1020
 gaggaagctg agctaaggaa acagaggcct gaagaactaa aacagcagca gaaacttgac
 1080
 aggcagaagg aacta
 1095

<210> 6114
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 6114
 Met Cys Phe Phe Val Glu Leu Lys Lys Ala Ser Lys Arg Met Thr Cys


```

      1           5           10           15
His Lys Arg Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys
      20           25           30
Leu Arg Lys Glu Ala Lys Lys Arg Gly His Lys Lys Pro Arg Lys Asp
      35           40           45
Pro Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Glu Glu
      50           55           60
Ala Glu Leu Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys
      65           70           75           80
Leu Asp Arg Gln Lys Glu Leu
      85

```

<210> 6115

<211> 411

<212> DNA

<213> Homo sapiens

<400> 6115

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120
actgtggcgt cccagggcgg tggagggagc aacttcgggg gcacgtcctc gtaaatcccc
180
tggaggacac tgaccctgta cccaccctc gagccagaa gtcggttctt ttgggggaac
240
tgagggcgca gagcactcgc cccctgact tgcaaaagtg cgctctttac ttggcctccg
300
ggattctgcg catggcgtgt ctccaggctg ctgatgggca agacagatgt gccaggtcca
360
gaatgaactt gagaagagtt tgtagccatt cctgaatcac cttatactag t
411

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<210> 6116

<211> 129

<212> PRT

<213> Homo sapiens

<400> 6116

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Met Ala Thr Asn Ser Ser Gln Val His Ser Gly Pro Gly Thr Ser Val
      1           5           10           15
Leu Pro Ile Ser Ser Leu Glu Thr Arg His Ala Gln Asn Pro Gly Gly
      20           25           30
Gln Val Lys Thr Pro Thr Leu Gln Val Arg Gly Ala Ser Ala Leu Ala
      35           40           45
Pro Gln Phe Pro Gln Arg Asn Arg Leu Leu Ala Ser Arg Val Gly Tyr
      50           55           60
Arg Val Ser Val Leu His Gly Ile Tyr Glu Asp Val Pro Pro Lys Leu
      65           70           75           80
Leu Pro Pro Pro Pro Trp Asp Ala Thr Val Arg Pro Ala Asp Glu Phe
      85           90           95
Leu Pro Gln Arg Pro Arg Glu Gly Gly Leu Arg Ala Ala Ala Ala Ala
      100          105          110
Thr Gly Gly Glu Ala Ser Ala Gly Asn Leu Gly Pro Gly Gly Ala Arg

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	115	120	125
Arg			
<210> 6117			
<211> 962			
<212> DNA			
<213> Homo sapiens			
<400> 6117			
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120			
tcgggagcgc acaagatgtt ctccctcaag aagtggaaac cggtggccat gtggagctgg			
180			
gacgtggagt gcgatactg cgccatctgc agggctccagg tgatggatgc ctgtcttaga			
240			
tgtcaagctg aaacaaaca agaggactgt gttgtggtct ggggagaatg taatcattcc			
300			
tccacaact gctgcatgtc cctgtgggtg aaacagaaca atcgtctgcc tctctgccag			
360			
caggactggg tggccaag aatcggaac tgagagtgg tagaaggctt cttagcgcag			
420			
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480			
gggatgaatt cttcaatag gagccgatg atctgtggtc ctttgggact catcaaagcc			
540			
ttggtttagc attttgtcag ttttatcttc agaaattctc tgcgattaag aagataattt			
600			
attaaagggt gtccttcta cctctgtggt gtgtgtcgcg cacacagctt agaagtgcta			
660			
taaaaaagg aagagctcca aattgaatca cttttataat ttaccattt ctatacaaca			
720			
ggcagtgaa gcagtttcag agaactttt gcctgcttat ggttgatcag ttaaaaaaga			
780			
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840			
aatacgattt ttggcaggg agagggaac gtccatgaaa tctttatgtg atataaggat			
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960			
aa			
962			
<210> 6118			
<211> 113			
<212> PRT			
<213> Homo sapiens			
<400> 6118			
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1 5 10 15			
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			

```

                20                25                30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
   35                40                45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
   50                55                60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys
   65                70                75                80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
   85                90                95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
   100                105                110
Lys

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<210> 6119

<211> 375

<212> DNA

<213> Homo sapiens

<400> 6119

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120
tggccccaca gaactcatgc ctgcttgctt taaaccaccc aatgaaaact ccccatggga
180
aacctgcttg gataatactt tggaccoccaa taaatgcttt aatcccacaa gtccctctgtc
240
tctgectctc tcttgcccct acccactggt tgagcatgtg tgtcccaaac ggccttgcaa
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ggtgtgtgac cctgttcttt ctgggctctg tcaaggaate aaactgcttc tgttatgtga
360
tgtgtcatgt tgtgc
375

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<210> 6120

<211> 118

<212> PRT

<213> Homo sapiens

<400> 6120

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Met Gly Lys Leu Asp Thr Ala Pro Trp Thr Cys Pro Thr Asp Pro His
1      5      10      15
Thr Pro His Gly Leu His Gly Asn Ile Thr Val Thr Ile Ser Gln Ser
20     25     30
Gln Arg Gly Pro Thr Glu Leu Met Pro Ala Cys Phe Lys Pro Thr Asn
35     40     45
Glu Asn Ser Pro Trp Glu Thr Cys Leu Asp Asn Thr Leu Asp Pro Asn
50     55     60
Lys Cys Phe Asn Pro Thr Ser Pro Leu Ser Leu Pro Leu Ser Cys Pro
65     70     75     80
Tyr Pro Leu Val Glu His Val Cys Pro Lys Arg Pro Cys Lys Val Cys
85     90     95
Cys Pro Val Leu Ser Gly Leu Cys Gln Gly Ile Lys Leu Leu Leu Leu

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100
Cys Asp Val Ser Cys Cys
115

105

110

<210> 6121
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 6121
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ttgtaaacat tgatttgaat gatgacaaca ttgtcagtggt ttgtaaactg ggaacagaca
120
aagaaacact ctccttctgc cacatttgtt ttgagctaaa tattgagggg gtaccaaaagt
180
ctgatctctt gcacacaaaa tcattaaggg gccataaaga ctgctttgaa aaataccatt
240
taattgcaaa ccagggttgt cctcgatcta agctttcaaa aagtacttat gaagaagtta
300
aaaccatttt gagtaagaag ataaactgga ttgtgcagta tgcacaaaat aaggatctgg
360
attcagattc tgaatgttct aaaaagcccc agcatcatct gtttaatttc aggcataagc
420
cagaagaaaa attactccca cagtttgagt ccgaagtacc aaaaatttct gcaaaaatgga
480
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540
atacagactt tggactttct atgttacaag attcaggtgc cactttatgt cgtaacagtg
600
tattgtggcc tcatagtcac aaccaggcac agaaaaaga agagacaatc tctagtccag
660
aggctaattg ccagaccag catccacatt acagcagaga ggaataagt ttggaagat
720
taactcacca agtgcaagaa aaagattctt tggcctcaca gctccatgtc cgccacgttg
780
ccatgaaca gcttctgaag aactgttcta agttaccatg tctgcaagta gggcgaacag
840
gaatgaagtc gcacctacc ataaacaact gacctaaaca gacttacttc gtatgccctg
900
ccctttattg gtctcccaga catgcaaact ttgaagaagt ttgaagaaa ttgtggtccg
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1039

<210> 6122
<211> 221
<212> PRT
<213> Homo sapiens

<400> 6122
Met Asn Glu Glu Glu Gln Phe Val Asn Ile Asp Leu Asn Asp Asp Asn

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1           5           10           15
Ile Cys Ser Val Cys Lys Leu Gly Thr Asp Lys Glu Thr Leu Ser Phe
20
Cys His Ile Cys Phe Glu Leu Asn Ile Glu Gly Val Pro Lys Ser Asp
35
Leu Leu His Thr Lys Ser Leu Arg Gly His Lys Asp Cys Phe Glu Lys
50
Tyr His Leu Ile Ala Asn Gln Gly Cys Pro Arg Ser Lys Leu Ser Lys
65
Ser Thr Tyr Glu Glu Val Lys Thr Ile Leu Ser Lys Lys Ile Asn Trp
85
Ile Val Gln Tyr Ala Gln Asn Lys Asp Leu Asp Ser Asp Ser Glu Cys
100
Ser Lys Lys Pro Gln His His Leu Phe Asn Phe Arg His Lys Pro Glu
115
Glu Lys Leu Leu Pro Gln Phe Glu Ser Gln Val Pro Lys Tyr Ser Ala
130
Lys Trp Ile Asp Gly Ser Ala Gly Gly Ile Ser Asn Cys Thr Gln Arg
145
Ile Leu Glu Gln Arg Glu Asn Thr Asp Phe Gly Leu Ser Met Leu Gln
165
Asp Ser Gly Ala Thr Leu Cys Arg Asn Ser Val Leu Trp Pro His Ser
180
His Asn Gln Ala Gln Lys Lys Glu Glu Thr Ile Ser Ser Pro Glu Ala
195
Asn Val Gln Thr Gln His Pro His Tyr Ser Arg Glu Glu
210
215
220

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<210> 6123

<211> 900

<212> DNA

<213> Homo sapiens

<400> 6123

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120
gcgaacaac aagagaaaaa aaaggaagct gcctctctgcc caaaaccac gtcgaggtcc
180
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300
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360
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420
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480
ctctgggaat cctctgggag gaccttgat gactttctga ctttccccag gcacgttttc
540
agggtcatga tctgcccc cccgggggga tctactgtcc tccagtcac accctctcc
600

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ccgcaccgcc ttcttctgtgt cttctcttct tcccagaatg aagacatcac cgagccgcag
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 agcatcctgg cggtctgcaga gaaggctggt atgtctgcag aacaagccca gggacttctg
 720
 gaaaagatcg caacgccaac ggtgaagaac cagctcaagg agaccactga ggcagcctgc
 780
 agatacggag cctttgggct gcccatcacc gtggcccatg tggatggcca aaccacatg
 840
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 900

<210> 6124

<211> 300

<212> PRT

<213> Homo sapiens

<400> 6124

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 20 25 30
 Cys Thr Pro Ala Trp Ala Thr Arg Ala Lys Gln Gln Glu Lys Lys Lys
 35 40 45
 Glu Ala Ala Leu Cys Pro Lys Pro Thr Ser Arg Ser Pro Asn Leu Gly
 50 55 60
 Pro Leu Gly Leu Phe Ser Leu Ser Val Pro Asn Leu Leu Ala Gly
 65 70 75 80
 Asn Lys Pro Pro Gly Leu Leu Pro Arg Lys Gly Leu Tyr Met Ala Asn
 85 90 95
 Asp Leu Lys Leu Leu Arg His His Leu Gln Ile Pro Ile His Phe Pro
 100 105 110
 Lys Asp Phe Leu Ser Val Met Leu Glu Lys Gly Ser Leu Ser Ala Met
 115 120 125
 Arg Phe Leu Thr Ala Val Asn Leu Glu His Pro Glu Met Leu Glu Lys
 130 135 140
 Ala Ser Arg Glu Leu Trp Met Arg Val Trp Ser Arg Val Ser Val Gly
 145 150 155 160
 Leu Trp Glu Ser Ser Gly Arg Thr Leu Asp Asp Phe Leu Thr Phe Pro
 165 170 175
 Arg His Val Phe Arg Val Met Ile Leu Pro Pro Pro Gly Gly Ser Thr
 180 185 190
 Val Leu Pro Val Thr Pro Leu Ser Pro His Arg Leu Pro Ala Val Phe
 195 200 205
 Ser Ser Ser Gln Asn Glu Asp Ile Thr Glu Pro Gln Ser Ile Leu Ala
 210 215 220
 Ala Ala Glu Lys Ala Gly Met Ser Ala Glu Gln Ala Gln Gly Leu Leu
 225 230 235 240
 Glu Lys Ile Ala Thr Pro Lys Val Lys Asn Gln Leu Lys Glu Thr Thr
 245 250 255
 Glu Ala Ala Cys Arg Tyr Gly Ala Phe Gly Leu Pro Ile Thr Val Ala
 260 265 270
 His Val Asp Gly Gln Thr His Met Leu Phe Gly Ser Asp Arg Met Glu
 275 280 285
 Leu Leu Ala His Leu Leu Gly Glu Lys Trp Met Gly

```

290                                295                                300

<210> 6125
<211> 468
<212> DNA
<213> Homo sapiens

<400> 6125
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120
ggagaattga aggggctgca ggagcaaata gcagaaacca aagcccggct tatcacgcag
180
cagcatgac gggccaaga gcagagtgc catgccttga tgctgcgtga gctccagaag
240
ctgtgcgagg aggagaggac ccagcgccag gacttggagc ttaggttaga agagacccga
300
gaagccttgg caggacgagc atatgcagct gaacagatgg aaggatttga actgcagacc
360
aagcagctga cccgtgaggt ggaggagctg aaaagtgaac tgaggccat tcgagatgag
420
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468

<210> 6126
<211> 156
<212> PRT
<213> Homo sapiens

<400> 6126
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Asp Lys Lys Lys Met Lys Gln Asp Leu Glu Asp Ala Ser Asn Lys Ala
20          25          30
Glu Glu Glu Arg Ala Arg Leu Glu Gly Glu Leu Lys Gly Leu Gln Glu
35          40          45
Gln Ile Ala Glu Thr Lys Ala Arg Leu Ile Thr Gln Gln His Asp Arg
50          55          60
Ala Gln Glu Gln Ser Asp His Ala Leu Met Leu Arg Glu Leu Gln Lys
65          70          75          80
Leu Leu Gln Glu Glu Arg Thr Gln Arg Gln Asp Leu Glu Leu Arg Leu
85          90          95
Glu Glu Thr Arg Glu Ala Leu Ala Gly Arg Ala Tyr Ala Ala Glu Gln
100         105         110
Met Glu Gly Phe Glu Leu Gln Thr Lys Gln Leu Thr Arg Glu Val Glu
115         120         125
Glu Leu Lys Ser Glu Leu Gln Ala Ile Arg Asp Glu Lys Asn Gln Pro
130         135         140
Asp Pro Arg Leu Gln Glu Leu Gln Glu Glu Ala Ala
145         150         155

<210> 6127
<211> 1900

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<212> DNA

<213> Homo sapiens

<400> 6127

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 120
 cgggcaagag actccaatat ggtgagggcg gcagcagagc tggccctgag ctgcctgcct
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 240
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 360
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 420
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 480
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 540
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 600
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 660
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 720
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 960
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 1080
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 1140
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 1260
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 1320
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 1380
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<210> 6128

<211> 530

<212> PRT

<213> Homo sapiens

<400> 6128

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Gly Met Met Gln Phe Asn Asp Ile Leu Gln Asn Leu Lys Arg Ser Lys
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<211> 2012

<212> DNA

<213> Homo sapiens

<400> 6129

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<210> 6130

<211> 364

<212> PRT

<213> Homo sapiens

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Ile Ile Ile Trp Arg Phe Ala Gly Asn Phe Glu Arg Thr Val Gly Thr
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<211> 3526

<212> DNA

<213> Homo sapiens

<400> 6131

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<211> 167

<212> PRT

<213> Homo sapiens

<400> 6132

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<212> DNA

<213> Homo sapiens

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<210> 6134

<211> 595

<212> PRT

<213> Homo sapiens

<400> 6134

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 35 40 45
 Arg Gly Leu Val Pro Thr Asp Tyr Val Glu Ile Leu Pro Ser Asp Gly
 50 55 60
 Lys Asp Gln Phe Ser Cys Gly Asn Ser Val Ala Asp Gln Ala Phe Leu
 65 70 75 80
 Asp Ser Leu Ser Ala Ser Thr Ala Gln Ala Ser Ser Ser Ala Ala Ser
 85 90 95
 Asn Asn His Gln Val Gly Ser Gly Asn Asp Pro Trp Ser Ala Trp Ser
 100 105 110
 Ala Ser Lys Ser Gly Asn Trp Glu Ser Ser Glu Gly Trp Gly Ala Gln

5315

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545                550                555                560
Tyr Asp Tyr Asn Ser Val Ile Arg Leu Tyr Leu Glu Gln Gln Val Gln
                    565                570                575
Phe Tyr Glu Thr Ile Ala Glu Lys Leu Arg Gln Ala Leu Ser Arg Phe
                    580                585                590
Pro Val Met
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<210> 6135
<211> 526
<212> DNA
<213> Homo sapiens

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180
gtcccccaag tgcgtcttcc agtagtgaca tgtctctctc agaacctcca cagcctcttg
240
caagaaaaa cttgatggaa tctacatgga tgcagcctga aagattgagc ccacaagttc
300
accattctca accacagcct ttgctggaa cagctggaag tttactctcc catctcttga
360
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420
atcataatat ggcttcaagg ccattaactt ttacacctca accatatgtg acctcaccag
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526

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<210> 6136
<211> 105
<212> PRT
<213> Homo sapiens

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Glu Ser Thr Trp Met Gln Pro Glu Arg Leu Ser Pro Gln Val His His
20          25          30
Ser Gln Pro Gln Pro Phe Ala Gly Thr Ala Gly Ser Leu Leu Ser His
35          40          45
Leu Leu Ser Leu Glu His Val Gly Ile Leu His Lys Asp Phe Glu Ser
50          55          60
Ile Leu Pro Thr Arg Lys Asn His Asn Met Ala Ser Arg Pro Leu Thr
65          70          75          80
Phe Thr Pro Gln Pro Tyr Val Thr Ser Pro Ala Ala Tyr Thr Asp Ala
85          90          95
Leu Val Lys Pro Ser Ala Ser Gln Tyr
100          105

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<210> 6137
<211> 2073
<212> DNA
<213> Homo sapiens

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180
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240
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300
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 1920
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<210> 6138

<211> 550

<212> PRT

<213> Homo sapiens

<400> 6138

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			20					25					30		
Arg	Lys	Glu	Ala	Lys	Lys	Gln	Gly	His	Lys	Lys	Pro	Arg	Lys	Asp	Pro
			35				40					45			
Gly	Val	Pro	Asn	Ser	Ala	Pro	Phe	Lys	Glu	Ala	Leu	Leu	Arg	Glu	Ala
	50					55					60				
Glu	Leu	Arg	Lys	Gln	Arg	Leu	Glu	Glu	Leu	Lys	Gln	Gln	Gln	Lys	Leu
	65				70					75				80	
Asp	Arg	Gln	Lys	Glu	Leu	Glu	Lys	Lys	Arg	Lys	Leu	Glu	Thr	Asn	Pro
				85					90					95	
Asp	Ile	Lys	Xaa	Ile	Lys	Cys	Gly	Thr	Xaa	Met	Glu	Lys	Glu	Phe	Gly
			100					105						110	
Leu	Cys	Lys	Thr	Glu	Asn	Lys	Ala	Lys	Ser	Gly	Lys	Gln	Asn	Ser	Lys
		115					120					125			
Lys	Leu	Tyr	Cys	Gln	Glu	Leu	Lys	Lys	Val	Ile	Glu	Ala	Ser	Asp	Val
	130					135					140				
Val	Leu	Glu	Val	Leu	Asp	Ala	Arg	Asp	Pro	Leu	Gly	Cys	Arg	Cys	Pro
	145				150				155					160	
Gln	Val	Glu	Glu	Ala	Ile	Val	Gln	Ser	Gly	Gln	Lys	Lys	Leu	Val	Leu
				165					170					175	
Ile	Leu	Asn	Lys	Ser	Asp	Leu	Val	Pro	Lys	Glu	Asn	Leu	Glu	Ser	Trp
			180					185					190		
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195                200                205
Thr Lys Pro Lys Asp Lys Gly Lys Ile Thr Lys Arg Val Lys Ala Lys
210                215                220
Lys Asn Ala Ala Pro Phe Arg Ser Glu Val Cys Phe Gly Lys Glu Gly
225                230                235                240
Leu Trp Lys Leu Leu Gly Gly Phe Gln Glu Thr Cys Ser Lys Ala Ile
245                250                255
Arg Val Gly Val Ile Gly Phe Pro Asn Val Gly Lys Ser Ser Ile Ile
260                265                270
Asn Ser Leu Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly
275                280                285
Leu Thr Arg Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile
290                295                300
Ile Asp Ser Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala
305                310                315                320
Leu Ala Leu Arg Ser Pro Ala Ser Ile Glu Val Val Lys Pro Met Glu
325                330                335
Ala Ala Ser Ala Ile Leu Ser Gln Ala Asp Ala Arg Gln Val Val Leu
340                345                350
Lys Tyr Thr Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Val
355                360                365
Leu Ala Gln Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val
370                375                380
Glu Gly Ala Ala Lys Leu Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu
385                390                395                400
Ala Tyr Tyr Cys His Pro Pro Thr Ser Trp Thr Pro Pro Pro Tyr Phe
405                410                415
Asn Glu Ser Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu
420                425                430
Leu Glu Lys Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His
435                440                445
Leu Ala Asn Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile
450                455                460
Ile Glu Glu Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg
465                470                475                480
Lys Gln Glu Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val
485                490                495
Asp Glu Glu Val Asp Glu Asn Ser Ser Gly Met Phe Ala Ala Glu Glu
500                505                510
Thr Gly Glu Ala Leu Ser Glu Glu Thr Thr Ala Gly Glu Gln Ser Thr
515                520                525
Arg Ser Phe Ile Leu Asp Lys Ile Ile Glu Glu Asp Asp Ala Tyr Asp
530                535                540
Phe Ser Thr Asp Tyr Val
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<210> 6139

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 6139

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120
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<210> 6140

<211> 381

<212> PRT

<213> Homo sapiens

<400> 6140

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			20				25					30			
Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	Gln	Ala	Glu
			35				40					45			
Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	Ala	His	Ile
			50				55				60				
Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	Val	Lys	Leu
			65				70				75			80	
Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Xaa	Phe	Gly	Pro	Xaa
			85					90					95		
Cys	Lys	Thr	Arg	Asp	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile
			100				105					110			
Arg	Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	Lys	Gly
			115				120				125				
Leu	Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser
			130				135				140				
Ser	Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu
			145				150				155			160	
Thr	Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser
			165				170					175			
Lys	Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp
			180				185					190			
Asp	Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val
			195				200					205			
Leu	Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala

210		215		220
Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg				
225		230	235	240
Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu				
	245		250	255
Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly				
	260	265	270	
Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met				
	275	280	285	
Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys				
	290	295	300	
Gly Ser Cys Ala Gly Cys Asp Leu Leu Phe Ser Gln Glu Thr Val Met				
305		310	315	320
Lys Phe Val Pro Arg Tyr Ser Leu Val Leu Glu Leu Ser Asp Ser Gly				
	325	330	335	
Ala Phe Arg Arg Ser Leu His Asp Pro Asp Gly Leu Val Ala Thr Tyr				
	340	345	350	
Ile Ser Glu Val His Glu His Asp Gly His Leu Tyr Leu Gly Ser Phe				
	355	360	365	
Arg Ser Pro Phe Leu Cys Arg Leu Ser Leu Gln Ala Val				
	370	375	380	

<210> 6141

<211> 5651

<212> DNA

<213> Homo sapiens

<400> 6141

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<210> 6142

<211> 513

<212> PRT

<213> Homo sapiens

<400> 6142

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 35          40          45
Ser Pro Gly Arg Thr Glu Gln Pro Pro Ser Pro Gln Ser Ser Ser
 50          55          60
Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
 65          70          75          80
Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
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His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu
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Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
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Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
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Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
 145          150          155          160
Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro
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Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
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Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
 195          200          205
Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
 210          215          220
Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
 225          230          235          240
Asn Leu Ser Gln Ile Pro Glu Gly Gly Val Val Thr Ala Ala Glu Phe
 245          250          255
Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
 260          265          270
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 275          280          285
Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
 290          295          300
Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
 305          310          315          320
Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
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Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
 340          345          350
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<210> 6144

<211> 141

<212> PRT

<213> Homo sapiens

<400> 6144

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			20					25					30		
Ser	Gly	Ser	Arg	Gln	Ala	Trp	Val	His	Pro	Pro	Ala	Gln	Pro	Arg	Thr
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Ala	Gly	Pro	Glu	Leu	Gly	Gly	Gln	Gly	Ile	Pro	Ser	Pro	Gly	Cys	Ala
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Cys	Gln	Arg	Gly	Glu	Ala	Gly	Gly	Gly	Asn	Ala	Val	Leu	Pro	Gln	
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Glu	Ser	Val	Leu	Arg	Ala	Ser	Ala	Val	Gly	Arg	Gly	Ala	Glu	Gly	Pro
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			100					105					110		
Pro	Gly	Glu	Lys	Gly	Cys	Trp	Cys	Arg	Thr	Ala	Ser	Gly	Ala	Gly	Pro
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<210> 6145

<211> 766

<212> DNA

<213> Homo sapiens

<400> 6145

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<210> 6146

<211> 100

<212> PRT

<213> Homo sapiens

<400> 6146

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 35 40 45
 Gln Pro Pro Pro Val Lys Cys Gln Glu Thr Cys Ala Pro Lys Thr Lys
 50 55 60
 Asp Pro Cys Ala Pro Gln Val Lys Lys Gln Cys Pro Pro Lys Asp Thr
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<210> 6147

<211> 1852

<212> DNA

<213> Homo sapiens

<400> 6147

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<210> 6148

<211> 410

<212> PRT

<213> Homo sapiens

<400> 6148

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Gly Trp Ile Lys Lys Gly Thr Asp Val Asp Val Gly Pro Phe Leu Asn
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Ser Leu Val Gln Glu Gly Glu Trp Glu Arg Ala Ala Val Ala Leu
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Phe Asn Leu Asp Ile Arg Arg Ala Ile Gln Ile Leu Asn Glu Gly Ala
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Ser Ser Glu Lys Gly Asp Leu Asn Leu Asn Val Val Ala Met Ala Leu
 85           90           95
Ser Gly Tyr Thr Asp Glu Lys Asn Ser Leu Trp Arg Glu Met Cys Ser
100          105          110
Thr Leu Arg Leu Gln Leu Asn Asn Pro Tyr Leu Cys Val Met Phe Ala
115          120          125
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Lys Val Ala Val Arg Asp Arg Val Ala Phe Ala Cys Lys Phe Leu Ser
145          150          155          160
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180          185          190
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195          200          205
Thr Ala Ser Tyr Cys Met Leu Gln Gly Ser Pro Leu Asp Val Leu Lys
210          215          220
Asp Glu Arg Val Gln Tyr Trp Ile Glu Asn Tyr Arg Asn Leu Leu Asp
225          230          235          240
Ala Trp Arg Phe Trp His Lys Arg Ala Glu Phe Asp Ile His Arg Ser
245          250          255
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275          280          285
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290          295          300
Ser Lys Val Thr Ser Cys Pro Gly Cys Arg Lys Pro Leu Pro Arg Cys
305          310          315          320
Ala Leu Cys Leu Ile Asn Met Gly Thr Pro Val Ser Ser Cys Pro Gly
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Gly Thr Lys Ser Asp Glu Lys Val Asp Leu Ser Lys Asp Lys Lys Leu
340          345          350
Ala Gln Phe Asn Asn Trp Phe Thr Trp Cys His Asn Cys Arg His Gly
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Gly His Ala Gly His Met Leu Ser Trp Phe Arg Asp His Ala Glu Cys
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<210> 6149
<211> 1949
<212> DNA
<213> Homo sapiens

<400> 6149
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<210> 6150

<211> 508

<212> PRT

<213> Homo sapiens

<400> 6150

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			20					25					30		
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Lys	Glu	Val	Arg	Glu	Arg	Ala	Ser	Lys	Arg	Lys	Leu	Pro	Phe	Thr	Ala
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Glu	Arg	Lys	Arg	Ile	Lys	Lys	Glu	Pro	Val	Thr	Arg	Lys	Ala	Gly	Leu
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<211> 648

<212> DNA

<213> Homo sapiens

<400> 6151

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<210> 6152

<211> 130

<212> PRT

<213> Homo sapiens

<400> 6152

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 35 40 45
 Ala Gly Thr Val Asp Thr His Leu Pro Ser Leu Leu Pro Val Ile
 50 55 60
 Leu His Pro Leu Gly Ala Ala Ser Ala Gly Arg Ala Leu Glu Pro Lys
 65 70 75 80
 Ala Asp Pro His Thr Cys Pro Tyr Gly Arg Lys Glu Ser Arg Gly Glu
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<210> 6153

<211> 1810

<212> DNA

<213> Homo sapiens

<400> 6153

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<210> 6154

<211> 388

<212> PRT

<213> Homo sapiens

<400> 6154

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Ser Arg Ala Tyr Arg Phe Thr Gly His Lys Asp Ala Val Thr Cys Val
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Asn Phe Ser Pro Ser Gly His Leu Ala Ser Gly Ser Arg Asp Lys
          50           55           60
Thr Val Arg Ile Trp Val Pro Asn Val Lys Gly Glu Ser Thr Val Phe
65          70           75           80
Arg Ala His Thr Ala Thr Val Arg Ser Val His Phe Cys Ser Asp Gly
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Gln Ser Phe Val Thr Ala Ser Asp Asp Lys Thr Val Lys Val Trp Ala
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Thr His Arg Gln Lys Phe Leu Phe Ser Leu Ser Gln His Ile Asn Trp
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Val Arg Cys Ala Lys Phe Ser Pro Asp Gly Arg Leu Ile Val Ser Ala
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Ser Asp Asp Lys Thr Val Lys Leu Trp Asp Lys Ser Ser Arg Glu Cys
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Val His Ser Tyr Cys Glu His Gly Gly Phe Val Thr Tyr Val Asp Phe
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His Pro Ser Gly Thr Cys Ile Ala Ala Ala Gly Met Asp Asn Thr Val
          180          185          190
Lys Val Trp Asp Val Arg Thr His Arg Leu Leu Gln His Tyr Gln Leu
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His Ser Ala Ala Val Asn Gly Leu Ser Phe His Pro Ser Gly Asn Tyr
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Leu Ile Thr Ala Ser Ser Asp Ser Thr Leu Lys Ile Leu Asp Leu Met
225          230          235          240
Glu Gly Arg Leu Leu Tyr Thr Leu His Gly His Gln Gly Pro Ala Thr
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Thr Val Ala Phe Ser Arg Thr Gly Glu Tyr Phe Ala Ser Gly Gly Ser
          260          265          270
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Met Gly Asn Leu Pro Glu Val Asp Phe Pro Val Pro Pro Gly Arg Gly
305          310          315          320
Trp Ser Val Glu Ser Val Gln Ser Gln Pro Gln Glu Pro Val Ser Val
          325          330          335
Pro Gln Thr Leu Thr Ser Thr Leu Glu His Ile Val Gly Gln Leu Asp
          340          345          350
Val Leu Thr Gln Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr
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<210> 6155
<211> 995
<212> DNA
<213> Homo sapiens

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<210> 6156
<211> 164
<212> PRT
<213> Homo sapiens

<400> 6156
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<210> 6158

<211> 455

<212> PRT

<213> Homo sapiens

<400> 6158

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Ile	Ser	Tyr	Asp	Tyr	Leu	Thr	Ser	Leu	Lys	Ser	Val	Pro	Tyr	Gly	Ser				
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Glu	Glu	Tyr	Leu	Gln	Leu	Arg	Ser	Lys	Ile	His	Asp	Leu	Phe	Gln	Ser				
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Glu	Ile	Arg	Asn	Asn	Ala	Ala	Asn	Tyr	Leu	Pro	Gln	Ile	Ser	His	Leu				
			340					345					350						
Leu	Asn	His	Val	Pro	Arg	Gln	Met	Leu	Leu	Ile	Leu	Lys	Thr	Asn	Asp				
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Leu	Leu	Arg	Gly	Ile	Glu	Ala	Ala	Leu	Gly	Thr	Arg	Ala	Ser	Ala	Ser				
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Ser	Phe	Leu	Asn	Met	Ser	Arg	Cys	Ile	Arg	Ala	Leu	Ala	Glu	His					
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<210> 6159
 <211> 4310
 <212> DNA
 <213> Homo sapiens

455

<400> 6159
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<210> 6160

<211> 551

<212> PRT

<213> Homo sapiens

<400> 6160

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Ser	Val	Leu	Ile	Gln	Phe	Ala	Thr	Pro	Asn	Asp	Phe	Cys	Ser	Phe	Tyr
50					55					60					
Asn	Ile	Leu	Lys	Thr	Cys	Arg	Gly	His	Thr	Leu	Glu	Arg	Ser	Val	Phe
65	70					75					80				
Ser	Glu	Arg	Thr	Glu	Glu	Ser	Ser	Ala	Val	Gln	Tyr	Phe	Gln	Phe	Tyr
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Gly	Tyr	Leu	Ser	Gln	Gln	Gln	Asn	Met	Gln	Asp	Tyr	Val	Arg	Thr	
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Gly	Thr	Tyr	Gln	Arg	Ala	Ile	Leu	Gln	Asn	His	Thr	Asp	Phe	Lys	Asp
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Lys	Ile	Val	Leu	Asp	Val	Gly	Cys	Gly	Ser	Gly	Ile	Leu	Ser	Phe	Phe
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Ala	Ala	Gln	Ala	Gly	Ala	Arg	Lys	Ile	Tyr	Ala	Val	Glu	Ala	Ser	Thr
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Met	Ala	Gln	His	Ala	Glu	Val	Leu	Val	Lys	Ser	Asn	Asn	Leu	Thr	Asp
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245					250					255					
Tyr	Gln	Pro	Ser	Phe	His	Gly	Val	Asp	Leu	Ser	Ala	Leu	Arg	Gly	Ala
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Met	Leu	His	Ser	Gly	Leu	Val	His	Gly	Leu	Ala	Phe	Trp	Phe	Asp	Val
325					330					335					
Ala	Phe	Ile	Gly	Ser	Ile	Met	Thr	Val	Trp	Leu	Ser	Thr	Ala	Pro	Thr
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405					410					415					
Phe	Arg	Tyr	Thr	Gly	Thr	Thr	Pro	Ser	Pro	Pro	Pro	Gly	Ser	His	Tyr
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Thr	Ser	Pro	Ser	Glu	Asn	Met	Trp	Asn	Thr	Gly	Ser	Thr	Tyr	Asn	Leu
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465              470              475              480
Leu Ala Asn Thr Gly Ile Val Asn His Thr His Ser Arg Met Gly Ser
      485              490              495
Ile Met Ser Thr Gly Ile Val Gln Gly Ser Ser Gly Ala Gln Gly Ser
      500              505              510
Gly Gly Gly Ser Thr Ser Ala His Tyr Ala Val Asn Ser Gln Phe Thr
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<210> 6161

<211> 1489

<212> DNA

<213> Homo sapiens

<400> 6161

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1020

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<210> 6162

<211> 58

<212> PRT

<213> Homo sapiens

<400> 6162

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			20				25						30		
Arg	Lys	Gly	Thr	Glu	Pro	Gly	Val	Val	Ala	His	Ala	Cys	Asn	Pro	Xaa
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<210> 6163

<211> 713

<212> DNA

<213> Homo sapiens

<400> 6163

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 300
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 480

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<210> 6164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 6164

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			20					25					30		
Pro	Leu	Pro	Gly	Lys	Ala	Gly	Leu	Ala	Leu	Leu	Lys	Pro	Gln	Ser	Arg
			35				40					45			
Ser	Asp	Gly	Tyr	Arg	Tyr	Leu	Gly	Lys	Asp	Thr	Val	Asp	Gly	Leu	Asp
	50				55					60					
Ser	Ser	Leu	Leu	Lys	Cys	Thr	Arg	Arg	Cys	Met	Arg	Gly	Phe	Arg	Leu
	65				70				75					80	
Pro	Glu	Lys	Gln	Pro	Ser	Lys	Thr	Arg	Val	Ser	Phe	Leu	Glu	Ser	Lys
			85					90					95		
Arg	Lys	Glu	Gly	Ser	Gly	Trp	Leu	His	Trp	Ser	Val	Thr	Arg	Ser	Gly
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Ala	Phe	Arg	Leu	Lys	Val	Thr	Val								
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<210> 6165

<211> 1004

<212> DNA

<213> Homo sapiens

<400> 6165

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<210> 6166

<211> 239

<212> PRT

<213> Homo sapiens

<400> 6166

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 35 40 45
 Glu Met Leu Ser Lys Lys Gln Glu Phe Leu Glu Lys Lys Ile Glu Gln
 50 55 60
 Glu Leu Thr Ala Ala Lys Lys His Gly Thr Lys Asn Lys Arg Ala Ala
 65 70 75 80
 Leu Gln Ala Leu Lys Arg Lys Lys Arg Tyr Glu Lys Gln Leu Ala Gln
 85 90 95
 Ile Asp Gly Thr Leu Ser Thr Ile Glu Phe Gln Arg Glu Ala Leu Glu
 100 105 110
 Asn Ala Asn Thr Asn Thr Glu Val Leu Lys Asn Met Gly Tyr Ala Ala
 115 120 125
 Lys Ala Met Lys Ala Ala His Asp Asn Met Asp Ile Asp Lys Val Asp
 130 135 140
 Glu Leu Met Gln Asp Ile Ala Asp Gln Gln Glu Leu Ala Glu Glu Ile
 145 150 155 160
 Ser Thr Ala Ile Ser Lys Pro Val Gly Phe Gly Glu Glu Phe Asp Glu
 165 170 175
 Asp Glu Leu Met Ala Glu Leu Glu Glu Leu Glu Gln Glu Glu Leu Asp
 180 185 190
 Lys Asn Leu Leu Glu Ile Ser Gly Pro Glu Thr Val Pro Leu Pro Asn
 195 200 205
 Val Pro Ser Ile Ala Leu Pro Ser Lys Pro Ala Lys Lys Lys Glu Glu
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225

230

235

<210> 6167

<211> 1220

<212> DNA

<213> Homo sapiens

<400> 6167

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 720
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 780
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 1220

<210> 6168

<211> 90

<212> PRT

<213> Homo sapiens

<400> 6168

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Ala Lys Trp  Gln Ile Trp Thr Val Ser  Ile Asp Ala Asp Glu Pro His
 1           5           10          15
Pro Gly Thr  Gly Glu Val Glu Asp  Ile Glu Gln Leu Asn Gln Cys Leu
          20           25           30
Ile Gln His  Phe His Leu Ile Lys Thr Ser Leu Ile Phe Leu Cys Phe
          35           40           45
Leu Phe His  Gly Ile His Glu Asn Leu Leu Thr Val Gly Val Ser Lys
          50           55           60
Glu Ala Tyr  Leu Met Thr Ser Val Asn Gly Lys Asn Lys Thr Lys Met
65           70           75           80
Leu Tyr Gly  Gln Ser His Lys Gly Lys Asp
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<210> 6169

<211> 720

<212> DNA

<213> Homo sapiens

<400> 6169

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120
cagtgcaccc aggcctttta tggctgtgaa acacgttaaa atttcagggt aagacgtgac
180
cttttgaggt gactataact gaagattgct ttacagaagc ccaaaaagg tttttgagtc
240
atgatgcaag aatctgggac tgagacaaaa agtaacggtt cagccatcca gaatgggtcg
300
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360
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420
tggcatctca taaaccatca gccctctagg agtccagca gttggcttaa gagactaatt
480
tcaagccctt gggagttgga agtcctgcag gtcctctgtg gggagcagtt gctgagacga
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600
gagaaatggt tcccactgct ttcatgcaaa aataaaaatt aaacgaaaaa cagcttaagc
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720

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<210> 6170

<211> 101

<212> PRT

<213> Homo sapiens

<400> 6170

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Met Met Gln Glu Ser Gly Thr Glu Thr Lys Ser Asn Gly Ser Ala Ile

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Gln Asn Gly Ser Gly Gly Ser Asn His Leu Leu Glu Cys Gly Gly Leu			
	20	25	30
Arg Glu Gly Arg Ser Asn Gly Glu Thr Pro Ala Val Asp Ile Gly Ala			
	35	40	45
Ala Asp Leu Ala His Ala Gln Gln Gln Gln Gln Trp His Leu Ile			
	50	55	60
Asn His Gln Pro Ser Arg Ser Pro Ser Ser Trp Leu Lys Arg Leu Ile			
	65	70	75
Ser Ser Pro Trp Glu Leu Glu Val Leu Gln Val Pro Cys Gly Glu Gln			
	85	90	95
Leu Leu Arg Arg Arg			
	100		

<210> 6171

<211> 1130

<212> DNA

<213> Homo sapiens

<400> 6171

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180
cgggacaggg atgtctacct ggtaatatagag gacttgaagc agaaagcaag tgaatacagag
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660
ggcatgggat cttctctgtc tcatcagtc ttagtagcac tatcagagaa actggcaaga
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960
ctaataacaa aactttctgt gttcttagat tacagaatat cataattgat agaatatggg
1020

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ttcttactgt gtgttgccatt ttgtgcccc aatacatagt tttcatatta aaaagccttt

1080

tctcttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

1130

<210> 6172

<211> 292

<212> PRT

<213> Homo sapiens

<400> 6172

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 20 25 30
 Phe Gly Asp His Pro Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr
 35 40 45
 Glu Ile Leu His His Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Asp
 50 55 60
 Val Tyr Leu Val Ile Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu
 65 70 75 80
 Ser Glu Ala Lys Tyr Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe
 85 90 95
 Ser Pro Ala Asn Leu Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu
 100 105 110
 Val Asp Ser Ala Val Ala Leu Glu Thr Lys Asp Thr Ser Leu Ala Ser
 115 120 125
 Phe Ile Pro Ala Val Asn Asp Leu Thr Ser Asp Leu Phe Arg Thr Lys
 130 135 140
 Ser Lys Ser Glu Glu Ile Lys Lys Ile Glu Leu Glu Lys Leu Glu Lys Asn
 145 150 155 160
 Leu Thr Ala Thr Leu Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys
 165 170 175
 Lys Ala Glu Leu His Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg
 180 185 190
 Arg Gln Asn Met Asp Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe
 195 200 205
 Gly Ile Lys Ala Ala Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala
 210 215 220
 Ser Leu Ser His Gln Ser Leu Val Ala Leu Ser Glu Lys Leu Ala Arg
 225 230 235 240
 Leu Lys Gln Gln Thr Ile Pro Leu Lys Lys Lys Leu Glu Ser Tyr Leu
 245 250 255
 Asp Leu Met Pro Asn Pro Ser Leu Ala Gln Val Lys Ile Glu Glu Ala
 260 265 270
 Lys Arg Glu Leu Asp Ser Ile Glu Ala Glu Leu Thr Arg Arg Val Asp
 275 280 285
 Met Met Glu Leu
 290

<210> 6173

<211> 1483

<212> DNA

<213> Homo sapiens

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120
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180
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240
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1483

<210> 6174

<211> 299

<212> PRT

<213> Homo sapiens

<400> 6174

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Gln Leu Ala Glu Asn Ser Leu Leu Ala Lys Val Phe Ile Thr Lys Gln
      20           25           30
Gly Tyr Ala Leu Leu Val Ser Asp Leu Gln Gln Val Trp His Glu Gln
      35           40           45
Val Asp Thr Ser Val Val Ser Gln Arg Ala Lys Glu Leu Asn Lys Arg
      50           55           60
Leu Thr Ala Pro Pro Ala Ala Phe Leu Cys His Leu Asp Asn Leu Leu
      65           70           75           80
Arg Pro Leu Leu Lys Asp Ala Ala His Pro Ser Glu Ala Thr Phe Ser
      85           90           95
Cys Asp Cys Val Ala Asp Ala Leu Ile Leu Arg Val Arg Ser Glu Leu
      100          105          110
Ser Gly Leu Pro Phe Tyr Trp Asn Phe His Cys Met Leu Ala Ser Pro
      115          120          125
Ser Leu Val Ser Gln His Leu Ile Arg Pro Leu Met Gly Met Ser Leu
      130          135          140
Ala Leu Gln Cys Gln Val Arg Glu Leu Ala Thr Leu Leu His Met Lys
      145          150          155          160
Asp Leu Glu Ile Gln Asp Tyr Gln Glu Ser Gly Ala Thr Leu Ile Arg
      165          170          175
Asp Arg Leu Lys Thr Glu Pro Phe Glu Glu Asn Ser Phe Leu Glu Gln
      180          185          190
Phe Met Ile Glu Lys Leu Pro Glu Ala Cys Ser Ile Gly Asp Gly Lys
      195          200          205
Pro Phe Val Met Asn Leu Gln Asp Leu Tyr Met Ala Val Thr Thr Gln
      210          215          220
Glu Val Gln Val Gly Gln Lys His Gln Gly Ala Gly Asp Pro His Thr
      225          230          235          240
Ser Asn Ser Ala Ser Leu Gln Gly Ile Asp Ser Gln Cys Val Asn Gln
      245          250          255
Pro Glu Gln Leu Val Ser Ser Ala Pro Thr Leu Ser Ala Pro Glu Lys
      260          265          270
Glu Ser Thr Gly Thr Ser Gly Pro Leu Gln Arg Pro Gln Leu Ser Lys
      275          280          285
Val Lys Arg Lys Asn Pro Arg Gly Leu Phe Ser
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<210> 6175

<211> 349

<212> DNA

<213> Homo sapiens

<400> 6175

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120

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aaaactgttc agtttggtgg aactgtgaca gaagtcttgc tgaagtacaa aaaggggtgaa
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acaaatgact ttgagttggt gaagaaccag ctgtagatc cagacataaa gagattgcct
240
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349

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<210> 6176

<211> 90

<212> PRT

<213> Homo sapiens

<400> 6176

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Met Arg Ala Leu Glu Asn Asp Phe Phe Asn Ser Pro Pro Arg Lys Thr
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Val Gln Phe Gly Gly Thr Val Thr Glu Val Leu Leu Lys Tyr Lys Lys
20          25          30
Gly Glu Thr Asn Asp Phe Glu Leu Leu Lys Asn Gln Leu Leu Asp Pro
35          40          45
Asp Ile Lys Arg Leu Pro Trp Leu Asn Arg Ser Gln Thr Val Val Glu
50          55          60
Glu Tyr Leu Ala Phe Leu Gly Asn Leu Val Ser Ala Gln Thr Val Phe
65          70          75          80
Leu Arg Pro Cys Leu Ser Met Ile Ala Ser
85          90

```

<210> 6177

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 6177

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120
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600

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gccctacga cagtgagacag aacccacgcc ctgatgaaga agattgganc agtccccat
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<210> 6178

<211> 310

<212> PRT

<213> Homo sapiens

<400> 6178

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			20					25				30			
Arg	Asn	Ala	Leu	Glu	Asn	Ile	Arg	Lys	Glu	Met	Lys	Leu	Leu	Glu	Gln
			35				40					45			
Ala	Gly	Ser	Leu	Lys	Gly	Ser	Leu	Ser	Val	Glu	Glu	Gln	Leu	Ser	Leu
	50					55				60					
Ile	Ser	Gly	Cys	Pro	Asn	Ile	Gln	Glu	Ala	Val	Glu	Gly	Ala	Met	His
	65				70				75				80		
Ile	Gln	Glu	Cys	Val	Pro	Glu	Asp	Leu	Glu	Leu	Lys	Lys	Lys	Ile	Phe
			85				90						95		
Ala	Gln	Leu	Asp	Ser	Ile	Ile	Asp	Arg	Val	Ile	Leu	Ser	Ser	Ser	
			100				105					110			
Thr	Ser	Cys	Leu	Met	Pro	Ser	Lys	Leu	Phe	Ala	Gly	Leu	Val	His	Val

	115		120		125	
Lys	Gln	Cys	Ile	Val	Ala	His
130						Pro
Leu	Val	Glu	Leu	Val	Pro	His
145						Pro
Arg	Thr	His	Ala	Leu	Met	Lys
						Lys
Pro	Glu	Gly	Gly	Arg	Leu	Arg
						Ser
His	Gln	Arg	Gly	Leu	Ala	Ala
						Ser
Val	Thr	Trp	Xaa	Leu	Val	Met
						Ser
Phe	Ile	Gly	Pro	Leu	Glu	Thr
225						Met
Ser	Tyr	Cys	Asp	Arg	Tyr	Ser
						Glu
Phe	Gly	Pro	Ile	Pro	Glu	Phe
						Ser
Gln	Asp	Met	Cys	Met	Lys	Val
						Pro
Arg	Arg	Gln	Trp	Arg	Asp	Glu
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<210> 6179

<211> 2940

<212> DNA

<213> Homo sapiens

<400> 6179

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2280

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<210> 6180

<211> 751

<212> PRT

<213> Homo sapiens

<400> 6180

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Tyr	Leu	Leu	Ile	Thr	Val	Gly	Val	Val	Tyr	Val	Lys	Ser	Phe	Pro	Gln
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Ser	Arg	Lys	Asp	Ile	Leu	Lys	Asp	Leu	Val	Glu	Met	Cys	Arg	Gly	Val
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Gln	His	Pro	Leu	Arg	Gly	Leu	Phe	Leu	Arg	Asn	Tyr	Leu	Leu	Gln	Cys
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Val	Phe	Pro	Asp	Glu	Phe	His	Leu	Gln	Thr	Leu	Asn	Pro	Phe	Leu	Arg														
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Ala	Cys	Ala	Glu	Leu	His	Gln	Asn	Val	Asn	Val	Lys	Asn	Ile	Ile	Ile														
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Ala	Leu	Ile	Asp	Arg	Leu	Ala	Leu	Phe	Ala	His	Arg	Glu	Asp	Gly	Pro														
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Gly	Ile	Pro	Ala	Asp	Ile	Lys	Leu	Phe	Asp	Ile	Phe	Ser	Gln	Gln	Val														
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Ala	Thr	Val	Ile	Gln	Ser	Arg	Gln	Asp	Met	Pro	Ser	Glu	Asp	Val	Val														
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Ser	Leu	Gln	Val	Ser	Leu	Ile	Asn	Leu	Ala	Met	Lys	Cys	Tyr	Pro	Asp														
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Asn	Lys	Leu	Asn	Leu	Glu	His	Ile	Ala	Thr	Ser	Ser	Ala	Val	Ser	Lys														
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Glu	Leu	Thr	Arg	Leu	Leu	Lys	Ile	Pro	Val	Asp	Thr	Tyr	Asn	Asn	Ile														
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Ser	Lys	Ala	Gln	Leu	Ala	Ala	Ile	Thr	Leu	Ile	Ile	Gly	Thr	Phe	Glu														
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						610					615																		
Ala	Glu	His	Leu	Cys	Thr	Ser	Leu	Trp	Ser	Gly	Arg	Asn	Thr	Asp	Lys														

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625          630          635          640
Asn Gly Glu Glu Leu His Gly Gly Lys Arg Val Met Glu Cys Leu Lys
          645          650          655
Lys Ala Leu Lys Ile Ala Asn Gln Cys Met Asp Pro Ser Leu Gln Val
          660          665          670
Gln Leu Phe Ile Glu Ile Leu Asn Arg Tyr Ile Tyr Phe Tyr Glu Lys
          675          680          685
Glu Asn Asp Ala Val Thr Ile Gln Val Leu Asn Gln Leu Ile Gln Lys
          690          695          700
Ile Arg Glu Asp Leu Pro Asn Leu Glu Ser Ser Glu Glu Thr Glu Gln
705          710          715          720
Ile Asn Lys His Phe His Asn Thr Leu Glu His Leu Arg Leu Arg Arg
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<210> 6181

<211> 1135

<212> DNA

<213> Homo sapiens

<400> 6181

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960

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<210> 6182
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 6182
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 20 25 30
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 35 40 45
 Asp Ala Gln Lys His Asp Val Glu Val Leu Glu Arg Asn Phe Gln Thr
 50 55 60
 Ile Leu Cys Glu Phe Glu Thr Leu Tyr Lys Ala Phe Ser Asn Cys Ser
 65 70 75 80
 Leu Pro Gln Gly Trp Lys Met Asn Ser Thr Pro Ser Gly Glu Trp Phe
 85 90 95
 Thr Phe Tyr Leu Val Asn Gln Gly Val Cys Val Pro Arg Asn Cys Arg
 100 105 110
 Lys Cys Pro Arg Thr Tyr Arg Leu Leu Gly Ser Leu Arg Thr Cys Ile
 115 120 125
 Gly Asn Asn Val Phe Gly Asn Ala Cys Ile Ser Val Leu Ser Pro Gly
 130 135 140
 Thr Val Ile Thr Glu His Tyr Gly Pro Thr Asn Ile Arg Ile Arg Cys
 145 150 155 160
 His Leu Gly Leu Lys Thr Pro Asn Gly Cys Glu Leu Val Val Gly Gly
 165 170 175
 Glu Pro Gln Cys Trp Ala Glu Gly Arg Cys Leu Leu Phe Asp Asp Ser
 180 185 190
 Phe Leu His Ala Ala Phe His Glu Gly Ser Ala Glu Asp Gly Pro Arg
 195 200 205
 Val Val Phe Met Val Asp Leu Trp His Pro Asn Val Ala Ala Ala Glu
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 Arg Gln Ala Leu Asp Phe Ile Phe Ala Pro Gly Arg
 225 230 235

<210> 6183
 <211> 2530
 <212> DNA
 <213> Homo sapiens

<400> 6183
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1740

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 2530

<210> 6184

<211> 308

<212> PRT

<213> Homo sapiens

<400> 6184

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 35 40 45
 Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly
 50 55 60
 Ala Arg Gly Gly Lys Ala Glu Asp Lys Glu Trp Met Pro Val Thr Lys
 65 70 75 80
 Leu Gly Arg Leu Val Lys Asp Met Lys Ile Lys Ser Leu Glu Glu Ile
 85 90 95
 Tyr Leu Phe Ser Leu Pro Ile Lys Glu Ser Glu Ile Ile Asp Phe Phe
 100 105 110
 Leu Gly Ala Ser Leu Lys Asp Glu Val Leu Lys Ile Met Pro Val Gln
 115 120 125
 Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala Phe Val Ala
 130 135 140
 Ile Gly Asp Tyr Asn Gly His Val Gly Leu Gly Val Lys Cys Ser Lys

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145          150          155          160
Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu Ala Lys Leu Ser
165          170          175
Ile Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro
180          185          190
His Thr Val Pro Cys Lys Val Thr Gly Arg Cys Gly Ser Val Leu Val
195          200          205
Arg Leu Ile Pro Ala Pro Arg Gly Thr Gly Ile Val Ser Ala Pro Val
210          215          220
Pro Lys Lys Leu Leu Met Met Ala Gly Ile Asp Asp Cys Tyr Thr Ser
225          230          235          240
Ala Arg Gly Cys Thr Ala Thr Leu Gly Asn Phe Ala Lys Ala Thr Phe
245          250          255
Asp Ala Ile Ser Lys Thr Tyr Ser Tyr Leu Thr Pro Asp Leu Trp Lys
260          265          270
Glu Thr Val Phe Thr Lys Ser Pro Tyr Gln Glu Phe Thr Asp His Leu
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Val Ala Thr Thr
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<210> 6185

<211> 1231

<212> DNA

<213> Homo sapiens

<400> 6185

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780

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<210> 6186

<211> 133

<212> PRT

<213> Homo sapiens

<400> 6186

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 Gly Tyr Ile Cys Arg Ile Cys His Lys Phe Tyr His Ser Asn Ser Gly
 35 40 45
 Ala Gln Leu Ser His Cys Lys Ser Leu Gly His Phe Glu Asn Leu Gln
 50 55 60
 Lys Tyr Lys Ala Ala Lys Asn Pro Ser Pro Thr Thr Arg Pro Val Ser
 65 70 75 80
 Arg Arg Cys Ala Ile Asn Ala Arg Asn Ala Leu Thr Ala Leu Phe Thr
 85 90 95
 Ser Ser Gly Arg Pro Pro Ser Gln Pro Asn Thr Gln Asp Lys Thr Pro
 100 105 110
 Ser Lys Val Thr Ala Arg Pro Ser Gln Pro Pro Leu Pro Arg Arg Ser
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 Thr Arg Leu Lys Thr
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<210> 6187

<211> 909

<212> DNA

<213> Homo sapiens

<400> 6187

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<210> 6188

<211> 227

<212> PRT

<213> Homo sapiens

<400> 6188

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		20					25						30		
Glu	Ala	Leu	Leu	Asp	Glu	Asp	Thr	Leu	Phe	Cys	Gln	Gly	Leu	Glu	Val
		35					40					45			
Phe	Tyr	Pro	Glu	Leu	Gly	Asn	Ile	Gly	Cys	Lys	Val	Val	Pro	Asp	Cys
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Pro	Asp	Ala	Pro	Ser	Arg	Ala	Glu	Pro	Arg	Gln	Arg	Phe	Trp	Arg	His
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<211> 3021

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<213> Homo sapiens

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<213> Homo sapiens

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 Gln Asp Ala His Gly Gln Pro Asp Val Ser Ala Phe Asp Phe Thr Ser
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<213> Homo sapiens

<400> 6194

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 35 40 45
 Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His
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 Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly
 65 70 75 80
 Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val
 85 90 95
 Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu
 100 105 110
 Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu
 115 120 125
 Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala Val His Val Leu Glu
 130 135 140
 Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu Ala Cys Ser Ala Asn
 145 150 155 160
 Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg Trp Glu Ile Leu Trp

165										170										175									
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180										185										190									
Pro	Cys	Ile	Lys	Gln	Ile	Asn	Phe	Pro	Thr	Asn	Leu	Ile	Arg	Leu	Glu														
195										200										205									
Val	Asn	Ser	Ser	Leu	Leu	Glu	Tyr	Tyr	Thr	Glu	Leu	Asp	Ala	Val	Val														
210										215										220									
Leu	His	Gly	Val	Lys	Asp	Lys	Pro	Val	Leu	Ser	Leu	Lys	Thr	Ser	Leu														
225										230										235									
Ile	Asp	Met	Asn	Asp	Ile	Glu	Asp	Asp	Ala	Tyr	Ala	Glu	Lys	Asp	Gly														
245										250										255									
Cys	Gly	Met	Asp	Ser	Leu	Asn	Lys	Lys	Phe	Ser	Ser	Ala	Val	Leu	Gly														
260										265										270									
Glu	Gly	Pro	Asn	Asn	Gly	Tyr	Phe	Asp	Lys	Leu	Pro	Tyr	Glu	Leu	Ile														
275										280										285									
Gln	Leu	Ile	Leu	Asn	His	Leu	Thr	Leu	Pro	Asp	Leu	Cys	Arg	Leu	Ala														
290										295										300									

	595		600		605
Ser	Phe	Pro	Lys	Val	Phe
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			Ser	Phe	Thr
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<210> 6195

<211> 518

<212> DNA

<213> Homo sapiens

<400> 6195

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<210> 6196

<211> 117

<212> PRT

<213> Homo sapiens

<400> 6196

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			20					25					30		
Leu	Leu	Leu	Ser	Arg	Thr	Thr	Arg	Val	Lys	Pro	His	Pro	Tyr	Lys	Tyr
			35				40					45			
Gln	Val	His	Pro	Asn	Ser	Ser	Leu	Ala	Gln	Lys	Trp	Cys	Tyr	Ile	His
			50			55					60				
Trp	Glu	Gln	Thr	Cys	Ile	Pro	Thr	Pro	Arg	His	Val	Thr	Thr	Gly	Thr
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Ala	Asn	Glu	Leu	Cys	Pro	Gly	Asn	Ser	Phe	Thr	Pro	Ser	Ser	Cys	Ser
				85					90					95	
Phe	His	Ser	His	Leu	Leu	Ser	Thr	Asn	Tyr	Ala	Lys	Asn	Tyr	Val	Gln
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His	Arg	Thr	Gly	Trp											
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<210> 6197

<211> 2841

<212> DNA

<213> Homo sapiens

<400> 6197

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420
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<210> 6198

<211> 124

<212> PRT

<213> Homo sapiens

<400> 6198

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	20	25	30
Ser Ser Gln His His Gly Leu Asn Thr His Trp Ala Pro Thr Leu Gly			
	35	40	45
Pro Gly Trp Gly Met Trp Gly Gln Glu Ala Ala Gln Ser Gly Arg Gln			
	50	55	60
Arg Glu Lys Cys Val Gln Arg Ala Pro Ile Ser Gly Cys Asn Val Val			
65	70	75	80
Leu Arg Leu Trp Leu Gly Ser Ala Ser Arg Val Ser Tyr Val Leu Cys			
	85	90	95
Ser Tyr Phe Leu Ser Pro Thr Leu Pro Cys Arg Asn Pro Ser Glu Tyr			
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Val Ala Thr Ile Leu Glu Leu Ser Ala Leu Ile Val			
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<210> 6199

<211> 1777

<212> DNA

<213> Homo sapiens

<400> 6199

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 1777

<210> 6200

<211> 164

<212> PRT

<213> Homo sapiens

<400> 6200

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		20						25					30		
Pro	Pro	Lys	Pro	Asp	Cys	Gln	Gln	Lys	Pro	Ser	Pro	Ser	Glu	Gly	Gln
		35					40					45			
Val	Gly	Val	Pro	Xaa	Arg	Ser	Pro	His	Pro	Gln	Gly	Gly	Phe	Thr	His
	50				55					60					
Cys	Pro	Val	Pro	Gly	Met	Pro	Gly	Gly	Arg	Pro	Leu	Cys	Cys	Cys	His
	65				70				75					80	
Cys	Cys	Gln	His	Cys	Pro	Ala	Cys	Glu	Ala	Arg	Arg	Ser	Pro	Cys	Pro
			85					90						95	
Thr	Arg	Cys	Cys	Cys	Ser	Ser	Asp	Pro	Cys	Cys	Glu	Glu	Trp	Asp	Ser
			100				105						110		
Trp	Ser	Lys	Lys	Leu	Val	Phe	Leu	Phe	Cys	Ile	Asn	Glu	Lys	Asn	Pro
		115					120					125			
Gly	Glu	Ala	Ala	Thr	Leu	Pro	Ser	Gln	Arg	Asp	Ala	Leu	Pro	Cys	Phe
	130				135						140				
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145
Ser Ser Trp Phe

150

155

160

<210> 6201
<211> 604
<212> DNA
<213> Homo sapiens

<400> 6201
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604

<210> 6202
<211> 124
<212> PRT
<213> Homo sapiens

<400> 6202
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35 40 45
Ala Gly Leu Arg Gly Cys Arg Glu Glu Phe Gly Gly Lys Gly Gln Pro
50 55 60
Gln Ser Leu Ser Cys Ala Ser Trp Glu Arg Gly Met Thr Gly Arg His
65 70 75 80
Thr Asn Val Ser Gln Gly Arg Trp Ala Trp Gly His Arg Ala Pro Arg
85 90 95
Gly Gly Ser Gly Glu Gly Glu Pro Ala Glu Glu Arg Pro Gly Arg Ala
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Gly Asp His Ala Gly Ala Gln Gly Glu Arg Gln Asp

115

120

<210> 6203

<211> 3462

<212> DNA

<213> Homo sapiens

<400> 6203

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<210> 6204

<211> 486

<212> PRT

<213> Homo sapiens

<400> 6204

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Asp	Gly	His	Arg	Leu	Cys	Ser	Asp	Leu	Met	Asn	Cys	Leu	His	Glu	Arg
			35				40					45			
Ala	Arg	Ile	Glu	Lys	Ala	Tyr	Ala	Gln	Gln	Leu	Thr	Glu	Trp	Ala	Arg
	50					55					60				
Arg	Trp	Arg	Gln	Leu	Val	Glu	Lys	Gly	Pro	Gln	Tyr	Gly	Thr	Val	Glu
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Lys	Ala	Trp	Met	Ala	Phe	Met	Ser	Glu	Ala	Glu	Arg	Val	Ser	Glu	Leu
			85					90					95		
His	Leu	Glu	Val	Lys	Ala	Ser	Leu	Met	Asn	Asp	Asp	Phe	Glu	Lys	Ile
			100				105					110			
Lys	Asn	Trp	Gln	Lys	Glu	Ala	Phe	His	Lys	Gln	Met	Met	Gly	Gly	Phe
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Lys	Glu	Thr	Lys	Glu	Ala	Glu	Asp	Gly	Phe	Arg	Lys	Ala	Gln	Lys	Pro
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Trp	Ala	Lys	Lys	Leu	Lys	Glu	Val	Glu	Ala	Ala	Lys	Lys	Ala	His	His
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			180					185					190		
Lys	Ile	Glu	Lys	Cys	Lys	Gln	Asp	Val	Leu	Lys	Thr	Lys	Glu	Lys	Tyr
		195				200					205				
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		210				215					220				
Asn	Met	Glu	Gln	Val	Phe	Glu	Gln	Cys	Gln	Gln	Phe	Glu	Glu	Lys	Arg
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Leu Ser Asn Val Ala Gly Tyr Lys Ala Ile Tyr His Asp Leu Glu Gln
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Ser Ile Arg Ala Ala Asp Ala Val Glu Asp Leu Arg Trp Phe Arg Ala
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Asn His Gly Pro Gly Met Ala Met Asn Trp Pro Gln Phe Glu Glu Trp
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Ser Ala Asp Leu Asn Arg Thr Leu Ser Arg Arg Glu Lys Lys Lys Ala
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Thr Asp Gly Val Thr Leu Thr Gly Ile Asn Gln Thr Gly Asp Gln Ser
                325                330                335
Leu Pro Ser Lys Pro Ser Ser Thr Leu Asn Val Pro Ser Asn Pro Ala
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Gln Ser Ala Gln Ser Gln Ser Ser Tyr Asn Pro Phe Glu Asp Glu Asp
                355                360                365
Asp Thr Gly Ser Thr Val Ser Glu Lys Asp Asp Thr Lys Ala Lys Asn
                370                375                380
Val Ser Ser Tyr Glu Lys Thr Gln Ser Tyr Pro Thr Asp Trp Ser Asp
                385                390                395                400
Asp Glu Ser Asn Asn Pro Phe Ser Ser Thr Asp Ala Asn Gly Asp Ser
                405                410                415
Asn Pro Phe Asp Asp Asp Ala Thr Ser Gly Thr Glu Val Arg Val Arg
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Ala Leu Tyr Asp Tyr Glu Gly Gln Glu His Asp Glu Leu Ser Phe Lys
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Ala Gly Asp Glu Leu Thr Lys Met Glu Asp Glu Asp Glu Gln Gly Trp
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Cys Lys Gly Arg Leu Asp Asn Gly Gln Val Gly Leu Tyr Pro Ala Asn
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Tyr Val Glu Ala Ile Gln
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<210> 6205

<211> 926

<212> DNA

<213> Homo sapiens

<400> 6205

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240
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300
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360
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420
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480

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<210> 6206

<211> 92

<212> PRT

<213> Homo sapiens

<400> 6206

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			20				25					30			
Arg	Glu	Gly	Lys	Glu	Phe	Ala	Asp	Ser	Gln	Lys	Leu	Leu	Phe	Met	Glu
			35				40				45				
Thr	Ser	Ala	Lys	Leu	Asn	His	Gln	Val	Ser	Glu	Val	Phe	Asn	Thr	Val
			50			55					60				
Ala	Gln	Glu	Leu	Leu	Gln	Arg	Ser	Asp	Glu	Glu	Gly	Gln	Ala	Leu	Xaa
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<210> 6207

<211> 1384

<212> DNA

<213> Homo sapiens

<400> 6207

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<210> 6208

<211> 290

<212> PRT

<213> Homo sapiens

<400> 6208

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 35 40 45
 Ser Ala Ala Ala Thr Val Arg Glu Ala Gln Gly Leu Met Ala Gly Gly
 50 55 60
 Phe Leu Cys Phe Ser Leu Ala Phe Xaa Ala Gln Val Gln Val Val Phe
 65 70 75 80
 Trp Arg Leu His Ser Pro Thr Gln Val Glu Asp Ala Met Leu Asp Thr

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      85              90              95
Tyr Asp Leu Val Tyr Glu Gln Ala Met Lys Gly Thr Ser His Val Arg
      100              105              110
Arg Gln Glu Leu Ala Ala Ile Gln Asp Val Phe Leu Cys Cys Gly Lys
      115              120              125
Lys Ser Pro Phe Ser Arg Leu Gly Ser Thr Glu Ala Asp Leu Cys Gln
      130              135              140
Gly Glu Glu Ala Ala Arg Glu Asp Cys Leu Gln Gly Ile Arg Ser Phe
      145              150              155              160
Leu Arg Thr His Gln Gln Val Ala Ser Ser Leu Thr Ser Ile Gly Leu
      165              170              175
Ala Leu Thr Val Ser Ala Leu Leu Phe Ser Ser Phe Leu Trp Phe Ala
      180              185              190
Ile Arg Cys Gly Cys Ser Leu Asp Arg Lys Gly Lys Tyr Thr Leu Thr
      195              200              205
Pro Arg Ala Cys Gly Arg Gln Pro Gln Glu Pro Ser Leu Leu Arg Cys
      210              215              220
Ser Gln Gly Gly Pro Thr His Cys Leu His Ser Glu Ala Val Ala Ile
      225              230              235              240
Gly Pro Arg Gly Cys Ser Gly Ser Leu Arg Trp Leu Gln Glu Ser Asp
      245              250              255
Ala Ala Pro Leu Pro Leu Ser Cys His Leu Ala Ala His Arg Ala Leu
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Ser Asp
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<210> 6209

<211> 2269

<212> DNA

<213> Homo sapiens

<400> 6209

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<210> 6210

<211> 165

<212> PRT

<213> Homo sapiens

<400> 6210

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		20					25					30			
Ser	Pro	Ser	Leu	Arg	Gly	Thr	His	Leu	Leu	Phe	Leu	Pro	Gln	Ala	Asp
		35				40				45					
Val	Val	Asp	Glu	Ala	Ile	Asp	Ser	Leu	Ala	Arg	Thr	Lys	Gly	Val	Met
	50				55					60					
Lys	Pro	Pro	Cys	Ser	Glu	Gly	Ser	Pro	Trp	Arg	Cys	Pro	His	Phe	Thr
65				70					75					80	
Cys	Trp	Val	Leu	Gln	Ala	Arg	Lys	Pro	Gly	Ser	Gly	Gly	Thr	Arg	Glu
			85						90				95		
Arg	Gln	Ala	Cys	Val	Trp	Thr	Ser	Ala	Gly	Ala	Ala	Ala	Leu	Arg	Leu
		100					105						110		
Ala	Arg	Glu	Arg	Gln	Arg	Trp	Val	Phe	Arg	Phe	His	Ala	Tyr	Val	Trp
		115				120					125				
Ala	His	Ser	Gln	His	Gly	Arg	Val	Ser	Ala	Val	Leu	Val	Leu	Thr	Leu
	130				135					140					
Pro	Glu	Gln	Gln	Trp	Thr	Asp	Glu	Ile	Arg	Leu	Phe	Gln	Lys	Gln	Arg
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<210> 6211

<211> 2163

<212> DNA

<213> Homo sapiens

<400> 6211

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<210> 6212

<211> 209

<212> PRT

<213> Homo sapiens

<400> 6212

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 35 40 45
 Ala Phe Glu Gly Ser Tyr Leu Glu Asp Thr Gln Met Tyr Gly Asn Ile
 50 55 60
 Ile Arg Gly Trp Xaa Ser Val Ser Asp Gln Pro Xaa Lys Asn Ser Asn
 65 70 75 80
 Ser Lys Asn Asp Arg Arg Asn Arg Lys Phe Lys Glu Ala Glu Arg Leu
 85 90 95
 Phe Ser Lys Ser Ser Val Thr Ser Ala Ala Val Ser Ala Leu Ala
 100 105 110
 Gly Val Gln Asp Gln Leu Ile Glu Lys Arg Glu Pro Gly Ser Gly Thr
 115 120 125
 Glu Ser Asp Thr Ser Pro Asp Phe His Asn Gln Glu Asn Glu Pro Ser
 130 135 140
 Gln Glu Asp Pro Glu Asp Leu Asp Gly Ser Val Gln Gly Val Lys Pro
 145 150 155 160
 Gln Lys Ala Ala Ser Ser Thr Ser Ser Gly Ser His His Ser Ser His
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 195 200 205
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<210> 6213

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 6213

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<211> 101

<212> PRT

<213> Homo sapiens

<400> 6214

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 Pro Pro Pro Pro Pro Thr Pro Pro Pro Thr Cys Ile Ala Gln Ile Gln
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<211> 651

<212> DNA

<213> Homo sapiens

<400> 6215

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<210> 6216

<211> 87

<212> PRT

<213> Homo sapiens

<400> 6216

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Glu Ala Val Ala Ile Gly Pro Arg Gly Cys Ser Gly Ser Leu Arg Trp
35          40          45
Leu Gln Glu Ser Asp Ala Ala Pro Leu Pro Leu Ser Cys His Leu Ala
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<211> 2955

<212> DNA

<213> Homo sapiens

<400> 6217

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<210> 6218

<211> 133

<212> PRT

<213> Homo sapiens

<400> 6218

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Gly Tyr Ile Cys Arg Ile Cys His Lys Phe Tyr His Ser Asn Ser Gly
      35             40             45
Ala Gln Leu Ser His Cys Lys Ser Leu Gly His Phe Glu Asn Leu Gln
      50             55             60
Lys Tyr Lys Ala Ala Lys Asn Pro Ser Pro Thr Thr Arg Pro Val Ser
      65             70             75             80
Arg Arg Cys Ala Ile Asn Ala Arg Asn Ala Leu Thr Ala Leu Phe Thr
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Ser Ser Gly Arg Pro Pro Ser Gln Pro Asn Thr Gln Asp Lys Thr Pro
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<210> 6219

<211> 2495

<212> DNA

<213> Homo sapiens

<400> 6219

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Gly Gly Pro Ala Pro Ser Pro Gln Xaa Tyr Ile His Asp Ser Pro Ser
 50 55 60
 Cys Trp Pro Trp Thr Lys Ala Gly Ser Ser Xaa Cys Pro Val Arg Ser
 65 70 75 80
 Pro Tyr Ser Pro Pro Ala Ala Arg Pro Gly Pro Gly Xaa Pro Leu Trp
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 Cys Gln Arg Val Ser Gln Asn Pro Gly Pro Ser Pro Ser Xaa Gly Pro
 100 105 110
 Leu Pro Ser Pro Arg Pro Val Cys Trp Asp Gly Ala Ser Thr Leu Arg
 115 120 125
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<210> 6221
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 <212> DNA
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<210> 6222

<211> 330

<212> PRT

<213> Homo sapiens

<400> 6222

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 35 40 45
 Pro Thr Ser Gly Asp Glu Tyr Ser Arg Gly Phe Leu Gln Asn Leu Asn
 50 55 60
 Leu Ile Gln Asp Gln Asn Ala Gln Thr Arg Trp Lys Gln Gly Arg Tyr
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 Asp Glu Asp Gly Lys Pro Phe Asn Gln Arg Ser Leu Leu Leu Gly His
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<211> 944

<212> DNA

<213> Homo sapiens

<400> 6223

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<210> 6224

<211> 156

<212> PRT

<213> Homo sapiens

<400> 6224

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Ala	Glu	Gly	His	Val	Gly	Gln	Gly	Ala	Pro	Gly	Leu	Met	Gly	Asn	Met
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Asn	Pro	Glu	Gly	Gly	Val	Asn	His	Glu	Asn	Gly	Met	Asn	Arg	Asp	Gly
	50				55					60					
Gly	Met	Ile	Pro	Glu	Gly	Gly	Gly	Asn	Gln	Glu	Pro	Arg	Gln	Gln	
65				70				75					80		
Pro	Gln	Pro	Pro	Pro	Glu	Glu	Pro	Ala	Gln	Ala	Ala	Met	Glu	Gly	Pro
			85					90					95		
Gln	Pro	Glu	Asn	Met	Gln	Pro	Arg	Thr	Arg	Arg	Thr	Lys	Phe	Thr	Leu
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Leu	Gln	Val	Glu	Glu	Leu	Glu	Ser	Val	Phe	Arg	His	Thr	Gln	Tyr	Pro
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Asp	Val	Pro	Thr	Arg	Arg	Glu	Leu	Ala	Glu	Asn	Leu	Gly	Val	Thr	Glu
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<210> 6225

<211> 3851

<212> DNA

<213> Homo sapiens

<400> 6225

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<212> DNA

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<210> 6228

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<213> Homo sapiens

<400> 6228

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<210> 6229

<211> 3105

<212> DNA

<213> Homo sapiens

<400> 6229

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<211> 944

<212> PRT

<213> Homo sapiens

<400> 6230

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 Glu Ala Glu His Pro Lys Lys Val Gln Arg Gly Glu Gly Gly Gly Arg
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 Ser Leu Pro Arg Ser Ser Leu Glu His Gly Ser Asp Val Tyr Leu Leu
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 Gly Arg Ala Ser Val Val Pro Leu Pro Tyr Glu Arg Leu Leu Arg Glu
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His	Ser</														

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<211> 471

<212> DNA

<213> Homo sapiens

<400> 6231

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<210> 6232

<211> 138

<212> PRT

<213> Homo sapiens

<400> 6232

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<211> 894

<212> DNA

<213> Homo sapiens

<400> 6233

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<210> 6234

<211> 230

<212> PRT

<213> Homo sapiens

<400> 6234

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Lys	Lys	Arg	Arg	Val	Gly	Asp	Leu	Leu	Ala	Ser	Tyr	Ile	Pro	Glu	Asp
			20					25					30		
Glu	Ala	Leu	Met	Leu	Arg	Asp	Gly	Arg	Phe	Ala	Cys	Ala	Ile	Cys	Pro
			35				40					45			
His	Arg	Pro	Val	Leu	Asp	Thr	Leu	Ala	Met	Leu	Thr	Ala	His	Arg	Ala
			50			55					60				
Gly	Lys	Lys	His	Leu	Ser	Ser	Leu	Gln	Leu	Phe	Tyr	Gly	Lys	Lys	Gln
65				70					75					80	
Pro	Gly	Lys	Glu	Arg	Lys	Gln	Asn	Pro	Lys	His	Gln	Asn	Glu	Leu	Arg
			85					90					95		
Arg	Glu	Glu	Thr	Lys	Ala	Glu	Ala	Pro	Leu	Leu	Thr	Gln	Thr	Arg	Leu
			100				105						110		
Ile	Thr	Gln	Ser	Ala	Leu	His	Arg	Ala	Pro	His	Tyr	Asn	Ser	Cys	Cys
			115				120					125			
Arg	Arg	Lys	Tyr	Arg	Pro	Glu	Ala	Pro	Gly	Pro	Ser	Val	Ser	Leu	Ser
			130			135					140				
Pro	Met	Pro	Pro	Ser	Glu	Val	Lys	Leu	Gln	Ser	Gly	Lys	Ile	Ser	Arg
145				150					155					160	
Glu	Pro	Glu	Pro	Ala	Ala	Gly	Pro	Gln	Ala	Glu	Glu	Ser	Ala	Thr	Val
			165						170					175	
Ser	Ala	Pro	Ala	Pro	Met	Ser	Pro	Thr	Arg	Arg	Arg	Ala	Leu	Asp	His
			180					185					190		
Tyr	Leu	Thr	Leu	Arg	Ser	Ser	Gly	Trp	Ile	Pro	Asp	Gly	Arg	Gly	Arg
			195				200					205			
Trp	Val	Lys	Asp	Glu	Asn	Val	Glu	Phe	Asp	Ser	Asp	Glu	Glu	Glu	Pro

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Pro Asp Leu Pro Leu Asp		
225	230	

<210> 6235
 <211> 3427
 <212> DNA
 <213> Homo sapiens

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<210> 6236

<211> 820

<212> PRT

<213> Homo sapiens

<400> 6236

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 Pro Glu Gly Gly Leu Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys
 35 40 45
 Lys Ala Thr Gly Ser Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro
 50 55 60
 Gly Ala Glu Glu Gln Thr Gln Val Ala Lys Ala Phe Lys Arg Phe
 65 70 75 80
 Lys Thr Leu Arg His Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu
 85 90 95
 Thr Glu Lys Cys Leu His Val Val Thr Glu Ala Val Thr Pro Leu Gly
 100 105 110
 Ile Tyr Leu Lys Ala Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu
 115 120 125
 Ile Ser Trp Gly Leu His Gln Ile Val Lys Ala Leu Ser Phe Leu Val
 130 135 140
 Asn Asp Cys Ser Leu Ile His Asn Asn Val Cys Met Ala Ala Val Phe
 145 150 155 160
 Val Asp Arg Ala Gly Glu Trp Lys Leu Gly Gly Leu Asp Tyr Met Tyr
 165 170 175
 Ser Ala Gln Gly Asn Gly Gly Gly Pro Pro Arg Lys Gly Ile Pro Glu
 180 185 190
 Leu Glu Gln Tyr Asp Pro Pro Glu Leu Ala Asp Ser Ser Gly Arg Val
 195 200 205
 Val Arg Glu Lys Trp Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile
 210 215 220
 Trp Glu Val Phe Asn Gly Pro Leu Pro Arg Ala Ala Ala Leu Arg Asn

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225          230          235          240
Pro Gly Lys Ile Pro Lys Thr Leu Val Pro His Tyr Cys Glu Leu Val
245          250          255
Gly Ala Asn Pro Lys Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn
260          265          270
Cys Arg Ala Pro Gly Gly Phe Met Ser Asn Arg Phe Val Glu Thr Asn
275          280          285
Leu Phe Leu Glu Glu Ile Gln Ile Lys Glu Pro Ala Glu Lys Gln Lys
290          295          300
Phe Phe Gln Glu Leu Ser Lys Ser Leu Asp Ala Phe Pro Glu Asp Phe
305          310          315
Cys Arg His Lys Val Leu Pro Gln Leu Leu Thr Ala Phe Glu Phe Gly
325          330          335
Asn Ala Gly Ala Val Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe
340          345          350
Leu Ser Ala Glu Glu Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys
355          360          365
Met Phe Ser Ser Thr Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln
370          375          380
Met Glu Gln Phe Ile Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln
385          390          395
Ile Phe Pro His Val Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile
405          410          415
Arg Glu Gln Thr Val Lys Ser Met Leu Leu Leu Ala Pro Lys Leu Asn
420          425          430
Glu Ala Asn Leu Asn Val Glu Leu Met Lys His Phe Ala Arg Leu Gln
435          440          445
Ala Lys Asp Glu Gln Gly Pro Ile Arg Cys Asn Thr Thr Val Cys Leu
450          455          460
Gly Lys Ile Gly Ser Tyr Leu Ser Ala Ser Thr Arg His Arg Val Leu
465          470          475
Thr Ser Ala Phe Ser Arg Ala Thr Arg Asp Pro Phe Ala Pro Ser Arg
485          490          495
Val Ala Gly Val Leu Gly Phe Ala Ala Thr His Asn Leu Tyr Ser Met
500          505          510
Asn Asp Cys Ala Gln Lys Ile Leu Pro Val Leu Cys Gly Leu Thr Val
515          520          525
Asp Pro Glu Lys Ser Val Arg Asp Gln Ala Phe Lys Ala Ile Arg Ser
530          535          540
Phe Leu Ser Lys Leu Glu Ser Val Ser Glu Asp Pro Thr Gln Leu Glu
545          550          555
Glu Val Glu Lys Asp Val His Ala Ala Ser Ser Pro Gly Met Gly Gly
565          570          575
Ala Ala Ala Ser Trp Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu
580          585          590
Thr Ser Lys Leu Ile Arg Ser His Pro Thr Thr Ala Pro Thr Glu Thr
595          600          605
Asn Ile Pro Gln Arg Pro Thr Pro Glu Gly Val Pro Ala Pro Ala Pro
610          615          620
Thr Pro Val Pro Ala Thr Pro Thr Thr Ser Gly His Trp Glu Thr Gln
625          630          635
Glu Glu Asp Lys Asp Thr Ala Glu Asp Ser Ser Thr Ala Asp Arg Trp
645          650          655
Asp Asp Glu Asp Trp Gly Ser Leu Glu Gln Glu Ala Glu Ser Val Leu

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        660              665              670
Ala Gln Gln Asp Asp Trp Ser Thr Gly Gly Gln Val Ser Arg Ala Ser
      675              680              685
Gln Val Ser Asn Ser Asp His Lys Ser Ser Lys Ser Pro Glu Ser Asp
      690              695              700
Trp Ser Ser Trp Glu Ala Glu Gly Ser Trp Glu Gln Gly Trp Gln Glu
      705              710              715              720
Pro Ser Ser Gln Glu Pro Pro Pro Asp Gly Thr Arg Leu Ala Ser Glu
      725              730              735
Tyr Asn Trp Gly Gly Pro Glu Ser Ser Asp Lys Gly Asp Pro Phe Ala
      740              745              750
Thr Leu Ser Ala Arg Pro Ser Thr Gln Pro Arg Pro Asp Ser Trp Gly
      755              760              765
Glu Asp Asn Trp Glu Gly Leu Glu Thr Asp Ser Arg Gln Val Lys Ala
      770              775              780
Glu Leu Ala Arg Lys Lys Arg Glu Glu Arg Arg Glu Met Glu Ala
      785              790              795              800
Lys Arg Ala Glu Arg Lys Val Ala Lys Gly Pro Met Lys Leu Gly Ala
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Arg Lys Leu Asp
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<210> 6237

<211> 494

<212> DNA

<213> Homo sapiens

<400> 6237

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120
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180
atggaatgag tagcaagagt cgaaagagaa tcattgcccga ccctgtgacg gagccccctg
240
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300
gcatggaagg tcattgcccc catcatttta agctgggtctc agtgcattgt ttcattcgcc
360
acggagacag gtaccactg tatgtcattt ccaaaacaaa gcgaccagaa attgactgca
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<210> 6238

<211> 141

<212> PRT

<213> Homo sapiens

<400> 6238

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20	25	30	
Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met			
35	40	45	
Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala			
50	55	60	
Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly			
65	70	75	80
His Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile Arg			
85	90	95	
His Gly Asp Arg Tyr Pro Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro			
100	105	110	
Glu Ile Asp Cys Thr Leu Val Ala Asn Arg Lys Pro Tyr His Pro Lys			
115	120	125	
Leu Glu Ala Phe Ile Ser His Met Leu Arg Gly Ser Gly			
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<210> 6239

<211> 911

<212> DNA

<213> Homo sapiens

<400> 6239

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aaaaaaaaa a
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<210> 6240
<211> 235
<212> PRT
<213> Homo sapiens

<400> 6240
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35 40 45
Phe Arg Lys Phe Gln Val Trp Arg Leu Val Thr Asn Phe Leu Phe Phe
50 55 60
Gly Pro Leu Gly Phe Ser Phe Phe Phe Asn Met Leu Phe Val Phe Arg
65 70 75 80
Tyr Cys Arg Met Leu Glu Glu Gly Ser Phe Arg Gly Arg Thr Ala Asp
85 90 95
Phe Val Phe Met Phe Leu Phe Gly Gly Val Leu Met Thr Leu Leu Gly
100 105 110
Leu Leu Gly Ser Leu Phe Phe Leu Gly Gln Ala Leu Met Ala Met Leu
115 120 125
Val Tyr Val Trp Ser Arg Arg Ser Pro Arg Val Arg Val Asn Phe Phe
130 135 140
Gly Leu Leu Thr Phe Gln Ala Pro Phe Leu Pro Trp Ala Leu Met Gly
145 150 155 160
Phe Ser Leu Leu Leu Gly Asn Ser Ile Leu Val Asp Leu Leu Gly Ile
165 170 175
Ala Val Gly His Ile Tyr Tyr Phe Leu Glu Asp Val Phe Pro Asn Gln
180 185 190
Pro Gly Gly Lys Arg Leu Leu Gln Thr Pro Gly Phe Leu Lys Leu Leu
195 200 205
Leu Asp Ala Pro Ala Glu Asp Pro Asn Tyr Leu Pro Leu Pro Glu Glu
210 215 220
Gln Pro Gly Pro His Leu Pro Pro Pro Gln Gln
225 230 235

<210> 6241
<211> 1515
<212> DNA
<213> Homo sapiens

<400> 6241
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180
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240

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 420
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<210> 6242

<211> 245

<212> PRT

<213> Homo sapiens

<400> 6242

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   35                40                45
Gly Glu Pro Pro Pro Pro Glu Leu Ala Leu Leu Pro Pro Pro Pro Pro
   50                55                60
Pro Pro Pro Thr Pro Ala Thr Pro Thr Ser Ser Ala Ser Asn Leu Asp
   65                70                75                80
Leu Gly Glu Gln Arg Asp Ala Trp Glu Thr Phe Gln Lys Arg Gln Lys
   85                90                95
Leu Thr Ser Glu Gly Ala Ala Lys Leu Leu Asp Thr Phe Glu Tyr
   100                105                110
Gln Gly Leu Val Lys His Thr Gly Gly Cys His Cys Gly Ala Val Arg
   115                120                125
Phe Glu Val Trp Ala Ser Ala Asp Leu His Ile Phe Asp Cys Asn Cys
   130                135                140
Ser Ile Cys Lys Lys Lys Gln Asn Arg His Phe Ile Val Pro Ala Ser
   145                150                155                160
Arg Phe Lys Leu Leu Lys Gly Ala Glu His Ile Thr Thr Tyr Thr Phe
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1090          1095          1100
Ser Leu Glu Val Ile Glu Ile Gln Ala Arg Ser Ser Ala Gly Thr Pro
1105          1110          1115          1120
Ala Arg Ala Tyr Leu Asp Ile Pro Asn Pro Arg Tyr Leu Gly Pro Ala
          1125          1130          1135
Ile Ser Ser Gly Ala Ile Tyr Leu Ala Ser Ser Tyr Gln Asp Lys Leu
          1140          1145          1150
Arg Val Ile Cys Cys Lys Gly Asn Leu Val Lys Glu Ser Gly Thr Glu
          1155          1160          1165
His His Arg Gly Pro Ser Thr Ser Arg Ser Ser Pro Asn Lys Arg Gly
1170          1175          1180
Pro Pro Thr Tyr Asn Glu His Ile Thr Lys Arg Val Ala Ser Ser Pro
1185          1190          1195          1200
Ala Pro Pro Glu Gly Pro Ser His Pro Arg Glu Pro Ser Thr Pro His
          1205          1210          1215
Arg Tyr Arg Glu Gly Arg Thr Glu Leu Arg Arg Asp Lys Ser Pro Gly
          1220          1225          1230
Arg Pro Leu Glu Arg Glu Lys Ser Pro Gly Arg Met Leu Ser Thr Arg
          1235          1240          1245
Arg Glu Arg Ser Pro Gly Arg Leu Phe Glu Asp Ser Ser Arg Gly Arg
          1250          1255          1260
Leu Pro Ala Gly Ala Val Arg Thr Pro Leu Ser Gln Val Asn Lys Val
1265          1270          1275          1280
Trp Asp Gln Ser Ser Val
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<210> 6247

<211> 497

<212> DNA

<213> Homo sapiens

<400> 6247

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120
aaggctgcat ggggggtcctt gcccgggagg cgccccacct agagaaacag ccggcagccg
180
gcccgcagcg cgttctcccc ggagagaaat attattcatc tgtgccagag gaaggagggg
240
caacccatgt ctatcggtat cacagaggcg agtcgaagct gcacatgtgc ttggacatag
300
ggaatgggtca gagaaaagac agaaaaaaga catcccttgg tcctggaggc agctatcaaa
360

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tatcagagca tgctccagag gcatcccagc ctgtgagtac ggaactgctt acgcactggg
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 497

<210> 6248

<211> 142

<212> PRT

<213> Homo sapiens

<400> 6248

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Ser	Ala	Gly	Glu	Gly	Gln	Glu	Glu	Gly	Gly	Gly	Leu	Ala	Cys	Pro	Gly
			20					25					30		
Ala	Ser	Gln	Arg	Leu	His	Gly	Gly	Pro	Cys	Pro	Gly	Gly	Ala	Pro	Pro
			35				40					45			
Arg	Glu	Thr	Ala	Gly	Ser	Arg	Pro	Ala	Ala	Arg	Ser	Pro	Gly	Arg	Glu
	50					55					60				
Ile	Leu	Phe	Ile	Cys	Ala	Arg	Gly	Arg	Arg	Gly	Asn	Pro	Cys	Leu	Ser
65					70				75					80	
Leu	Ser	Gln	Arg	Arg	Val	Glu	Ala	Ala	His	Val	Leu	Gly	His	Arg	Glu
			85						90					95	
Trp	Ser	Glu	Lys	Arg	Gln	Lys	Lys	Asp	Ile	Pro	Trp	Ser	Trp	Arg	Gln
			100				105						110		
Leu	Ser	Asn	Ile	Arg	Ala	Cys	Ser	Arg	Gly	Ile	Pro	Ala	Cys	Glu	Tyr
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Gly	Thr	Ala	Tyr	Ala	Leu	Gly	Phe	Thr	Thr	Val	Ala	Thr	Pro		
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<210> 6249

<211> 1217

<212> DNA

<213> Homo sapiens

<400> 6249

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 180
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 240
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 attaatgagt ccaaacttca ggaactggaa aagtacccgg gtattcaaac tcgtgtcctt
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 420
 ctctttaatg ttgctggttt tgtccatcat ggaactgtcc tggattgtga ggagaaagac
 480

tgggacttct cgatgaatct caatgtgcgc agcatgtacc tgatgatcaa ggcattcctt
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 720
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 840
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 960
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 1020
 taatcacatg ttaatgaaaa taagctcttt ttaatgatgt cactgtttgc aagagtctga
 1080
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 1200
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 1217

<210> 6250

<211> 245

<212> PRT

<213> Homo sapiens

<400> 6250

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 20 25 30
 Val Ile Ala Thr Asp Ile Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys
 35 40 45
 Tyr Pro Gly Ile Gln Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln
 50 55 60
 Ile Asp Gln Phe Ala Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn
 65 70 75 80
 Val Ala Gly Phe Val His His Gly Thr Val Leu Asp Cys Glu Glu Lys
 85 90 95
 Asp Trp Asp Phe Ser Met Asn Leu Asn Val Arg Ser Met Tyr Leu Met
 100 105 110
 Ile Lys Ala Phe Leu Pro Lys Met Leu Ala Gln Lys Ser Gly Asn Ile
 115 120 125
 Ile Asn Met Ser Ser Val Ala Ser Ser Val Lys Gly Val Val Asn Arg
 130 135 140
 Cys Val Tyr Ser Thr Lys Lys Ala Ala Val Ile Gly Leu Thr Lys Ser
 145 150 155 160
 Val Ala Ala Asp Phe Ile Gln Gln Gly Ile Arg Cys Asn Cys Val Cys

165					170					175						
Pro	Gly	Thr	Val	Asp	Thr	Pro	Ser	Leu	Gln	Glu	Arg	Ile	Gln	Ala	Arg	
180					185					190						
Gly	Asn	Pro	Glu	Glu	Ala	Arg	Asn	Asp	Phe	Leu	Lys	Arg	Gln	Lys	Thr	
195					200					205						
Gly	Arg	Phe	Ala	Thr	Ala	Glu	Glu	Ile	Ala	Met	Leu	Cys	Val	Tyr	Leu	
210					215					220						
Ala	Ser	Asp	Glu	Ser	Ala	Tyr	Val	Thr	Gly	Asn	Pro	Val	Ile	Ile	Asp	
225					230					235					240	
Gly	Gly	Trp	Ser	Leu												
245																

<210> 6251

<211> 1611

<212> DNA

<213> Homo sapiens

<400> 6251

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120					
ttttgtgact	ttttccgttt	ctttacaata	ggacttctct	cagtgtgtga	caccagtgaa
180					
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240					
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300					
aaggaggaga	aagaccacgc	acgggcagca	gcctggaggg	acccggtggg	ctgctgagag
360					
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420					
gctgggagcc	ctaggccgga	ctgcatttcc	gctcccgcat	gagactttct	atgaaataaa
480					
tatagaaaag	agggcatccc	ccagccccc	agcacaaagc	cctggccctc	agcgctggac
540					
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600					
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660					
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720					
gaaactgagg	cacaaggagg	tttgggaact	tgcccgaagt	cactcacagt	gagtcagctt
780					
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840					
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900					
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960					
aagtccagta	agggcaaggg	gagggggcat	tctggtgaga	acagctattt	tgccaagacg
1020					
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1080					

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 1320
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 1440
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 1500
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<210> 6252
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 6252
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 Ala Lys Ser Ser Lys Gly Lys Gly Arg Gly His Ser Gly Glu Asn Ser
 20 25 30
 Ile Ser Gly Lys Thr Gly Ile His Phe Lys Ile Ser Ala Gln Lys Gly
 35 40 45
 Ser Arg Ala Val Leu Lys Pro Gly Arg Gln Gly Pro Pro Ile Pro Thr
 50 55 60
 Ile Leu Leu Ser Pro Ser Pro Pro Trp Arg Thr Leu Ala Arg Val Tyr
 65 70 75 80
 Arg Glu Ser His His Ile Tyr Tyr Glu Ala Arg Ala Leu Gly Tyr Val
 85 90 95
 Pro Thr Ile Pro
 100

<210> 6253
 <211> 1953
 <212> DNA
 <213> Homo sapiens

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 120
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 180
 ggaccgaaga tgagcttcc cttcagcagc cgctcttcta aaacattcaa accaaagaag
 240

aatatccctg aaggatctca tcagtatgaa ctcttaaaac atgcagaagc aactctagga
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360
gctgtgaaca ctgtggattt cttaaccag atcaacatgt tatatggaac tattacagaa
420
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480
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540
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720
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1080
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1260
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1320
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1440
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1500
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1680
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1800
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1860

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1920

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa

1953

<210> 6254

<211> 216

<212> PRT

<213> Homo sapiens

<400> 6254

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      20           25           30
Glu Ala Thr Leu Gly Ser Gly Asn Leu Arg Gln Ala Val Met Leu Pro
      35           40           45
Glu Gly Glu Asp Leu Asn Glu Trp Ile Ala Val Asn Thr Val Asp Phe
      50           55           60
Phe Asn Gln Ile Asn Met Leu Tyr Gly Thr Ile Thr Glu Phe Cys Thr
      65           70           75           80
Glu Ala Ser Cys Pro Val Met Ser Ala Gly Pro Arg Tyr Glu Tyr His
      85           90           95
Trp Ala Asp Gly Thr Asn Ile Lys Lys Pro Ile Lys Cys Ser Ala Pro
      100          105          110
Lys Tyr Ile Asp Tyr Leu Met Thr Trp Val Gln Asp Gln Leu Asp Asp
      115          120          125
Glu Thr Leu Phe Pro Ser Lys Ile Gly Val Pro Phe Pro Lys Asn Phe
      130          135          140
Met Ser Val Ala Lys Thr Ile Leu Lys Arg Leu Phe Arg Val Tyr Ala
      145          150          155          160
His Ile Tyr His Gln His Phe Asp Ser Val Met Gln Leu Gln Glu Glu
      165          170          175
Ala His Leu Asn Thr Ser Phe Lys His Phe Ile Phe Phe Val Gln Glu
      180          185          190
Phe Asn Leu Ile Asp Arg Arg Glu Leu Ala Pro Leu Gln Glu Leu Ile
      195          200          205
Glu Lys Leu Gly Ser Lys Asp Arg
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<210> 6255

<211> 622

<212> DNA

<213> Homo sapiens

<400> 6255

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  120
aaagccacag tggtgcctt cacagccagc gagggccacg cacatccagc ggtagtggag
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ctaccaaga cggtgaggg cctaggcttc aacatcatgg gtggcacaaga gcaaaactcg
  240
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cccatctaca tctccgggt catcccagg ggtgtggctg accgccatgg aggcctcaag
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360
gcgggtggagc tgctgaaggc ggcccagggc tcggtgaagc tggttgctcc ttacacaccg
420
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622

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<210> 6256
<211> 150
<212> PRT
<213> Homo sapiens

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<400> 6256
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Lys Lys Lys Ala Thr Val Ala Ala Phe Thr Ala Ser Glu Gly His Ala
20 25 30
His Pro Arg Val Val Glu Leu Pro Lys Thr Asp Glu Gly Leu Gly Phe
35 40 45
Asn Ile Met Gly Gly Lys Glu Gln Asn Ser Pro Ile Tyr Ile Ser Arg
50 55 60
Val Ile Pro Gly Gly Val Ala Asp Arg His Gly Gly Leu Lys Arg Gly
65 70 75 80
Asp Gln Leu Leu Ser Val Asn Gly Val Ser Val Glu Gly Glu Gln His
85 90 95
Glu Lys Ala Val Glu Leu Leu Lys Ala Ala Gln Gly Ser Val Lys Leu
100 105 110
Val Val Arg Tyr Thr Pro Arg Val Leu Glu Glu Met Glu Ala Arg Phe
115 120 125
Glu Lys Met Arg Ser Ala Arg Arg Gln Gln His Gln Ser Tyr Ser
130 135 140
Ser Leu Glu Ser Arg Gly
145 150

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<210> 6257
<211> 2216
<212> DNA
<213> Homo sapiens

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<400> 6257
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120
tcctctgttg aggggaaggtc ttgggtccca gatgcctact ctgcaggaga gggaggaacc
180

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ttgtcccttt ggggagtcg ctggtctctt ctgttgtggg gaagaaggaa ggtgggaggg
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1560
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1800

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 1860
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 1980
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<210> 6258

<211> 340

<212> PRT

<213> Homo sapiens

<400> 6258

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Phe	Gln	Ala	Leu	Gln	Arg	Leu	His	Met	Thr	Ile	Phe	Ser	Gln	Ser	Val
			20					25					30		
Ser	Pro	Cys	Gly	Lys	Phe	Leu	Ala	Ala	Gly	Asn	Asn	Tyr	Gly	Gln	Ile
		35					40					45			
Ala	Ile	Phe	Ser	Leu	Ser	Ser	Ala	Leu	Ser	Ser	Glu	Ala	Lys	Glu	Glu
	50					55					60				
Ser	Lys	Lys	Pro	Val	Val	Thr	Phe	Gln	Ala	His	Asp	Gly	Pro	Val	Tyr
	65				70					75				80	
Ser	Met	Val	Ser	Thr	Asp	Arg	His	Leu	Leu	Ser	Ala	Gly	Asp	Gly	Glu
			85						90					95	
Val	Lys	Ala	Trp	Leu	Trp	Ala	Glu	Met	Leu	Lys	Lys	Gly	Cys	Lys	Glu
			100					105					110		
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Thr	Leu	Trp	His	Leu	Arg	Ser	Ser	Thr	Pro	Thr	Thr	Ile	Phe	Pro	Ile
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<210> 6259

<211> 384

<212> DNA

<213> Homo sapiens

<400> 6259

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<210> 6260

<211> 128

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Gln Lys Asn Glu Lys Ile Lys Tyr Ser Arg Phe Ala Ala Thr Asn Thr
35          40          45
Arg Val Lys Ala Lys Gln Lys Pro Leu Ile Ser Asn Ser His Thr Asp
50          55          60
His Leu Met Gly Cys Thr Lys Ser Ala Glu Pro Gly Thr Glu Thr Ser
65          70          75          80
Gln Val Asn Ser Phe Ser Asp Leu Lys Ala Ser Thr Leu Val His Lys
85          90          95
Pro Gln Ser Asp Phe Thr Asn Asp Ala Leu Ser Pro Lys Phe Asn Leu
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<212> PRT

<213> Homo sapiens

<400> 6262

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Val	Arg	Leu	Gln	Asn	Glu	Thr	Ser	Tyr	Ser	Arg	Val	Leu	His	Gly	Tyr
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Ala	Ala	Gln	Gln	Leu	Pro	Ser	Leu	Leu	Lys	Glu	Arg	Glu	Phe	His	Leu
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Val	Val	Cys	Gly	Thr	Lys	Cys	Asn	Thr	Leu	Phe	Val	Val	Asp	Val	Gln
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Gly	Val	Thr	Gln	Gln	Gly	Cys	Gly	Ile	His	Ala	Ile	Glu	Leu	Asn	Pro
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Ser	Arg	Thr	Leu	Leu	Ala	Thr	Gly	Gly	Asp	Asn	Pro	Asn	Ser	Leu	Ala
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Ile	Tyr	Arg	Leu	Pro	Thr	Leu	Asp	Pro	Val	Cys	Val	Gly	Asp	Asp	Gly
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Lys Asn Lys Glu Leu Gly Ala Val Ser Leu Asp Gly Tyr Phe His Leu		
245	250	255
Trp Lys Ala Glu Asn Thr Leu Ser Lys Leu Leu Ser Thr Lys Leu Pro		
260	265	270
Tyr Cys Arg Glu Asn Val Cys Leu Ala Tyr Gly Ser Glu Trp Ser Val		
275	280	285
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290	295	300
Pro Ser Tyr Asn Val Lys Ser Val Cys Ser Arg Glu Arg Gly Ser Gly		
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Ile Arg Ser Val Ser Phe Tyr Glu His Ile Thr Val Gly Thr Gly		
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Gln Gly Ser Leu Leu Phe Tyr Asp Ile Arg Ala Gln Arg Phe Leu Glu		
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Glu Arg Leu Ser Ala Cys Tyr Gly Ser Lys Pro Arg Leu Ala Gly Glu		
355	360	365
Asn Leu Lys Leu Thr Thr Gly Lys Gly Trp Leu Asn His Asp Glu Thr		
370	375	380
Trp Arg Asn Tyr Phe Ser Asp Ile Asp Phe Phe Pro Asn Ala Val Tyr		
385	390	395
Thr His Cys Tyr Asp Ser Ser Gly Thr Lys Leu Phe Val Ala Gly Gly		
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<212> DNA

<213> Homo sapiens

<400> 6263

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<212> PRT

<213> Homo sapiens

<400> 6264

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Ser	Ser	Ala	Phe	Arg	Pro	Val	Met	Pro	Ser	Arg	Gln	Ile	Val	Glu	Arg
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Gln	Pro	Arg	Met	Leu	Asp	Phe	Arg	Val	Glu	Tyr	Arg	Asp	Arg	Asn	Val
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			165					170					175		
Pro	Ser	Ser	Ser	Ser	His	Ala	Gly	Ala	Leu	Gln	Glu	Ser	Leu	Asn	Gln
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	195					200					205				
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      355              360              365
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      500              505              510
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      530              535              540
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      545              550              555              560
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      565              570              575
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      580              585              590
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      595              600              605
Ser Lys Gly Phe Pro Trp Asp Glu Tyr Lys Leu Leu Ser Thr Phe Pro
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<210> 6265

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 6265

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480
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780
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840
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960
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<210> 6266

<211> 240

<212> PRT

<213> Homo sapiens

<400> 6266

Xaa Ala Leu Pro Ala Ser His Arg Pro Gly Gln Gln Gly Leu Asn Pro

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Tyr Leu Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu
      20             25             30
Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Met Gln Ser
      35             40             45
Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn
      50             55             60
Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp
      65             70             75
Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn
      85             90             95
His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala
      100            105            110
Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met
      115            120            125
Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln
      130            135            140
Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp
      145            150            155
Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr
      165            170            175
Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser
      180            185            190
Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu
      195            200            205
Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro Glu
      210            215            220
Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val Asp Gly
      225            230            235            240

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<210> 6267

<211> 328

<212> DNA

<213> Homo sapiens

<400> 6267

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120
gatgagcctt tcttcagatt ccgaaggaac gtgttcttcc caaagcggcg ggagctccag
180
atccatgacg aggggtcctt ggggctgctc tatgaggagg ccaagggcaa cgtgctggct
240
gcacgggtacc cgtgcgacgt ggaggactgc gaggctctgg gcgccctggt gtgccgcgtg
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<210> 6268

<211> 83

<212> PRT

<213> Homo sapiens

<400> 6268

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 20 25 30
 Leu Gln Ile His Asp Glu Glu Val Leu Arg Leu Leu Tyr Glu Glu Ala
 35 40 45
 Lys Gly Asn Val Leu Ala Ala Arg Tyr Pro Cys Asp Val Glu Asp Cys
 50 55 60
 Glu Ala Leu Gly Ala Leu Val Cys Arg Val Gln Leu Gly Pro Tyr Gln
 65 70 75 80
 Pro Gly Arg

<210> 6269

<211> 923

<212> DNA

<213> Homo sapiens

<400> 6269

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 120
 aacgtgatgg ttctccagga cgaaaatttt gtcagtaaag aagagttcca ggcagtgagg
 180
 aagaagctgg tggaagagaa agctgcccat gccaaaaacca aggtcctcct ggccaaggaa
 240
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 300
 gagaagctgg cctttgaaaa agcgctctcc agtgtaaga gcaaatcctc tcaggagtcc
 360
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 420
 gaagatatac ttaatggcaa agagaatgag attaaagagt tgcagcaagt tatcagccag
 480
 cagaaacaga tcttcagccc accaccagcc gggtccgttg caggaatcac atgtctgact
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 gccgctttcc tgttctctgg ctgtaatccc cagcctctgc cttctctgct ctgggagctc
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 780
 ggggcttgta gcctagggga ggagctgggt ctttgtgtgc tggtaggcac caccgcttcc
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<210> 6270

<211> 307

<212> PRT

<213> Homo sapiens

<400> 6270

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Ser Val Cys Leu Ala Leu Asp Gln Leu Arg Asp Val Ile Glu Ser Gln
      20           25           30
Glu Glu Leu Ile His Gln Leu Arg Asn Val Met Val Leu Gln Asp Glu
 35           40           45
Asn Phe Val Ser Lys Glu Glu Phe Gln Ala Val Glu Lys Lys Leu Val
 50           55           60
Glu Glu Lys Ala Ala His Ala Lys Thr Lys Val Leu Leu Ala Lys Glu
 65           70           75           80
Glu Glu Lys Leu Gln Phe Ala Leu Gly Glu Val Glu Val Leu Ser Lys
      85           90           95
Gln Leu Glu Lys Glu Lys Leu Ala Phe Glu Lys Ala Leu Ser Ser Val
 100          105          110
Lys Ser Lys Val Leu Gln Glu Ser Ser Lys Lys Asp Gln Leu Ile Thr
 115          120          125
Lys Cys Asn Glu Ile Glu Ser His Ile Ile Lys Gln Glu Asp Ile Leu
 130          135          140
Asn Gly Lys Glu Asn Glu Ile Lys Glu Leu Gln Gln Val Ile Ser Gln
 145          150          155          160
Gln Lys Gln Ile Phe Ser Pro Pro Pro Ala Gly Ser Val Ala Gly Ile
      165          170          175
Thr Cys Leu Thr Ser Gly Ser Arg Ser Ser Arg Lys Ala Thr Trp Pro
 180          185          190
Arg Cys Trp Thr Arg Ser Ile Arg Lys Pro Gln Gly His Val Arg Pro
 195          200          205
Ala Ala Thr Ser Ile Pro Gly Lys Asn Lys Met Ala Ala Ala Phe Leu
 210          215          220
Phe Ser Gly Cys Asn Pro Gln Pro Leu Pro Ser Leu Leu Trp Glu Ser
 225          230          235          240
Pro Ala Ser Ser Pro Cys Tyr Phe Pro Pro Ser Trp Ile Val Val Gly
      245          250          255
Val His Lys Val Gly Ala Cys Ser Leu Gly Glu Glu Leu Gly Leu Cys
 260          265          270
Cys Leu Val Gly Thr Thr Ala Ser Phe Gly Tyr Leu Ile Pro Ser Tyr
 275          280          285
Ile Asn Ser Pro Gly Tyr Pro Val Ile Phe His Pro Thr Pro Ser Val
 290          295          300
Leu Val Asn
305

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<210> 6271

<211> 1437

<212> DNA

<213> Homo sapiens

<400> 6271

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 180
 agtggagctg gaatggtgag accaacaatcc gtgacacctg gactctttca ggttctgaag
 240
 gctgtatact ttgcattgta ctccaaagcc aaagagcaat ttaatggcat tttcgtgcct
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 aacagcaata ttgtgcattct tttctcagct ggctctgcag cttttatcac aaattcctta
 360
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 420
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 600
 actgagaaaa attccacaag tttttttgga cttatggcag ctgctgctct ttctaagggc
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 1320
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<210> 6272

<211> 296

<212> PRT

<213> Homo sapiens

<400> 6272

Xaa Met Ala Thr Gly Gly Gln Gln Lys Glu Asn Thr Leu Leu His Leu


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      20           25           30
Leu Glu Val Ile Lys Thr Arg Leu Gln Ser Ser Arg Leu Ala Leu Arg
      35           40           45
Thr Val Tyr Tyr Pro Gln Val His Leu Gly Thr Ile Ser Gly Ala Gly
      50           55           60
Met Val Arg Pro Thr Ser Val Thr Pro Gly Leu Phe Gln Val Leu Lys
      65           70           75           80
Ala Val Tyr Phe Ala Cys Tyr Ser Lys Ala Lys Glu Gln Phe Asn Gly
      85           90           95
Ile Phe Val Pro Asn Ser Asn Ile Val His Leu Phe Ser Ala Gly Ser
      100          105          110
Ala Ala Phe Ile Thr Asn Ser Leu Met Asn Pro Ile Trp Met Val Lys
      115          120          125
Thr Arg Met Gln Leu Glu Gln Lys Val Arg Gly Ser Lys Gln Met Asn
      130          135          140
Thr Leu Gln Cys Ala Arg Tyr Val Tyr Gln Thr Glu Gly Ile Arg Gly
      145          150          155          160
Phe Tyr Arg Gly Leu Thr Ala Ser Tyr Ala Gly Ile Ser Glu Thr Ile
      165          170          175
Ile Cys Phe Ala Ile Tyr Glu Ser Leu Lys Lys Tyr Leu Lys Glu Ala
      180          185          190
Pro Leu Ala Ser Ser Ala Asn Gly Thr Glu Lys Asn Ser Thr Ser Phe
      195          200          205
Phe Gly Leu Met Ala Ala Ala Ala Leu Ser Lys Gly Cys Ala Ser Cys
      210          215          220
Ile Ala Tyr Pro His Glu Val Ile Arg Thr Arg Leu Arg Glu Glu Gly
      225          230          235          240
Thr Lys Tyr Lys Ser Phe Val Gln Thr Ala Arg Leu Val Phe Arg Glu
      245          250          255
Glu Gly Tyr Leu Ala Phe Tyr Arg Gly Leu Phe Ala Gln Leu Ile Arg
      260          265          270
Gln Ile Pro Asn Thr Ala Ile Val Leu Ser Thr Tyr Glu Leu Ile Val
      275          280          285
Tyr Leu Leu Glu Asp Arg Thr Gln
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<210> 6273

<211> 2355

<212> DNA

<213> Homo sapiens

<400> 6273

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120
tggaactggt caccaaccag ccgcggccgg cagctgggtg acaaggacag caccttctc
180
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240
gctgacaagc gggaccaga gtttgtcttc tacgaccagc tgaagcaagt gatgaatgcg
300

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360
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420
t a c a a g a c c g t c c a g a g g c t g c t c g t g a a g g c c a a g a c a c a g t g a c a c a g c c a c c c c c a c
480
a g c c g g a g c c c c g c c g c t c c a c a g t c c c t g g g g c c g a g c a c g a g t g a g t g g a c a c t g c c
540
c g c c g c g g g c g g c c c t g c a g g g a c a g g g c c c t c t c c c t c c c c g g c g g t g g t t g g a a c a
600
c t g a a t t a c a g a g c t t t t t t c t g t t g c t c t c c g a g a c t g g g g g g a t t g t t c t c t c t t
660
t c c t t g t c t t t g a a c t t c c t t g g a g g a g a g c t t g g g a g a c g t c c c g g g g c c a g g c t a c g g
720
a c t t g c g g a c g a g c c c c c c a g t c c t g g g a g c c g g c c g c c c t c g g t c t g g t g t a a g c a c a c
780
a t g c a c g a t t a a a g a g g a g a c g c c g g g a c c c c t g c c c g a t c g c g c g c g g c c t c c g c c c a
840
c g c c t c c t g c c g c a a g g g g c c t g g a c t g c a g g c c t g a c t g t c c c t g c t c c g t g t c t g
900
t c c t a g g a c g t c c c c t c c c g c t c c c c g a t g t g g c g t g g a c a t g g t t a t t t a t c t c t g c t
960
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1020
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1080
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1140
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1200
g t t c c c c t g c a c t c c t e t t c t c c a g c c c a t c c c t c c g g c c c c t g t g c c t c t g c g g c c c c
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a g c c c a g c t c c a g g g c c g t c a c c t g c t t g g c c t g g c c a g t c c c t g c c c t a g a t c c t g
1320
a g c c a g t g c c t g g t g t t t c c t g g g c t c g g t a c t g g g c c c c a g g c n a t c c a g g g c t t t g c
1380
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1440
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1620
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1680
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1740
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1800
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1860
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1920

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 1980
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<210> 6274

<211> 70

<212> PRT

<213> Homo sapiens

<400> 6274

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		20						25					30		
Ala	Ala	Tyr	Leu	Gly	Met	Ala	Tyr	Val	Ala	Val	Gln	Val	Ser	Ser	Ala
		35					40					45			
Gln	Ala	Gln	His	Phe	Ser	Leu	Leu	Tyr	Lys	Thr	Val	Gln	Arg	Leu	Leu
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Val	Lys	Ala	Lys	Thr	Gln										
65														70	

<210> 6275

<211> 1534

<212> DNA

<213> Homo sapiens

<400> 6275

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 720
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 1440
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<210> 6276

<211> 172

<212> PRT

<213> Homo sapiens

<400> 6276

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 20 25 30
 Asp Asp Leu Ser Asn Ala Ala Arg Glu Leu Arg Val Leu Ile Asp Asp
 35 40 45
 Ser Gln Ser Ile Ile Phe Ile Asn Leu Asp Ser His Arg Asn Val Met
 50 55 60
 Ile Arg Leu Asn Leu Gln Leu Thr Met Gly Thr Phe Ser Leu Ser Leu

65		70		75		80									
Phe	Gly	Leu	Met	Gly	Val	Ala	Phe	Gly	Met	Asn	Leu	Glu	Ser	Ser	Leu
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<210> 6277

<211> 1206

<212> DNA

<213> Homo sapiens

<400> 6277

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<210> 6278

<211> 399

<212> PRT

<213> Homo sapiens

<400> 6278

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<210> 6279

<211> 2795

<212> DNA

<213> Homo sapiens

<400> 6279

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 <212> PRT
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 His Gly Leu Arg His Gly Asp Phe Gln Arg Tyr Arg Gly Tyr Cys Ser
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 85 90 95
 Arg His Lys Phe Thr Gly Lys Lys Val Thr Glu Glu Leu Leu Thr Asp
 100 105 110
 Asn Arg Tyr Leu Leu Val Leu Met Asp Ala Glu Arg Ala Trp Ser
 115 120 125
 Tyr Ala Met Gln Leu Lys Gln Glu Ala Asn Thr Glu Pro Arg Lys Arg
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 Phe His Leu Leu Ser Arg Leu Arg Lys Ala Val Lys His Ala Glu Glu
 145 150 155 160
 Leu Glu Arg Leu Cys Lys Ser Asn Arg Val Asp Ala Lys Thr Lys Leu
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 180 185 190
 His Gln Glu Trp Lys Ala Ala Ile Glu Ala Phe Asn Lys Cys Lys Thr
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 Ile Tyr Glu Lys Leu Ala Ser Ala Phe Thr Glu Glu Gln Ala Val Leu
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 Tyr Asn Gln Arg Val Glu Glu Ile Ser Pro Asn Ile Arg Tyr Cys Ala
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 Tyr Asn Ile Gly Asp Gln Ser Ala Ile Asn Glu Leu Met Gln Met Arg
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 275 280 285
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465          470          475          480
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485          490          495
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515          520          525
Asp Ala His Gln Thr Glu Thr Ser Ser Ser Gln Val Lys Asp Asn Lys
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Pro Leu Val Glu Arg Phe Glu Thr Phe Cys Leu Asp Pro Ser Leu Val
545          550          555          560
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565          570          575
Pro Cys Lys Pro Leu Phe Phe Asp Leu Ala Leu Asn His Val Ala Phe
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<210> 6281

<211> 741

<212> DNA

<213> Homo sapiens

<400> 6281

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<213> Homo sapiens

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Met	Gly	Lys	Leu	Glu	Thr	Asp	Phe	Lys	Arg	Ser	Arg	Ile	Ala	Tyr	Ser
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Asp	Glu	Val	Arg	Asn	Glu	Leu	Leu	Gly	Asp	Asp	Gly	Asn	Ser	Ser	Glu
			100					105				110			
Asn	Gln	Arg	Ala	His	Leu	Leu	Asp	Asn	Thr	Glu	Arg	Leu	Glu	Arg	Ser
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<211> 2312

<212> DNA

<213> Homo sapiens

<400> 6283

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<210> 6284

<211> 122

<212> PRT

<213> Homo sapiens

<400> 6284

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<210> 6285

<211> 2542

<212> DNA

<213> Homo sapiens

<400> 6285

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<210> 6286
<211> 57
<212> PRT
<213> Homo sapiens

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<210> 6287
<211> 1674
<212> DNA
<213> Homo sapiens

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<210> 6288

<211> 269

<212> PRT

<213> Homo sapiens

<400> 6288

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      35             40             45
Ser Val Lys Leu Asp Glu His Ile Ile Pro Leu Gly Ser Met Ala Ile
      50             55             60
Asn Ser Ile Ser Lys Leu Thr Gln Leu Thr Gln Ser Ser Met Tyr Ser
65             70             75             80
Leu Pro Asn Ala Pro Thr Leu Ala Asp Leu Glu Asp Asp Thr His Glu
      85             90             95
Ala Ser Asp Asp Gln Pro Glu Lys Pro His Phe Asp Ser Arg Ser Val
      100            105            110
Ile Phe Glu Leu Asp Ser Cys Asn Gly Ser Gly Lys Val Cys Leu Val
      115            120            125
Tyr Lys Ser Gly Lys Pro Ala Leu Ala Glu Asp Thr Glu Ile Trp Phe
      130            135            140
Leu Asp Arg Ala Leu Tyr Trp His Phe Leu Thr Asp Thr Phe Thr Ala
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Tyr Tyr Arg Leu Leu Ile Thr His Leu Gly Leu Pro Gln Trp Gln Tyr
      165            170            175
Ala Phe Thr Ser Tyr Gly Ile Ser Pro Gln Ala Lys Gln Trp Phe Ser
      180            185            190
Met Tyr Lys Pro Ile Thr Tyr Asn Thr Asn Leu Leu Thr Glu Glu Thr
      195            200            205
Asp Ser Phe Val Asn Lys Leu Asp Pro Ser Lys Val Phe Lys Ser Lys
      210            215            220
Asn Lys Ile Val Ile Pro Lys Lys Lys Gly Pro Val Gln Pro Ala Gly
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Gly Gln Lys Gly Pro Ser Gly Pro Ser Gly Pro Ser Thr Ser Ser Thr
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<210> 6289

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 6289

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<210> 6290

<211> 172

<212> PRT

<213> Homo sapiens

<400> 6290

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				20				25					30		
Ser	Pro	Asp	Glu	Gly	Leu	Ile	Glu	Asp	Leu	Thr	Ile	Glu	Asp	Lys	Ala
				35			40					45			
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Gln	Arg	Ser	Lys	Gln	Ala	Leu	Gln	Glu	Leu	Thr	Gln	Asn	Gln	Val	Val

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Ser Met Leu Asp Ile Asn Ala Leu Phe Ala Glu Ala Lys His Tyr His			
	100	105	110
Ala Lys Leu Val Asn Ile Arg Lys Glu Met Leu Met Leu His Glu Lys			
	115	120	125
Thr Ser Lys Leu Lys Lys Arg Ala Leu Lys Leu Gln Gln Lys Arg Gln			
	130	135	140
Lys Glu Glu Leu Glu Arg Glu Gln Gln Arg Glu Lys Gly Phe Glu Arg			
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<210> 6291

<211> 2718

<212> DNA

<213> Homo sapiens

<400> 6291

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<210> 6292

<211> 497

<212> PRT

<213> Homo sapiens

<400> 6292

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Ala	Leu	Trp	Leu	Arg	Phe	Lys	Tyr	Tyr	Ser	Phe	Phe	Asp	Leu	Asp	Pro
				85					90					95	
Lys	Thr	Asp	Pro	Val	Arg	Leu	Thr	Gln	Leu	Tyr	Glu	Gln	Ala	Arg	Trp
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Asp	Leu	Leu	Glu	Glu	Ile	Asp	Cys	Thr	Glu	Glu	Glu	Met	Met	Val	
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Ile	Phe	Arg	Pro	Arg	Lys	Leu	Thr	Leu	Lys	Gly	Tyr	Arg	Gln	His	Trp
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Val	Pro	Ser	Pro	Glu	Gly	Met	Ser	Glu	Ile	Tyr	Leu	Arg	Cys	Gln	Asp
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Ile Ser Tyr Val Met Val Arg Phe Lys Gly Ser Arg Lys Asp Glu Ile
          385          390          395          400
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          405          410          415
Asp Val Val Lys Thr Trp Arg Phe Ser Asn Met Arg Gln Trp Asn Val
          420          425          430
Asn Trp Asp Ile Arg Gln Val Ala Ile Glu Phe Asp Glu His Ile Asn
          435          440          445
Val Ala Phe Ser Cys Val Ser Ala Ser Cys Arg Ile Val His Glu Tyr
          450          455          460
Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg Glu Arg Ala Arg Gly Glu
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<210> 6293

<211> 750

<212> DNA

<213> Homo sapiens

<400> 6293

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480
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600
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660
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<210> 6294
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 6294
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 Gly Gly Thr Ala Ile Ala Gly Ser Val Glu Ala Val Ala Arg Leu Lys
 35 40 45
 Arg Ser Arg Leu Lys Val Arg Phe Cys Thr Asn Glu Ser Gln Lys Ser
 50 55 60
 Arg Ala Glu Leu Val Gly Gln Leu Gln Arg Leu Gly Phe Asp Ile Ser
 65 70 75 80
 Glu Gln Glu Val Thr Ala Pro Ala Pro Ala Ala Cys Gln Ile Leu Lys
 85 90 95
 Glu Arg Gly Leu Arg Pro Tyr Leu Leu Ile His Asp Gly Val Arg Ser
 100 105 110
 Glu Phe Asp Gln Ile Asp Thr Ser Asn Pro Asn Cys Val Val Ile Ala
 115 120 125
 Asp Ala Gly Glu Ser Phe Ser Tyr Gln Asn Met Asn Asn Ala Phe Gln
 130 135 140
 Val Leu Met Glu Leu Glu Lys Pro Val Leu Ile Ser Leu Gly Lys Gly
 145 150 155 160
 Arg Tyr Tyr Lys Glu Thr Ser Gly Leu Met Leu Asp Val Gly Pro Tyr
 165 170 175
 Met Lys Ala Leu Glu Tyr Ala Cys Gly Ile Lys Ala Glu Val Val Gly
 180 185 190
 Lys Pro Ser Pro Glu Phe Phe Lys Ser Ala Leu Gln Ala Ile Gly Val
 195 200 205
 Glu Ala His Gln Ala Val Met Ile Gly Asp Asp Ile Val Gly Asp Val
 210 215 220
 Gly Gly Ala Gln Arg Cys Gly Met Arg Ala Leu Gln Val Arg Thr Gly
 225 230 235 240
 Lys Phe Arg Pro Ser Asp Glu His His Pro
 245 250

<210> 6295
 <211> 2091
 <212> DNA
 <213> Homo sapiens

<400> 6295
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 cgcgcgcggg cagccctccg gctgtggggc cgggtagttg aacgggtcga ggccggggga
 180
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420
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1680
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1740
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1860

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 1920
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 1980
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 2091

<210> 6296

<211> 399

<212> PRT

<213> Homo sapiens

<400> 6296

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			20					25					30		
Ala	Cys	Gly	Cys	Arg	Leu	Val	Leu	Gly	Gly	Arg	Asp	Asp	Val	Ser	Ala
			35				40					45			
Gly	Leu	Arg	Gly	Ser	His	Gly	Ala	Arg	Gly	Glu	Pro	Leu	Asp	Pro	Ala
			50			55					60				
Arg	Pro	Leu	Gln	Arg	Pro	Pro	Arg	Pro	Glu	Val	Pro	Arg	Ala	Phe	Arg
					70					75				80	
Arg	Gln	Pro	Arg	Ala	Ala	Ala	Pro	Ser	Phe	Phe	Phe	Ser	Ser	Ile	Lys
				85					90					95	
Gly	Gly	Arg	Arg	Ser	Ile	Ser	Phe	Ser	Val	Gly	Ala	Ser	Ser	Val	Val
				100				105					110		
Gly	Ser	Gly	Gly	Ser	Ser	Asp	Lys	Gly	Lys	Leu	Ser	Leu	Gln	Asp	Val
			115				120						125		
Ala	Glu	Leu	Ile	Arg	Ala	Arg	Ala	Cys	Gln	Arg	Val	Val	Val	Met	Val
					135					140					
Gly	Ala	Gly	Ile	Ser	Thr	Pro	Ser	Gly	Ile	Pro	Asp	Phe	Arg	Ser	Pro
					150					155				160	
Gly	Ser	Gly	Leu	Tyr	Ser	Asn	Leu	Gln	Gln	Tyr	Asp	Leu	Pro	Tyr	Pro
				165				170						175	
Glu	Ala	Ile	Phe	Glu	Leu	Pro	Phe	Phe	Phe	His	Asn	Pro	Lys	Pro	Phe
			180					185					190		
Phe	Thr	Leu	Ala	Lys	Glu	Leu	Tyr	Pro	Gly	Asn	Tyr	Lys	Pro	Asn	Val
				195			200					205			
Thr	His	Tyr	Phe	Leu	Arg	Leu	Leu	His	Asp	Lys	Gly	Leu	Leu	Leu	Arg
				210			215				220				
Leu	Tyr	Thr	Gln	Asn	Ile	Asp	Gly	Leu	Glu	Arg	Val	Ser	Gly	Ile	Pro
					230					235				240	
Ala	Ser	Lys	Leu	Val	Glu	Ala	His	Gly	Thr	Phe	Ala	Ser	Ala	Thr	Cys
				245					250					255	
Thr	Val	Cys	Gln	Arg	Pro	Phe	Pro	Gly	Glu	Asp	Ile	Arg	Ala	Asp	Val
				260				265					270		
Met	Ala	Asp	Arg	Val	Pro	Arg	Cys	Pro	Val	Cys	Thr	Gly	Val	Val	Lys
				275			280					285			
Pro	Asp	Ile	Val	Phe	Phe	Gly	Glu	Pro	Leu	Pro	Gln	Arg	Phe	Leu	Leu
				290			295				300				
His	Val	Val	Asp	Phe	Pro	Met	Ala	Asp	Leu	Leu	Leu	Ile	Leu	Gly	Thr

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305          310          315          320
Ser Leu Glu Val Glu Pro Phe Ala Ser Leu Thr Glu Ala Val Arg Ser
          325          330          335
Ser Val Pro Arg Leu Leu Ile Asn Arg Asp Leu Val Gly Pro Leu Ala
          340          345          350
Trp His Pro Arg Ser Arg Asp Val Ala Gln Leu Gly Asp Val Val His
          355          360          365
Gly Val Glu Ser Leu Val Glu Leu Leu Gly Trp Thr Glu Glu Met Arg
          370          375          380
Asp Leu Val Gln Arg Glu Thr Gly Lys Leu Asp Gly Pro Asp Lys
385          390          395

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<210> 6297

<211> 472

<212> DNA

<213> Homo sapiens

<400> 6297

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ngggggcgct ggccgagagg ctgaggcggc gtcattgtcct ccgagggtgc cgccgcgccg
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120
ttcgggaagcc cgttcggcct ggaggagccg cagtgggtcc cggacaagga gtgtcggaga
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240
gggaagtgtc tctgcgacag gtgctgcagc cagaaggtgc cgctcgccg catgtgcttt
300
gtggagccccc tgcggcagtg cgcggagtg gccttggtgt ccctcaagga ggccgagttc
360
tacgacaagc agctcaaagt gctcctgagc ggtaaggacg ggtgtcctgc acagtctctg
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472

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<210> 6298

<211> 146

<212> PRT

<213> Homo sapiens

<400> 6298

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Ser Pro Ser Gly Leu Arg Met Val Pro Glu His Arg Ala Phe Gly Ser
          20          25          30
Pro Phe Gly Leu Glu Glu Pro Gln Trp Val Pro Asp Lys Glu Cys Arg
          35          40          45
Arg Cys Met Gln Cys Asp Ala Lys Phe Asp Phe Leu Thr Arg Lys His
          50          55          60
His Cys Arg Arg Cys Gly Lys Cys Phe Cys Asp Arg Cys Cys Ser Gln
65          70          75          80
Lys Val Pro Leu Arg Arg Met Cys Phe Val Asp Pro Val Arg Gln Cys
          85          90          95
Ala Glu Cys Ala Leu Val Ser Leu Lys Glu Ala Glu Phe Tyr Asp Lys

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	100		105		110
Gln	Leu	Lys	Val	Leu	Leu
	115		120		125
Cys	Ala	Leu	Arg	Gln	Pro
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Cys	Ala				
145					

<210> 6299

<211> 1466

<212> DNA

<213> Homo sapiens

<400> 6299

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 120
 ggcgccagcgc ccgccatttg gccagggag agcctgggttc tgtaccactg gaccagtgcc
 180
 ttcatctcgc agaaggtgcg gctggtgatc gccgagaagg gcctgggtgtg cgaggagcgg
 240
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 360
 gactatgtgg agcgcacatt cacaggagag cactgtgtgg ccctgatgcc cgagggtggc
 420
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 480
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 660
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 720
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 1200

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 1320
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 1466

<210> 6300

<211> 372

<212> PRT

<213> Homo sapiens

<400> 6300

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		20						25					30		
Ser	Gly	Gly	Pro	Arg	Arg	Ser	Arg	Gly	Gly	Gln	Pro	Ala	His	Trp	Pro
		35					40					45			
Arg	Glu	Ser	Leu	Val	Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	Ser	Gln
	50				55					60					
Lys	Val	Arg	Leu	Val	Ile	Ala	Glu	Lys	Gly	Leu	Val	Cys	Glu	Glu	Arg
65				70					75					80	
Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	Met	Arg
			85						90					95	
Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	Asn	Ile
			100					105					110		
Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr	Phe	Thr
		115				120						125			
Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	Gln	His
	130					135					140				
Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	Met	Asp
145				150					155					160	
Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Pro	Glu	Leu	Thr	Thr	Asp	Ser
			165						170					175	
Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	Ala	Asn
			180						185				190		
Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	Gln	Leu
	195						200						205		
Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	Ile	Leu
	210					215					220				
Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	Leu	Ala
225				230						235				240	
Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	Leu	Glu
			245						250					255	
Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	Phe	Thr
		260						265					270		
Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu
		275					280					285			
Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	Leu	Gln

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      290              295              300
Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu
305              310              315              320
Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe
      325              330              335
Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Gly Ala Ser Phe Leu
      340              345              350
Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys
      355              360              365
Lys Lys Tyr Ile
      370

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<210> 6301

<211> 911

<212> DNA

<213> Homo sapiens

<400> 6301

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120
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180
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240
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720
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<210> 6302

<211> 202

<212> PRT

<213> Homo sapiens

<400> 6302

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 Glu Ser Leu Lys Lys Lys Ile Gln Pro Lys Leu Ser Leu Thr Leu Ser
 35 40 45
 Ser Ser Val Ser Arg Gly Asn Val Ser Thr Pro Pro Arg His Ser Ser
 50 55 60
 Gly Ser Leu Thr Pro Val Thr Pro Pro Ile Thr Pro Ser Ser Ser
 65 70 75 80
 Phe Arg Ser Ser Thr Pro Thr Gly Ser Glu Tyr Asp Glu Glu Glu Val
 85 90 95
 Asp Tyr Glu Glu Ser Asp Ser Asp Glu Ser Trp Thr Thr Glu Ser Ala
 100 105 110
 Ile Ser Ser Glu Ala Ile Leu Ser Ser Met Cys Met Asn Gly Gly Glu
 115 120 125
 Glu Lys Pro Phe Ala Cys Pro Val Pro Gly Cys Lys Lys Arg Tyr Lys
 130 135 140
 Asn Val Asn Gly Ile Lys Tyr His Ala Lys Asn Gly His Arg Thr Gln
 145 150 155 160
 Ile Arg Val Arg Lys Lys Pro Phe Lys Cys Arg Cys Gly Lys Ser Tyr Lys
 165 170 175
 Thr Ala Gln Gly Leu Arg His His Thr Ile Asn Phe His Pro Pro Val
 180 185 190
 Ser Ala Glu Ile Ile Arg Lys Met Gln Gln
 195 200

<210> 6303

<211> 676

<212> DNA

<213> Homo sapiens

<400> 6303

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 120
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 240
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 300
 cggcatgcaa atacaatcag attatttggt ttgctacctg aacaatcccc agtatcttat
 360
 tccaaaagga cagcatacca gaaagctgga ggcgattctg gtaatgtgga tgatgactgt
 420
 gaaagagtca aaggacctgt aggaagccta aagctctgtg aagctattct agaagaagc
 480
 actgaaaaac tcaaaagctt gtcactgcag caacagcagg atggagataa tggggacagc
 540

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 660
 aaattttcag tctgaa
 676

<210> 6304
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 6304
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 Val Phe Val Glu Ser Ser Glu Thr Leu Asp Tyr Gln Met Ala Phe Ala
 35 40 45
 Asp Ser His Leu Trp Lys Leu Leu Asp Arg His Ala Asn Thr Ile Arg
 50 55 60
 Leu Phe Val Leu Leu Pro Glu Gln Ser Pro Val Ser Tyr Ser Lys Arg
 65 70 75 80
 Thr Ala Tyr Gln Lys Ala Gly Gly Asp Ser Gly Asn Val Asp Asp Asp
 85 90 95
 Cys Glu Arg Val Lys Gly Pro Val Gly Ser Leu Lys Ser Val Glu Ala
 100 105 110
 Ile Leu Glu Glu Ser Thr Glu Lys Leu Lys Ser Leu Ser Leu Gln Gln
 115 120 125
 Gln Gln Asp Gly Asp Asn Gly Asp Ser Ser Lys Ser Thr Glu Thr Ser
 130 135 140
 Asp Phe Glu Asn Ile Glu Ser Pro Leu Asn Glu Arg Asp Ser Ser Ala
 145 150 155 160
 Ser Val Asp Asn Arg Glu Leu Glu Gln His Ile Gln Thr Ser Asp Pro
 165 170 175
 Glu Lys Phe Ser Val
 180

<210> 6305
 <211> 3853
 <212> DNA
 <213> Homo sapiens

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<211> 474

<212> PRT

<213> Homo sapiens

<400> 6306

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			20					25				30			
Thr	Trp	Asp	Ser	Thr	Phe	Cys	Ala	Val	Asn	Pro	Lys	Phe	Leu	Ala	Val
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Lys	Thr	Gly	Arg	Ile	Asp	Lys	Ala	Tyr	Pro	Thr	Val	Cys	Gly	His	Thr
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Gly	Pro	Val	Leu	Asp	Ile	Asp	Trp	Cys	Pro	His	Asn	Asp	Gln	Val	Ile
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Asn	Gly	Leu	Thr	Ser	Pro	Leu	Thr	Glu	Pro	Val	Val	Val	Leu	Glu	Gly
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Cys	Lys	Asp	Lys	Ser	Val	Arg	Ile	Ile	Asp	Pro	Arg	Arg	Gly	Thr	Leu
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Ile	Phe	Leu	Ala	Asp	Gly	Lys	Val	Phe	Thr	Thr	Gly	Phe	Ser	Arg	Met
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Ser	Glu	Arg	Gln	Leu	Ala	Leu	Trp	Asn	Pro	Lys	Asn	Met	Gln	Glu	Pro
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Ile	Ala	Leu	His	Glu	Met	Asp	Thr	Ser	Asn	Gly	Val	Leu	Leu	Pro	Phe
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Tyr	Asp	Pro	Asp	Thr	Ser	Ile	Ile	Tyr	Leu	Cys	Gly	Lys	Gly	Asp	Ser

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  290              295              300
Leu Asn Thr Phe Ser Ser Lys Glu Pro Gln Arg Gly Met Gly Tyr Met
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Pro Lys Arg Gly Leu Asp Val Asn Lys Cys Glu Ile Ala Arg Phe Phe
      325              330              335
Lys Leu His Glu Arg Lys Cys Glu Pro Ile Ile Met Thr Val Pro Arg
      340              345              350
Lys Ser Asp Leu Phe Gln Asp Asp Leu Tyr Pro Asp Thr Ala Gly Pro
      355              360              365
Glu Ala Ala Leu Glu Ala Glu Glu Trp Phe Glu Gly Lys Asn Ala Asp
      370              375              380
Pro Ile Leu Ile Ser Leu Lys His Gly Tyr Ile Pro Gly Lys Asn Arg
 385              390              395
Asp Leu Lys Val Val Lys Lys Asn Ile Leu Asp Ser Lys Pro Thr Ala
      405              410              415
Asn Lys Lys Cys Asp Leu Ile Ser Ile Pro Lys Lys Thr Thr Asp Thr
      420              425              430
Ala Ser Val Gln Asn Glu Ala Lys Leu Asp Glu Ile Leu Lys Glu Ile
      435              440              445
Lys Ser Ile Lys Asp Thr Ile Cys Asn Gln Asp Glu Arg Ile Ser Lys
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<210> 6307

<211> 2119

<212> DNA

<213> Homo sapiens

<400> 6307

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<210> 6308

<211> 483

<212> PRT

<213> Homo sapiens

<400> 6308

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35      40      45
Phe Ile Gln Arg Phe Glu Met Lys Arg Ser Pro Glu Glu Lys Gln Glu
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Met Leu Gln Thr Glu Gly Ser Gln Cys Ala Lys Thr Phe Ile Asn Leu
65      70      75      80
Met Thr His Ile Cys Lys Glu Gln Thr Val Gln Tyr Ile Leu Thr Met
85      90      95
Val Asp Asp Met Leu Gln Glu Asn His Gln Arg Val Ser Ile Phe Phe
100     105     110
Asp Tyr Ala Arg Cys Ser Lys Asn Thr Ala Trp Pro Tyr Phe Leu Pro
115     120     125
Met Leu Asn Arg Gln Asp Pro Phe Thr Val His Met Ala Ala Arg Ile
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Leu Asn Tyr Tyr Phe Asn Trp Ile Lys Thr Gln Leu Ser Ser Gln Lys
165     170     175
Leu Arg Gly Ser Gly Val Ala Val Glu Thr Gly Thr Val Ser Ser Ser
180     185     190
Asp Ser Ser Gln Tyr Val Gln Cys Val Ala Gly Cys Leu Gln Leu Met
195     200     205
Leu Arg Val Asn Glu Tyr Arg Phe Ala Trp Val Glu Ala Asp Gly Val
210     215     220
Asn Cys Ile Met Gly Val Leu Ser Asn Lys Cys Gly Phe Gln Leu Gln
225     230     235     240
Tyr Gln Met Ile Phe Ser Ile Trp Leu Leu Ala Phe Ser Pro Gln Met
245     250     255
Cys Glu His Leu Arg Arg Tyr Asn Ile Ile Pro Val Leu Ser Asp Ile
260     265     270
Leu Gln Glu Ser Val Lys Glu Lys Val Thr Arg Ile Ile Leu Ala Ala
275     280     285
Phe Arg Asn Phe Leu Glu Lys Ser Thr Glu Arg Glu Thr Arg Gln Glu
290     295     300
Tyr Ala Leu Ala Met Ile Gln Cys Lys Val Leu Lys Gln Leu Glu Asn
305     310     315     320
Leu Glu Gln Gln Lys Tyr Asp Asp Glu Asp Ile Ser Glu Asp Ile Lys
325     330     335
Phe Leu Leu Glu Lys Leu Gly Glu Ser Val Gln Asp Leu Ser Ser Phe
340     345     350
Asp Glu Tyr Ser Ser Glu Leu Lys Ser Gly Arg Leu Glu Trp Ser Pro
355     360     365
Val His Lys Ser Glu Lys Phe Trp Arg Glu Asn Ala Val Arg Leu Asn
370     375     380
Glu Lys Asn Tyr Glu Leu Lys Ile Leu Thr Lys Leu Leu Glu Val
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Ser Asp Asp Pro Gln Val Leu Ala Val Ala Ala His Asp Val Gly Glu

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Arg Tyr Asn Ala Leu Leu Ala Val Gln Lys Leu Met Val His Asn Trp
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<210> 6309

<211> 564

<212> DNA

<213> Homo sapiens

<400> 6309

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<210> 6310

<211> 83

<212> PRT

<213> Homo sapiens

<400> 6310

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20     25     30
Leu Gln Glu Ala Arg Pro Leu Gly Leu Leu Val Pro Asp Ala Gly Asp
35     40     45
Leu Arg Leu Pro Glu Pro Gln Leu Leu Pro Glu Arg Val Leu Ala
50     55     60
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75

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<210> 6311
<211> 1548
<212> DNA
<213> Homo sapiens

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<210> 6312

<211> 234

<212> PRT

<213> Homo sapiens

<400> 6312

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		20					25					30			
Leu	Asp	Glu	Tyr	Lys	Glu	Gln	Tyr	Phe	Ser	Leu	Arg	Pro	Asp	Leu	Lys
	35					40					45				
Thr	Lys	Ser	Tyr	Gly	Asn	Ile	Ser	Glu	Arg	Val	Glu	Leu	Arg	Lys	Lys
	50				55					60					
Leu	Gly	Cys	Lys	Ser	Phe	Lys	Trp	Tyr	Leu	Asp	Asn	Val	Tyr	Pro	Glu
65				70				75				80			
Met	Gln	Ile	Ser	Gly	Ser	His	Ala	Lys	Pro	Gln	Gln	Pro	Ile	Phe	Val
			85					90				95			
Asn	Arg	Gly	Pro	Lys	Arg	Pro	Lys	Val	Leu	Gln	Arg	Gly	Arg	Leu	Tyr
			100					105				110			
His	Leu	Gln	Thr	Asn	Lys	Cys	Leu	Val	Ala	Gln	Gly	Arg	Pro	Ser	Gln
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Lys	Gly	Gly	Leu	Val	Val	Leu	Lys	Ala	Cys	Asp	Tyr	Ser	Asp	Pro	Asn
	130					135					140				
Gln	Ile	Trp	Ile	Tyr	Asn	Glu	Glu	His	Glu	Leu	Val	Leu	Asn	Ser	Leu
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What is claimed is:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2*n*, wherein *n* is any integer 1-3161, or the complement thereof.
2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*, wherein *n* is any integer 1-3161, or the complement thereof.
3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*.
4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.
5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprises the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein *n* is any integer 1-3161, or the complement thereof.
6. An oligonucleotide less than 100 nucleotides in length and comprising at least contiguous nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein *n* is any integer 1-3161, or the complement thereof.
7. A vector comprising the nucleic acid molecule of claim 1.

8. The vector of claim 7, wherein said vector is an expression vector.
9. A host cell comprising the isolated nucleic acid molecule of claim 1.
10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.
11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.
12. An antibody that selectively binds to the polypeptide of claim 10.
13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:
 - a) the nucleic acid of claim 1;
 - b) the polypeptide of claim 10; and
 - c) the antibody of claim 12;and a pharmaceutically acceptable carrier.
14. A kit comprising in one or more containers, a therapeutically or prophylactically effective amount of the pharmaceutical composition of claim 13.
15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.
16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said

compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe or primer bound to the nucleic acid molecule of claim 1 is present in the sample.

18. A method for modulating the activity of the polypeptide of claim 10, the method comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.

19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected from the group consisting of:

- a) the nucleic acid of claim 1;
- b) the polypeptide of claim 10; and
- c) the antibody of claim 12.

20. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:

- a) contacting a test compound with the polypeptide of claim 10; and
- b) determining if said test compound binds to said polypeptide,

wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.

21. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:

- a) administering a test compound to a test subject at an increased risk ORFX-associated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;

- b) measuring expression the activity of said protein in said test subject;
- c) measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and
- d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predisposition to an ORFX-associated disorder.

22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.

23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:

- a) measuring the amount of the polypeptide in a sample from said subject; and
- b) comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

24. The method of claim 23, wherein said subject is a human.

25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:

- a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and
- b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the control sample indicates the presence of or predisposition to said disease in said subject.

26. The method of claim 25, wherein said subject is a human.

27. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.

28. The method of claim 27, wherein said subject is a human.

29. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject a nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said pathological condition.

30. The method of claim 29, wherein said subject is a human.

31. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject an antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological condition.

32. The method of claim 31, wherein said subject is a human.